

Suiform Soundings

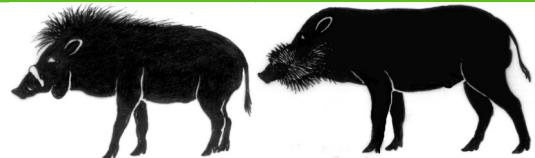
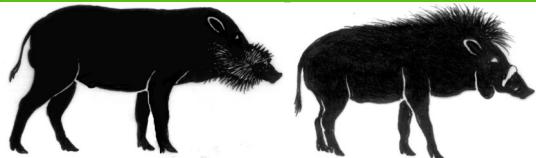


Newsletter of the IUCN / SSC Wild Pig,
Peccary and Hippo Specialist Groups



Volume 18(1)
August 2019
ISSN: 1446-991-X





Suiform Soundings is the newsletter of the IUCN/SSC Wild Pig, Peccary, and Hippo Specialist Groups.

This newsletter is electronically available at:

<https://sites.google.com/site/wildpigspecialistgroup/iucnssc-wild-pig-specialist-group/suiform-soundings-2>

Editor in Chief: Thiemo Braasch

Managing Editor / Production Editor: Thiemo Braasch and Rafael Reyna

Handling Editor Portuguese Section: Alessandra Nava

Handling Editor Spanish Section: Rafael Reyna

Handling Editor French Section: Jean-Pierre d'Huart

Handling Editor Africa Section: Rafael Reyna

Handling Editor Asian Section: Matthew Linkie

Contact address:

Thiemo Braasch

E-mail: salvanius@gmail.com

Photo front page:

Chaco peccary (*Catagonus wagneri*). Photo: Paul Smith.

Please email all contributions to future issues to Thiemo Braasch, email: salvanius@gmail.com. Articles, photos and comments are welcome and appreciated. **Please follow the guidelines for authors**, which can be found on the website listed above.



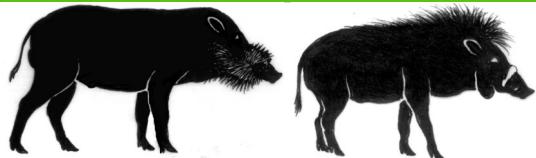


Table of Contents

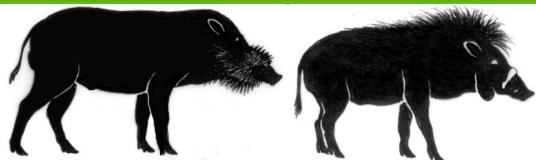


EDITORIAL by <i>Thiemo Braasch</i>	4
An observation in water-bathing in Chaco peccary by <i>Paul Smith</i>	7
Repertório acústico de caititus (<i>Pecari tajacu</i>) mantidos em cativeiro by <i>Selene S. C. Nogueira, José Pereira da Silva Neto and Sérgio L. G. Nogueira-Filho</i>	9
Tongue adaptations of suckling babirusa (<i>Babyrousa celebensis</i>) and other Suiformes by <i>Alastair A. Macdonald and Steven Mitchell</i>	20
NEW LITERATURE ON SUIFORMES	30
NEW BOOKS ABOUT SUIFORMES	77
ARTICLES IN THE NEWS	79

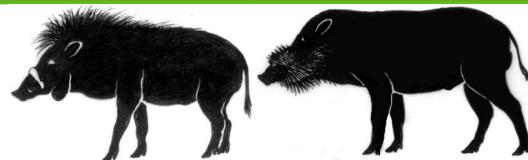


Chaco peccary (*Catagonus wagneri*). Photo: P. Smith





Editorial



Dear fellow reader,

I am glad to present you with the latest issue of Suiform Soundings. There have been some changes in the IUCN/SSC Wild Pig Specialist Group. As you remember from the editorial from the last issue, Erik Meijaard resigned as co-chair of this group and Johanna Rode-Margono has taken over since January this year. We welcome her warmly.

A short look back on 19 years of publishing Suiform Soundings



This issue is the 34th issue of Suiform Soundings. After more than 18 years of continuously publishing this newsletter it is now time for a short look back on all the years of publishing in Suiform Soundings, with the purpose to do an analysis of the main contributions the newsletter has provided and its history.

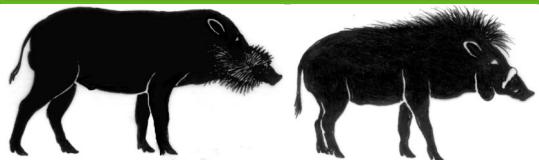
The newsletter started as Asian Wild Pig News in 2001. After five issues published from 2001 to 2004 the name changed its name to “Pigs, Peccaries and Hippos News” and after two years and three issues it changed again to the current name “Suiform Soundings”. From 2004 to today’s date it has comprised all three families of the suborder Suiformes: pigs (family Suidae), peccaries (family Tayassuidae) and hippos (family Hippopotamidae). Although recent investigations show that hippos are more related to Cetaceans (whales and dolphins) and build the group Whippomorpha with them (see e.g. Prothero, 2017) they are still included in this newsletter because of historical reasons.

Even if we do not consider the first five issues of the newsletter because they only dealt with Asian wild pigs, most of the articles in the newsletter have been about pig species from Asia (103 articles including 31 articles about the Eurasian wild pig *Sus scrofa* and its subspecies) whereas only 32 articles dealt with wild pigs in Africa, 112 articles about peccaries and 20 about the two hippo species. A simple explanation is that there are 14 species of wild pigs in Asia (including a so far unconfirmed species from the Sulu archipelago, Philippines, and the Eurasian Wild Boar *Sus scrofa*, which is now separated into eleven species (see Melletti and Meijaard, 2018). In contrast, there are only six wild pig species on the African continent (including the populations of *Sus scrofa* in Northern Africa), three peccary species and two hippo species.

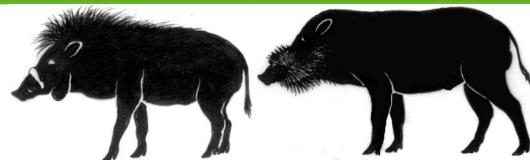
Asian wild pigs

Indonesia harbors eight pig species and therefore also most of the investigations presented in the article took place in this country (almost 60 %). Most of the articles were about introduced





Editorial



Eurasian wild boars, and Bearded pigs (31 articles and 25 articles respectively). This can be explained by the general interest in ecological and taxonomic differences of Eurasian wild boars (especially when comparing to other species) and the fundamental role Bearded pigs have in their ecosystems. Only nine articles have been published about the four Philippine wild pigs (seven about Visayan warty pigs, one about the Mindoro warty pig, one about the unconfirmed species of the Sulu archipelago and none about the Philippine warty pig). There is a strong need to get more information about all these species. Due to the ongoing successful conservation actions for the Pygmy hog, 13 articles have been published about this species (see Braasch (2018), for a description of these actions).

African wild pigs

Most of the articles about African pigs are about Common warthogs (*Phacochoerus africanus*) and Desert warthogs (*Phacochoerus aethiopicus*) (eleven and ten articles respectively) while none article has been published about the Bushpig. Most of the investigations presented in the articles took place in Kenya and Uganda (seven in both countries). It seems that the biology and ecology of Warthogs is relatively well known, but we need to increase research in the other forest species, especially on the Giant Forest Hog (*Hylochoerus meinertzhageni*) and the Bush Pigs and Red River Hog (*Potamochoerus porcus* and *P. larvatus*). These species are facing imminent threats of extinction as the African tropical forests are disappearing at alarming rates and hunting pressure is very high (see Reyna-Hurtado et al 2014).

Peccaries

112 articles about peccaries have been published in Suiform Soundings and its predecessor "Pigs, Peccaries and Hippos News" since 2003. Most of the articles were about the Collared peccary and the White-lipped peccary. Most of the investigations about peccaries published in this newsletter took place in Brazil (almost 48 %) - the biggest of all Latin-American countries and the one with more tropical forest extensions than any other country. There are still gaps in knowledge of these two species', and especially about the Chaco peccary'. This is the most threatened peccary species and future investigations might help to conserve this wonderful species. Both the Collared and the White-lipped peccaries play important roles in their ecosystems and are good models to answer ecological and behavioural questions. The white-lipped peccary is also facing imminent extinction threats in Mesoamerica (Reyna-Hurtado et al. 2017) and research should increase in this area with the aim to elaborate conservation actions.

Hippos

20 articles have been published about hippos (13 about Common hippos, seven about Pygmy hippos). There is no bias for a particular country. The Pygmy hippo has an elusive behavior and lives in small populations in the Upper Guinean Forests in Liberia, Cote d'Ivoire and adjacent countries. Therefore, there are only very few scientific investigations about this species in the native habitat (see Robinson et al., 2017). The common hippo has been decimated in a great portion of its historical range for meat consumption. Hopefully more articles about both hippo species will be published in order to raise awareness of the ongoing threats for them.

The analysis presented here only includes articles published in this newsletter and its two predecessors. Articles in other peer-reviewed journals have not been included. Therefore, this





Editorial

analysis covers only a tiny proportion of the articles published about Suiformes in the scientific literature. Most of the articles in this analysis deal with Asian pigs, especially the two most common species (the Eurasian wild boar and Bearded pigs). Only few articles have been published about African pigs and hippos and about one peccary species (the Chaco peccary). There is still a lack of knowledge about many species. It would be great to have more articles about endangered or critically endangered species such as Visayan warty pigs, Mindoro warty pig, Chaco peccary or Pygmy hippo but also about species like Bushpig, Red River Hog, Giant Forest Hog, Philippine warty pig or Common hippo which are not similarly close to extinction but still face many threats. Wild pigs, peccaries and hippos are amazing species that fulfill a role in the ecosystems as some of the largest herbivores and largest prey for carnivores, as well as dispersing seeds and predating on some plant species. They are also related to human communities in very different ways, as food or in cultural expressions. We need to conserve these species and one important step toward it is to get as much as possible scientific information on them. We can see that Suiform Soundings is playing an important role in publishing information about these wonderful species!

With warm regards,

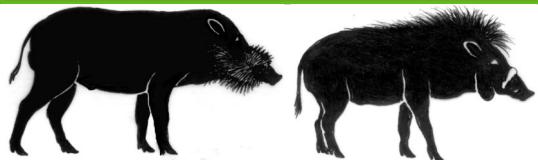
Thiemo Braasch
Chief Editor Suiform Soundings

References

- Braasch, T. 2018. The future is burning brighter – the remarkable comeback of the Pygmy hog (*Porcula salvania*). *Suiform Soundings* 17 (1): 6-13.
- Melletti, M. and E. Meijaard (eds.) 2018. *Ecology, Conservation and Management of Wild Pigs and Peccaries*. Cambridge University Press, Cambridge, UK.
- Prothero, D. R. 2017. *The Princeton Field Guide to Prehistoric Mammals*. Princeton University Press, Princeton, New Jersey, USA.
- Reyna-Hurtado R., Radachowsky, R., McLoughlin, L., Thornton, D., Moreira-Ramirez, J. F., Garcia-Anleu, R., Ponce-Santizo, G., McNab, R., Diaz-Santos, F., Elvir, F., Portillo-Reyes, O., Moreno, R., Meyer, N., Artavia, A., Amit, R., Hofman, M.P.G., Harmsen, B.J., Castañeda, F., Sanchez-Pinzon, K., Hernandez-Perez, E., Martinez, W., Mérida, M., Solis, N., Ramos, V.H., Juárez, D., Tot, C., Lopez, E., Leonardo, R., Machuca, O., Calderon, P., Estrada, C., Morales, C., Guerrero, S., Morazan, F., Carrillo, E., Cruz, J.C., Montalvo, V., Gonzalez-Maya, J.F., Gomez, D., Jiménez, J.J., Arroyo, S., Thomson, I., and J. Polisar. 2017. White-lipped Peccary in Mesoamerica: Status, Threats and Conservation Actions. *Suiform Soundings* 15(2), 31-35.
- Reyna-Hurtado, R., Tumukunde, A., Chapman, C.A., Rojas-Flores, E., Sanvicente, M., Sengupta R. and S. Calme. 2014. On the track of the Giant Forest Hog in Kibale, National Park, Uganda: a preliminary report on studying the species. *Suiform Soundings* 12:38-41.
- Robinson, P. T., Flacke, G. L. and K. M. Hentschel 2017. *The Pygmy Hippo Story – West Africa's Enigma of the Rainforest*. Oxford University Press, Oxford, UK.



Behaviour



An observation of water-bathing in Chaco Peccary

Paul Smith

FAUNA Paraguay, Encarnación, Dpto. Itapúa, Paraguay www.faunaparaguay.com,

and Para La Tierra, Centro IDEAL, Mariscal Estigarribia 321 c/ Tte. Capurro, Pilar, Dpto. Ñeembucú, Paraguay, www.paralatierra.org.

Contact email: faunaparaguay@gmail.com

Three species of peccary (Tayassuidae) are sympatric in the Paraguayan Dry Chaco: Collared peccary *Pecari tajacu*, White-lipped peccary *Tayassu pecari* and the endangered Chaco endemic Chaco peccary *Parachoerus wagneri* (Taber 1991). The latter was known only from fossil remains until its remarkable rediscovery alive in the Paraguayan Chaco (Wetzel et al. 1975) and it also occurs marginally into the Chaco of Bolivia and Argentina (Mayer & Wetzel 1986, Maffei et al. 2008, Torres et al. 2016). The species was initially classified in the genus *Catagonus* Ameghino, 1904 until it was recently reassigned to *Parachoerus* Rusconi, 1930 (Dutra et al. 2017).

Observations of individuals are very rare in the wild. Here I provide details of a wild individual bathing under natural conditions.

At around 9 am on 3 December 2018 a Chacoan peccary *Catagonus wagneri* was seen bathing in a puddle on the Transchaco Road at km 670 close to the entrance to Parque Nacional Teniente Enciso, Boquerón department, Paraguay. The habitat here is the typical xeric, low thorn forest of this region of the Paraguayan Chaco. The weather was warm and sunny, and the area had experienced heavy rain in the days previous. Though this is usually a social species, only one individual was observed.

The puddle was in the road, but close to the roadside and a couple of metres from forest cover. The animal was seen emerging from the forest close to the puddle. It then subsequently lay on its side, piloerecting, and moving the body rapidly in a squirming motion to cover itself with mud and water, pausing occasionally but without changing



Chaco peccaries (*Catagonus wagneri*). Photo: P. Smith





Behaviour

sides. Throughout the observation drops of water could be seen being cast up into the air by the motion. Unfortunately the animal was disturbed after fifteen seconds by a passing motorbike and returned to the forest.

Much of the natural history information we have for the Chaco Peccary is based on captive studies (Mayer & Wetzel 1986, Benirschke 1993), so wild behavioural observations are worthy of note. Water bathing in this species is apparently rare, with dust-bathing more frequent (Mayer & Wetzel 1986, Taber et al. 1993) and probably opportunistic.

With accelerating habitat destruction in the Chaco now reaching emergency levels (Caballero et al. 2014), additional information on the biology of this species is essential in order to adequately understand its conservation requirements (Altrichter et al. 2016b). A plan for the conservation of the species is in place (Altrichter et al. 2016a), but is complicated by the fact that only 46% of the entire Gran Chaco is suitable for habitation of the species, and of this suitable area just 12% is protected. The long term conservation of the species is still far from secure.

References

- Altrichter M, Saldívar S, Decarre J, Camino M, Yanosky A, Campos Krauer JM, Desbiez A, Leus K, Ferraz KM, Silva Angelieri CC, Cuéllar RL, Arévalos F, Cartes JL, Giordano AJ, Thompson J, Velilla M, Torres R, Neris N and Cabral H. 2016a. Situación de conservación del pecarí del Chaco o Tagua (*Catagonus wagneri*): Distribución, aptitud de hábitat y viabilidad poblacional. *Paraquaria Natural* 4(2): 30-39.
- Altrichter M, Desbiez A, Camino M and Decarre J. 2016b. Pecarí del Chaco o Tagua (*Catagonus wagneri*). Una estrategia para su conservación. UICN/SSC Grupo de Especialistas en Pecaríes, Asunción.
- Benirschke K and Heuschele WP. 1993. Proyecto Tagua: the Giant Chaco peccary *Catagonus wagneri* conservation project. *International Zoo Yearbook* 32: 28-31.
- Caballero J, Palacios F, Arévalos F, Rodas O, Yanosky A. 2014. Cambio de uso de la tierra en el Gran Chaco Americano en el año 2013. *Paraquaria Natural* 2(1): 21-28.
- Dutra RP, Casali D de M, Missaglia RV, Gasparini GM, Perini, FA and Cozzuol MA. 2017. Phylogenetic systematics of peccaries (Tayassuidae: Artiodactyla) and a classification of South American Tayassuids. *Journal of Mammalian Evolution* 24: 345-358.
- Maffei L, Cuéllar RL and Banegas J. 2008. Distribución del solitario (*Catagonus wagneri*) en Bolivia. *Ecología en Bolivia* 43(2): 1-5.
- Mayer JJ and Wetzel RM. *Catagonus wagneri*. *Mammalian Species* 259: 1-5.
- Taber AB. 1991. The status and conservation of the Chacoan peccary in Paraguay. *Oryx* 25(3): 147-155.
- Taber AB, Doncaster CP, Neris NN and Colman FH. 1993. Ranging behavior and population dynamics of the Chacoan peccary, *Catagonus wagneri*. *Journal of Mammalogy* 74(2): 443-454.
- Torres R, Tamburini D, Lescano J and Rossi E. 2017. New records of the Endangered Chacoan peccary *Catagonus wagneri* suggest a broader distribution than formerly known. *Oryx* 51(2): 286-289.
- Wetzel RM, Dubos RE, Martin RL and Myers P. 1975. *Catagonus*, an “extinct” peccary, alive in Paraguay. *Science* 189: 379-381.





Behaviour

Repertório acústico de caititus (*Pecari tajacu*) mantidos em cativeiro

Selene S. C. Nogueira^{1,2}, José Pereira da Silva Neto¹, Sérgio L. G. Nogueira-Filho^{1,2}

¹Laboratório de Etiologia Aplicada, Universidade Estadual de Santa Cruz, Rodovia Jorge Amado, km 16, Ilhéus, Bahia 45662-900, Brazil.

²National Institute of Science and Technology in Interdisciplinary and Transdisciplinary Studies in Ecology and Evolution (INCT IN-TREE), Bahia, Brazil

*Corresponding author: *selene@uesc.br or seleneuesc@gmail.com (SSCN)

Resumo

Caititus (*Pecari tajacu*) vivem em bandos e emitem chamados acústicos durante suas interações sociais. Com as novas ferramentas tecnológicas é possível caracterizar com mais acurácia os parâmetros acústicos destas emissões sonoras e melhor compreender a função e contexto destes chamados. Assim, o objetivo deste estudo foi analisar as emissões sonoras e comportamentos associados de caititus mantidos em cativeiro. Analisamos a diferença nos parâmetros acústicos entre machos e fêmeas, além de comparar o repertório encontrado com o já descrito nos anos 80 e 90. Oito tipos de chamados foram encontrados por meio de inspeção auditiva e visual por meio dos espectrogramas, no entanto, a análise funcional discriminante, confirmou um repertório com apenas sete chamados- grunhido, arfagem, rosnado, latido, ronco, dentada e whoof (Wilks Lambda= 0,25; P < 0,001; N = 268). Há diferença entre os sexos nos parâmetros acústicos dos roncos e grunhidos. Ambos os sexos emitiram todos os chamados exceto o whoof, que foi emitido apenas por machos. Em geral, as emissões acústicas apresentaram uma frequência dominante grave e estrutura ruidosa. As vocalizações estão presentes nas interações de conflito, deslocamento e exploração do ambiente, além do contato adulto-filhote e alarme.

Palavras-chave: bioacústica, comportamento social, comunicação animal, Tayassuidae

Abstract

Collared peccary (*Pecari tajacu*) lives in groups and emits acoustic calls during their social interactions. With the new technological tools it is possible to characterize more accurately the acoustic parameters of these sound emissions and to better understand the function and context of these calls. Thus, the objective of this study was to analyze the sound emissions and associated behaviors of captive collared peccaries. We analyzed the differences in acoustic parameters between males and females and compare the current repertoire with the already described in the 80's and 90's. Eight types of calls were found by auditory and visual inspection through the spectrograms. However, the discriminant functional analysis, has confirmed a repertoire with only seven calls – grunt, snarling, growl, barking, snoring, teeth chattering and whoof (Wilks Lambda= 0.25; P < 0,001; N = 268). There is difference between the sexes in the acoustic parameters of snores and grunts. Both sexes emitted all calls, but the whoof, which was emitted only by males. In general, the acoustic emissions showed a low dominant frequency and noisy structure. Vocalizations were present in conflict interactions, displacement and environment exploration, besides adult-juvenile contact and alarm.

Keywords: acoustic repertoire, collared peccary, animal communication, Tayassuidae





Behaviour

INTRODUÇÃO

O repertório acústico de uma dada espécie é o resultado de pressões seletivas do seu ambiente ao longo dos anos (Wiley & Richards, 1978; Charlton et al., 2007). A morfologia da espécie, por exemplo, pode interferir em seus parâmetros acústicos devido a capacidade torácica e assim, fornecer diferenças sonoras (Reby & McComb, 2003). A socialidade, também possibilita a seleção de chamados de comunicação (Briefer & McElligott, 2012; Freeberg et al., 2012), que podem promover o reconhecimento de grupos sociais diferentes (Barros et al., 2011), de chamados de submissão (Nogueira et al. 2016) ou até de assinaturas vocais com o reconhecimento individual (Lacerda et al., 2014).

O conhecimento sobre os sinais de comunicação podem, portanto, esclarecer características das relações sociais e possibilitar a compreensão da história evolutiva de uma espécie, além de revelar estratégias adaptativas que contribuem para sua sobrevivência na natureza (Bradbury & Vehrencamp, 1998) e manutenção em cativeiro buscando identificar sinais acústicos que viabilizem seu bem-estar (Nogueira et al., 2012). Desta forma, descrevemos o repertório acústico de caititus (*Pecari tajacu*) mantidos em cativeiro para melhor compreender aspectos de sua biologia e a função de tais vocalizações, aprimorando as informações adquiridas por outros autores no passado (Bissonette, 1982; Sowls, 1997).

O caititu é uma espécie que vive em socialidade com grupos de até quinze indivíduos (Kiltie & Terborgh, 1983; Sowls, 1997) e não possui um sistema de hierarquia de dominância social (Nogueira-Filho et al. 1999). Estudos previamente realizados registraram um repertório acústico variando entre oito e quinze chamados na espécie (Bissonette, 1982; Sowls, 1997). A tecnologia disponível atualmente, no entanto, pode aprimorar a caracterização destes sinais da espécie, viabilizando tanto seu monitoramento em vida livre (Jorge et al., 2018), como a compreensão de sinais associados ao seu bem-estar (Briefer, 2012), que possam ser usados como indicadores de bem-estar para animais mantidos em cativeiro.

MATERIAL E MÉTODOS

(a) Animais de estudo

Foi estudado o repertório acústico de um grupo de caititus mantidos em cativeiro no Laboratório de Etiologia Aplicada na Universidade Estadual de Santa Cruz, Ilhéus, Bahia, Brasil. O grupo corresponde a terceira geração de cativeiro e é mantido em piquete cercado por tela de alambrado de 1,5 m de altura, com chão de terra e vegetação natural. A área total é de 360 m². O alimento era oferecido rotineiramente duas vezes ao dia (às 10h e às 16h), água era disponibilizada ad libitum.

Os dados foram coletados em dois períodos, setembro de 2009 a setembro de 2010 e o segundo período foi de março de 2014 a agosto de 2014. Desta forma, a composição dos bandos variou entre 11 e 16 indivíduos (Tabela 1).

(b) Coleta de dados

Os animais foram habituados a presença do observador durante 14 dias. Os dados acústicos e comportamentais foram coletados a uma distância que variava entre 1 e 30 m dos animais. Foi aplicado o método de amostragem de todas as ocorrências (Altmann, 1974) para emissões





Behaviour

sonoras. Os animais foram observados e suas gravações registradas de forma contínua durante sessões não consecutivas de uma hora, totalizando 48 horas de registro. Para obtenção desses registros utilizamos um gravador digital portátil Marantz (PMD-671, Tóquio, Japão) e um microfone unidirecional Sennheiser (ME66, Wendemark, Alemanha). Os registros acústicos foram feitos no modo mono, no formato .wav, com taxa de amostragem de 44,1 kHz e resolução de 16 bits. Simultaneamente, filmamos o contexto comportamental utilizando uma câmera digital (Handycam JVC, Tóquio, Japão).

Tabela 1. Composição dos grupos de animais nos períodos observados.

	Período	
	2010	2014
Machos	2	5
Fêmea	3	7
Subadultos	4	-
Filhotes	2	4
Total	11	16

aos sons produzidos, os denominando de chamados, independente da via de produção.

Classificamos as emissões sonoras por inspeção auditiva e visual dos espectrogramas gerados no RAVEN 1.5 (Tamanho de janela: 1351 amostras, tipo: Hann, DFT de 2048 amostras e 85% de sobreposição quadro). Em seguida, usando o mesmo software, recortamos cada elemento dos chamados e salvamos individualmente em arquivos tipo .wav com as mesmas configurações da gravação original. Estes passos são necessários para selecionar os registros de maior qualidade, com maior razão sinal de interesse/ruído de fundo. Após essa etapa, os registros foram filtrados, eliminando os sons abaixo de 100 Hz, a fim de minimizar barulhos de fundo, e os normalizamos à mesma amplitude máxima de -1dB. O filtro de frequência foi estabelecido após uma inspeção visual dos registros acústicos de forma a nos certificar de que nenhum som de interesse fosse eliminado. Estes procedimentos são necessários para padronizar os registros e eliminar interferências de ruídos, de forma que os sinais acústicos e os seus limites fossem reconhecidos de forma correta pelo algoritmo de detecção automática utilizado para as medições dos parâmetros acústicos.

As medições acústicas foram feitas utilizando o programa Avisoft – SASLab Pro 5.2.05 (R. Specht, Berlim, Alemanha) seguindo a configuração: janela tipo Hamming, FFT de 1024 amostras, 87,5% de sobreposição de quadro, 2,7 ms de resolução de tempo e 47 Hz de resolução de frequência, utilizando a ferramenta de medição automática. Este método é baseado na continuidade espectral e em limiares de amplitude. Isto significa que enquanto forem detectados sons continuamente acima de uma certa amplitude (o limiar) estes serão considerados como um único sinal. Utilizamos dois limiares, um para detecção do sinal acústico, como explicado acima, e outro para detectar o início e o fim do sinal. Além dos limiares, determinamos como "tempo de espera" o intervalo de 80 ms. O "tempo de espera" é o intervalo dentro do qual as detecções de sons abaixo do limiar de detecção serão consideradas como parte do sinal se tiverem continuidade com este. O uso deste limiar é especialmente importante para sinais com grande modelação de amplitude, como é o caso das vocalizações dos pecarí. Não foi possível usar o mesmo limiar para todos os chamados dos pecarí devido a variação nas

(c) Análises acústicas

O cateto emite três tipos de sons: sons orais, produzidos pela passagem do ar através das vias aéreas e boca; sons nasais, produzidos pela exalação ou inalação através das narinas; e sons mecânicos, produzidos pela batida dos dentes. Nos referiremos de forma genérica





Behaviour

características dos diferentes sons, então usamos os seguintes valores (1º limiar/ 2º limiar): -10/-8 dB para o ronco baixo e -13/-13 dB para as demais emissões dos caitituss.

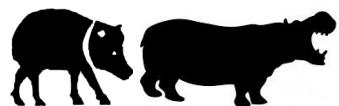
Medimos os seguintes parâmetros acústicos: duração (s), frequência dominante (kHz), frequência máxima (kHz), frequência mínima (kHz), intervalo da banda de frequência (kHz), entropia (dB) e razão harmônico-ruído RHR (dB). A duração corresponde a diferença de tempo entre o início e o fim de cada elemento. A frequência máxima é a frequência mais alta acima do limiar de amplitude, frequência mínima é a frequência mais baixa acima do limiar de amplitude, a frequência dominante é aquela com maior amplitude do espectro, o intervalo de banda é a diferença entre a frequência máxima e a frequência mínima. A entropia e a razão harmônico-ruído (RHR) são parâmetros de organização de energia. A entropia nos permite calcular a aleatoriedade (ou pureza) de um som; é a razão da média geométrica e da média aritmética do espectro. A RHR quantifica a razão de energia harmônica e a energia não harmônica (AVISOFT, 2010). Cada parâmetro foi medido no início, no fim, no centro, na região com pico de energia e no sinal como um todo (média).

(c) Análise comportamental

Para categorizar os contextos comportamentais das vocalizações, gravamos as atividades (ex: descanso, forrageamento, exploração) dos indivíduos e suas posturas, antes, durante e imediatamente depois das emissões. Também compararamos nossas observações com informações da literatura (e.g. Byers & Bekoff, 1981; Dubost, 1997; Sowls, 1997). Para quantificar a taxa de emissão relativa dos tipos vocais, calculamos a taxa de emissão (TE) de cada chamado pela razão entre o número de emissões (N) e o número de indivíduos (I) multiplicado pelo número total de horas de observação (H): $TE = N/H \times I$.

(e) Análise estatística

Para testar a validade das categorias vocais previamente reconhecidas, conduzimos uma Análise Funcional Discriminante (AFD) para cada espécie. Como os caititus podem produzir sons por meio de diferentes canais (nasal, oral e mecânica, ver resultados), a AFD foi conduzida de forma a comparar sons produzidos por meio do mesmo mecanismo ou origem. Assim, baseamos essa análise em 60 amostras escolhidas aleatoriamente para cada tipo vocal, ou todos os registros obtidos para categorias vocais menos frequentes (totalizando 268 para catetos, balanceadas por sexo e idade dos animais). Realizamos a AFD com cinco das variáveis acústicas medidas (duração, frequência mínima, frequência dominante, largura de banda, razão harmônico-ruído) uma vez que as demais variáveis estavam altamente correlacionadas com pelo menos uma outra variável (coeficiente de correlação de Spearman variando entre 0,60 e 0,99, $P < 0,05$). Uma vez que as variáveis utilizadas são medidas em unidades diferentes e não comparáveis (Hz, s e dB), antes de realizar a análise discriminante nós padronizamos as variáveis acústicas de forma a evitar atribuições espúrias de pesos a cada uma devido a diferenças de variância entre elas (Noy Meir, Walker, & Williams, 1975). Esta padronização é feita pela subtração do valor médio de cada variável do valor de cada observação, dividindo-se esse resultado pelo desvio padrão. Para testar a significância do modelo discriminante nós utilizamos uma MANOVA e posteriormente realizamos uma análise de validação cruzada para determinar se seria possível predizer corretamente cada tipo vocal com base nos parâmetros acústicos medidos e utilizados na análise discriminante. Para determinar a acurácia da análise





Behaviour

realizamos um teste binomial testando se a proporção de acerto da análise de validação cruzada seria maior que àquela esperada ao acaso (uma chance em cinco).

Para avaliar se as propriedades acústicas dos tipos vocais mais comumente utilizados por ambas espécies diferiam entre machos e fêmeas, primeiramente resumimos cinco parâmetros acústicos em um número menor de variáveis resposta compostas através de uma Análise de Componentes Principais baseada em matrizes de correlação (PCA; Tabela 5). Após realizar a PCA, escolhemos os primeiros fatores não rotacionados de componentes principais (PCs), que apresentassem autovalores maior que um e explicassem a maior parte da variância do conjunto de dados (Tabela 4) Comparamos então as variáveis compostas (PCs) representantes dos parâmetros acústicos (variáveis dependentes) entre os sexos (variável independente categórica). Para cada PC foi calculado a sua diferença absoluta entre vocalizações de machos e fêmeas, depois compararamos essas diferenças com a distribuição de diferenças esperadas sob a hipótese nula, ou seja, as medições acústicas tomadas de vocalizações de machos e fêmeas não eram diferentes. A distribuição das diferenças esperadas sob hipótese nula foi gerada por 1000 simulações (simulação de Monte Carlo; Manly, 1997) para calcular o valor de P associado. Em seguida, usamos a correção do valor do P para falsas descobertas (para a taxa de descobrimento (Taxa de Falsas Descobertas) devido a comparações múltiplas, que corresponde a uma correção menos conservadora e, portanto, mais poderosa que a correção de Bonferroni (Benjamini & Hochberg, 1995).

Estas análises foram realizadas no software R versão R 3.1.2 (R Development Core Team, 2014) utilizando os pacotes "MASS" versão 7.3-35 (Venables & Ripley, 2002) e "FactoMineR" versão 1.7 (Husson, Josse, Le, & Maze, 2014). Para todas as análises estatísticas usamos nível de significância de $P < 0,05$.

RESULTADOS

(a) Repertório acústico

Por meio dos espectrogramas identificamos inicialmente oito tipos de chamados (Fig. 1). Seis chamados orais (latido, ronco, rosnado, choramingo, grunhido e whoof), um chamado nasal (arfagem) e um chamado mecânico (batida de dentes). Aanálise discriminante confirmou diferenças entre os chamados vocais ($\text{Wilks Lambda} = 0,25$; $P < 0,001$; $N = 268$). A validação cruzada classificou corretamente os chamados com uma precisão total de 60 %. Esta precisão é significativamente maior do que o esperado ao acaso (Teste binomial: $P_s < 0,001$). A acurácia da validação cruzada para as categorias dos chamados variou de zero (rosnado) a 70% (choramingo) (Tabela 2). A primeira e a segunda função discriminante explicaram 99% da variância entre os tipos de chamados. Os parâmetros acústicos mais importantes para discriminar os tipos vocais foram a duração, frequência dominante e intervalo de frequência (Tabela 2).



Behaviour

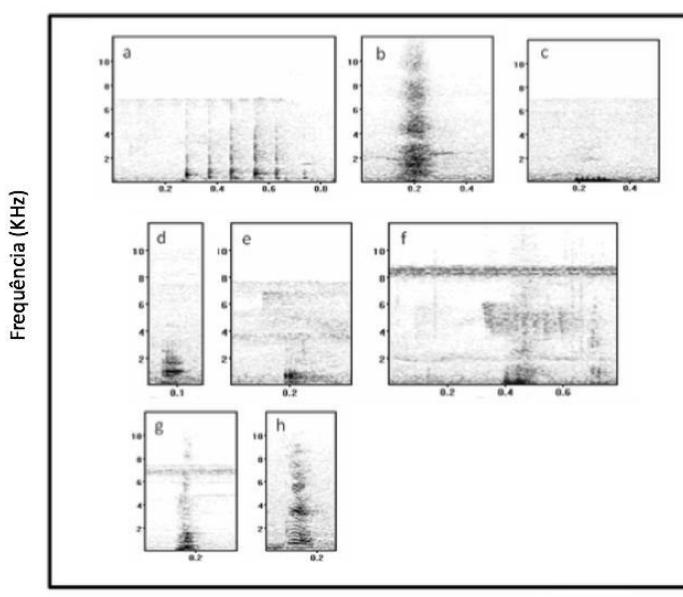
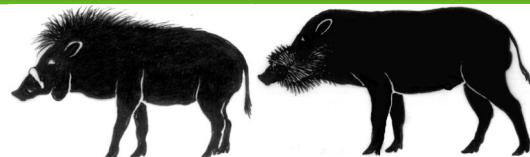
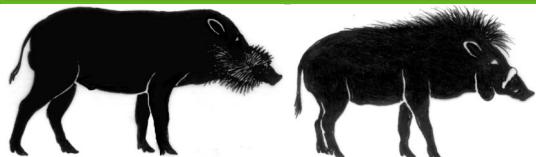


Figura 1. Espectrogramas dos chamados de caititus: série de batidas de dentes (a), arfagem

(b), ronco (c), grunhido (d), rosnado (e), whoof (f), latido (g), choramingo (h-f).

Tabela 2. Parâmetros acústicos dos chamados de catetos (média ± desvio-padrão) e relação das funções discriminantes (DF1 e DF2) com os parâmetros acústicos utilizados na análise discriminante. Os valores em negrito destacam as variáveis mais importantes para discriminação entre tipos vocais.

Chamado	DF1	DF2	Grunhido	Ronco	Rosnado	Choramingo	Whoof	Latido	Arfagem	Batida de dentes	Média
N*	-	-	60	60	32	60	56	-	-	-	-
Validação Cruzada	-	-	0,68	0,70	0,00	0,70	0,64	-	-	-	-
Duração (s)	0,14	1,15	0,06 ± 0,04	0,13 ± 0,07	0,04 ± 0,02	0,08 ± 0,05	0,05 ± 0,02	0,04 ± 0,01	0,09 ± 0,04	0,01 ± 0,01	0,07 ± 0,05
Frequência Min (Hz)	-0,27	0,08	103,67 ± 56,18	51,50 ± 21,06	91,50 ± 41,65	186,00 ± 231,24	65,0 ± 44,09	117,20 ± 97,92	55,83 ± 25,20	134,17 ± 66,44	99,37 ± 105,78
Frequência Máx (Hz)	-	-	2093,17 ± 1079,46	806,00 ± 194,21	994,67 ± 323,00	6818,50 ± 3829,12	760,17 ± 320,94	1638,00 ± 723,71	5210,17 ± 2786,82	6803,83 ± 2002,09	3258,74 ± 3214,79
Frequência Dominante (Hz)	-0,65	-0,57	542,17 ± 225,34	168,33 ± 77,02	450,83 ± 141,51	1607,00 ± 1149,51	248,33 ± 152,04	442,40 ± 340,35	714,50 ± 543,47	831,67 ± 1093,06	640,07 ± 764,41
Largura de banda (Hz)	-0,89	0,34	1986,33 ± 1092,34	748,50 ± 198,01	899,83 ± 322,25	6627,17 ± 3847,51	688,17 ± 306,14	1516,40 ± 718,70	5148,67 ± 2776,45	6665,83 ± 2004,21	3154,56 ± 3194,23
Entropia (dB)	-	-	0,26 ± 0,05	0,24 ± 0,04	0,21 ± 0,03	0,43 ± 0,12	0,21 ± 0,04	0,24 ± 0,04	0,41 ± 0,10	0,44 ± 0,07	0,31 ± 0,12
RHR** (dB)	0,14	-0,12	30,07 ± 9,28	29,68 ± 12,75	31,67 ± 10,62	24,27 ± 12,46	29,62 ± 12,62	27,85 ± 9,59	26,54 ± 9,46	32,10 ± 10,26	29,06 ± 11,27

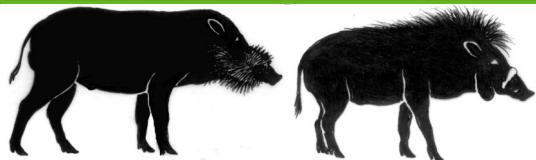
* número de amostras que entram na AFD

** razão harmônio-ruido.

Tabela 3. Autovalores e variância acumulada dos principais fatores não rotacionados da análise de componentes principais (variáveis compostas) e a comparação desses fatores entre os sexos em queixadas e catetos.

Chamado	Componente principal	Autovalor	Variância acumulada (%)	Média dos machos	Média das fêmeas	Diferença observada	Diferença Esperada	Valor de p	p corrigido
Grunhido	1	1,46	29,2	-0,13	0,12	0,25	0,12	0,050	0,062
	2	1,25	54,2	-0,41	0,40	0,80	0,11	0,001	0,002
Ronco	1	1,41	28,3	-0,15	0,07	0,22	0,20	0,202	0,242
	2	1,19	23,8	-0,51	0,26	0,77	0,18	0,001	0,003
	3	1,10	21,8	-0,31	0,15	0,46	0,17	0,011	0,016





Behaviour



Com relação ao uso dos tipos vocais, ambos os sexos emitiram os chamados grunhido, arfagem, rosnado, latido, ronco e dentada. Whoof só foi emitido por machos. Quanto à frequência de emissão de chamados, machos adultos emitiram (38% na fase 1 e 34% na fase 2) mais chamados do que as fêmeas (30% na fase 1 e 12% na fase 2). O tipo de chamado mais emitido pelas fêmeas foi o ronco (N= 27 no período 1, N=12 no período 2). Os machos emitiram mais dentada (N=18) e arfagem (N=14), e o chamado que menos foi emitido foi o latido (N=1). O de menor emissão foi o latido.

Tabela 4 Contribuição dos parâmetros acústicos para a discriminação dos chamados entre machos e fêmeas em caititus. Os fatores que mais contribuíram por componente principal aparecem em negrito.

Chamado	CP*	Duração	Frequência dominante	Frequência mínima	Frequência máxima	Razão harmônico/ ruído
Grunhido	1	39,47	3,48	9,70	20,5	26,85
	2	0,46	40,43	18,10	28,35	12,67
Ronco	1	7,12	11,56	18,26	26,20	36,87
	2	59,16	1,73	8,61	27,36	3,14
	3	0,18	55,06	40,25	2,44	2,08

*Componente principal

No período 1 do estudo, os catetos adultos emitiram 68% das vocalizações, subadultos 8% e os filhotes 23% do total. No entanto, no período 2, os filhotes emitiram mais vocalizações (54%) que os adultos (46%). Os tipos de chamado emitidos por cada faixa etária estão na Tabela 5.

(c) Contextos comportamentais

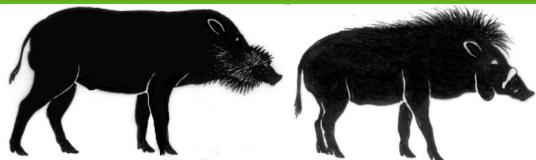
Considerando as atividades e posturas dos animais, classificamos os chamados em sete contextos: ameaça, contato, submissão/dominância, defesa, alarme, isolamento e incômodo (Tabela 5). Entre os catetos, no primeiro período de observação os chamados de isolamento foram os mais emitidos, seguido dos chamados de contato e de ameaça. No segundo período, os chamados de ameaça foram os mais emitidos seguidos dos chamados de isolamento e de contato.

DISCUSSÃO

Catetos possuem um repertório de pelo menos seis chamados acusticamente distintos. Os chamados são utilizados em diferentes contextos, principalmente na resolução de conflitos e para contato entre indivíduos que estão dispersos do grupo. Os parâmetros acústicos mais importantes para a discriminação dos chamados vocais dos catetos foram a duração, a frequência dominante e a largura de banda.

O repertório acústico dos catetos foi descrito por Sowls (Sowls, 1997) como contendo oito chamados e Bissonette (1982) encontrou 15. Este último autor identificou tantos chamados porque assumiu graduações como diferentes tipos vocais, mas através de nossa análise não pudemos identificar os seguintes sons: yip-yip, yip-ou, yelp, repetitive grunt, alternating grunt, feeding growl, purring e também não diferenciamos chamados de batidas de dentes como realizado pelo autor (Bissonette, 1982). Baseado na descrição do contexto das categorias descritas por Sowls (1997), assumimos os seguintes sinônimos: choramingo para complaining call, o ronco seria low grunt, o rosnado como growl, o latido como bark, a batida de dentes seria tooth click e o grunhido, o squeal. Também identificamos algumas categorias descritas por Bissonette (1982): o whoof seria o huff/woof, o latido está descrito como bark e o rosnado como growl. Em nossa AFD o rosnado se confunde com o whoof e com o grunhido, a análise visual





Behaviour



Tabela 5. Descrição das categorias comportamentais e contextos dos chamados acústicos de caititus.

Categoría funcional	Chamado (classe etária)	Contexto
Ameaça	Grunhido (A, S) Batida de dente (A)	O chamado é emitido durante a disputa por alimento. Ocorre quando um indivíduo ameaça após ser ameaçado por outro membro do grupo.
Submissão		Um indivíduo adota uma postura submissa, abaixando a cabeça e vocaliza quando ameaçado por outro membro do grupo, durante encontros frontais após perseguição ou lutas, ou quando o animal dá lugar a outro indivíduo em uma fonte de água ou alimento.
Contato	Ronco (A)	Esta vocalização ocorre quando um animal afasta-se de um grupo ou é emitido durante o esfregamento mútuo ou <i>grooming</i> .
	Choramigo (F)	Este chamado é emitido durante o forrageio, em geral os animais estão mais dispersos.
Defesa	Whoof (A) Arfagem (A) Batidas de dentes (A)	Os filhotes emitem esse chamado quando separados de adultos ou da mãe; quando um animal junta-se a um grupo de indivíduos deitados, ou quando um animal deitado move-se ou enquanto indivíduos exploram o ambiente cavando o solo ou comendo vegetação, o movimento de um animal em direção ao outro pode provocar a emissão sonora do segundo animal. Ou quando um animal deslocando-se pelo ambiente "atropela" o filhote.
Alarme	Latido (A, S, F)	Os chamados whoof, Arfagem e batida de dentes, em geral, ocorrem em sequência, quando um animal ameaça um ser humano, movendo-se em sua direção enquanto vocaliza. A piloereção pode ser observada. O indivíduo permanece parado emitindo os chamados associados a este contexto repetidamente enquanto encara o observador.
		Este chamado é emitido quando um indivíduo é surpreendido por uma perturbação sonora.





Behaviour

mostra que pode se tratar de uma estrutura acústica intermediária uma vez que os três chamados -whoof, rosnado, grunhido- são vocalizações de banda larga de curta duração. Além disso, esta pouca discriminação entre esses chamados pode estar relacionado com a presença de gradações, como argumentado por Bissonette (1982), no repertório da espécie.

O latido, é um som curto explosivo emitido quando um animal é surpreendido por uma perturbação no ambiente. Esse chamado é frequentemente emitido por filhotes enquanto exploram o ambiente e quando estão brincando, mas é ignorado pelos adultos. Quando o latido é emitido por um adulto, todos os indivíduos sempre respondem com a fuga. O ronco, por sua vez, é a vocalização com frequência dominante mais baixa dentre todos os chamados. Esta característica torna a comunicação à distância mais eficiente porque diminui a velocidade de perda de energia do sinal para o ambiente, possibilitando que a mensagem alcance animais mais distantes (Fletcher, 2004). Há, portanto, maior evidência de tal característica como uma adaptação para facilitar a comunicação aumentando seu alcance, na razão harmônico-ruído, que é maior no ronco e no whoof dos catetos do que em outros chamados. Aumentar a razão harmônico-ruído é uma estratégia de otimização, no sentido evolutivo, para superar o barulho de fundo e melhorar a detecção do sinal (Fletcher, 2004). Esse resultado constitui mais uma evidência para a função de contato deste chamado. O whoof, por sua vez, foi emitido quando o cateto visualizava um ser humano. O animal assume uma postura de alerta encarando o indivíduo e emite este chamado junto com batidas de dentes e arfagem repetidamente, provavelmente este chamado tem uma função de alerta ou ameaça.

Os chamados de catetos, podem alcançar frequências mais baixas devido a sua massa corporal menor quando comparada aos queixadas (Sowls, 1997). Este fato influencia na distância com que o animal pode se comunicar eficientemente (Fletcher, 2004). Estes animais parecem explorar tal habilidade uma vez que são encontrados forrageando guardando um certo distanciamento do grupo por algumas horas do dia e depois reúnem-se novamente em seu bando (Keuroghlian et al., 2004). Esta habilidade comunicativa, encontrada no ronco baixo, também pode facilitar o reagrupamento do grupo após uma fissão devido a ataques de predadores (Sowls, 1997). O arranjo espacial exerce influência sobre o tipo de chamado emitido pelos pecaris, corroborando a afirmação de que eles utilizam a comunicação acústica para manterem a coesão do grupo (Bissonette, 1982; Sowls, 1997).

Foi observado que houve uma mudança entre os dois períodos na taxa de emissão dos chamados de contato e ameaça. No primeiro período, os chamados de contato foram mais emitidos do que os chamados de ameaça e no segundo período houve uma inversão. Uma explicação para isso pode ser o aumento do número de indivíduos nos piquetes, principalmente de adultos, uma vez que a proporção animal/m² exerce uma pressão sobre a expressão de comportamentos agonísticos nos catetos, quanto menor a área maior a taxa de comportamentos agonísticos (Nogueira et al., 2010).

As observações mostraram que quando os animais estão mais próximos, forrageando lado a lado, compartilhando uma mesma fonte de alimento ou local de descanso, surgem ameaças e agressões acompanhadas por algumas vocalizações. Os caititus utilizam o grunhido e a batida de dentes nestes contextos, e a medida que os indivíduos afastam- se, emitem chamados para





Behaviour

manterem o contato. O ronco é o chamado utilizado neste contexto. Este chamado é suave e repetitivo como discutido acima, enquanto o grunhido, o rosnado e a batida de dentes podem soar bastante ruidosos e agressivos. Chamados ruidosos são difíceis de ignorar e são frequentemente produzidos por animais em perigo (Fitch et al., 2002).

Foi encontrado diferença nos parâmetros acústicos entre os sexos, apesar dos caititus não possuírem dimorfismo sexual aparente, exceto pela presença do escroto nos machos. No entanto, algumas características osteológicas do crânio e características do aparato mandibular são diferentes entre machos e fêmeas (Sicuro et al., 2011) e podem interferir na sonoridade dos chamados uma vez que as fêmeas são menores do que os machos (Dubost et al., 2003).

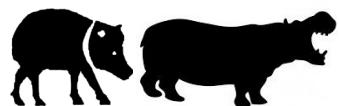
Neste estudo, descrevemos a estrutura acústica dos chamados acústicos de caititus mantidos em cativeiro, cuja análise estrutural mostra a presença de dimorfismo sexual nos parâmetros acústicos. O repertório acústico possui importante papel em manter a coesão espacial do grupo e resolver conflitos relacionados a proximidade e competição por recursos. Há evidências da presença de graduações e maior flexibilidade na taxa de emissão de chamados, o que pode indicar maior complexidade deste repertório.

AGRADECIMENTOS

À Christine Barbosa Caselli pelo auxílio com a análise estatística. Este estudo recebeu apoio da CAPES/PNPD#2951/2010

REFERÊNCIAS

- Altmann, J. (1974). Observational Study of Behavior: Sampling Methods. *Behavior*.
- Barros, K. S., Tokumaru, R. S., Pedroza, J. P., & Nogueira, S. S. C. (2011). Vocal Repertoire of Captive Capybara (*Hydrochoerus hydrochaeris*): Structure, Context and Function. *Ethology*, 117(1). <https://doi.org/10.1111/j.1439-0310.2010.01853.x>
- Benjamini, Y., & Hochberg, Y. (1995). Controlling the false discovery rate: a practical and powerful approach to multiple testing. *Journal of the Royal Statistical Society. Series B (Methodological)*, 57(1), 289–300.
- Bissonette, J. A. (1982). Ecology and Social Behavior of the Collared Peccary in Big Bend National Park. Washington, DC: US Dept of the Interior.
- Bradbury, J. W., & Vehrencamp, S. L. (1998). Principles of animal communication (1st ed.). Sunderland, MA: Sianuer.
- Briefer, E. F. (2012). Vocal expression of emotions in mammals: mechanisms of production and evidence. *Journal of Zoology*, 288(1), 1–20. <https://doi.org/10.1111/j.1469-7998.2012.00920.x>
- Briefer, Elodie F., & McElligott, A. G. (2012). Social effects on vocal ontogeny in an ungulate, the goat, *Capra hircus*. *Animal Behaviour*, 83, 991–1000. <https://doi.org/10.1016/j.anbehav.2012.01.020>
- Byers, J. A., & Bekoff, M. (1981). Social, Spacing, and Cooperative Behavior of the Collared Peccary, *Tayassu tajacu*. *Journal of Mammalogy*, 62(4), 767–785.
- Dubost, G. (1997). Comportements comparés du Pécari À lèvres blanches, *Tayassu pecari*, et du Pécari à collier, *T. tajacu* (Artiodactyles, Tayassuidés). *Mammalia*, 61(3), 313–343.
- Dubost, G., Dutertre, C., & Henry, O. (2003). Body weight increase in the two peccary species of

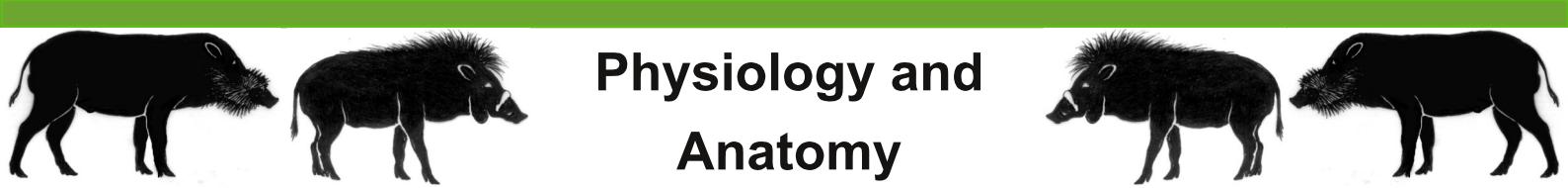




Behaviour

- the genus *Tayassu* (Tayassuidae, Artiodactyla). *Mammalia*, 67, 55–64.
<https://doi.org/10.1515/mamm.2003.67.1.55>
- Fitch, W. T., Neubauer, J., & Herzel, H. (2002). Calls out of chaos: the adaptive significance of nonlinear phenomena in mammalian vocal production. *Animal Behaviour*, 63(3), 407–418.
<https://doi.org/10.1006/anbe.2001.1912>
- Fletcher, N. H. (2004). A simple frequency-scaling rule for animal communication. *The Journal of the Acoustical Society of America*, 115(January), 2334–2338.
<https://doi.org/10.1121/1.1694997>
- Freeberg, T. M., Dunbar, R. I. M., & Ord, T. J. (2012). Social complexity as a proximate and ultimate factor in communicative complexity. *Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences*, 367(1597), 1785–1801.
<https://doi.org/10.1098/rstb.2011.0213>
- Husson, F., Josse, J., Le, S., & Maze, J. (2014). Multivariate Exploratory Data Analysis and Data Mining with R., <https://rdrr.io/cran/FactoMineR/man/FactoMineR-package.html>
- Jorge, F. C., Machado, C. G., Nogueira, S. S. da C., & Nogueira-Filho, S. L. G. (2018). The effectiveness of acoustic indices for forest monitoring in Atlantic rainforest fragments. *Ecological Indicators*, 91(April), 71–76. <https://doi.org/10.1016/j.ecolind.2018.04.001>
- Keuroghlian, A., Eaton, D. P., & Longland, W. S. (2004). Area use by white-lipped and collared peccaries (*Tayassu pecari* and *Tayassu tajacu*) in a tropical forest fragment. *Biological Conservation*, 120(3), 411–425. <https://doi.org/10.1016/j.biocon.2004.03.016>
- Kiltie, R. A., & Terborgh, J. (1983). Observations on the Behavior of Rain Forest Peccaries in Perú: Why do White-lipped Peccaries Form Herds? *Zeitschrift Für Tierpsychologie*, 62, 241–255.
- Lacerda, P. O., Tokumaru, R. S., & Nogueira, S. S. C. (2014). Vocal signature in capybara, *Hydrochoerus hydrochaeris*. *Acta Ethologica*, 17(2). <https://doi.org/10.1007/s10211-013-0162-4>
- Manly, B. F. J. (1997). Randomization, Bootstrap and Monte Carlo Methods in Biology (2nd ed.). London: Chapman and Hall.
- Nogueira-Filho, S. L. G., Sato, T., & Nogueira, S. S. C. (1999). A Organização social de queixadas (*Tayassu pecari*) e caititus (*T. tajacu*) em cativeiro. *Revista de Etologia*, 1(2), 89–98.
- Nogueira, S. S. C., Barros, K. S., Almeida, M. H., Pedroza, J. P., Nogueira Filho, S. L. G., & Tokumaru, R. S. (2012). Ultrasound call detection in capyba. *Pesquisa Veterinaria Brasileira*, 32(7). <https://doi.org/10.1590/S0100-736X2012000700014>
- Nogueira, S. S. C., Caselli, C. B., Costa, T. S. O., Moura, L. N., & Nogueira-Filho, S. L. G. (2016). The role of grunt calls in the social dominance hierarchy of the white-lipped peccary (mammalia, tayassuidae). *PLoS ONE*, 11(7). <https://doi.org/10.1371/journal.pone.0158665>
- Nogueira, S. S. C., Silva, M. G., Dias, C. T. S., Pompéia, S., Cetra, M., & Nogueira-filho, S. L. G. (2010). Social behaviour of collared peccaries (*Pecari tajacu*) under three space. *Animal Welfare*, 19: 243–248.
- Noy Meir, I., Walker, D., & Williams, W. T. (1975). Data transformations in ecological ordination. II. On the meaning of data standardization. *Journal of Ecology*, 63, 779–800.
- Reby, D. D., & McComb, D. K. (2003). Anatomical constraints generate honesty: acoustic cues to age and weight in the roars of red deer stags. *Animal Behavior*, 65, 519–530.
<https://doi.org/10.1006/anbe.2003.2078>





Physiology and Anatomy

- Sicuro, F. L., Neves, L. F. M., & Oliveira, L. F. B. (2011). Sex- and age-related morphofunctional differences in skulls of *Tayassu pecari* and *Pecari tajacu* (Artiodactyla: Tayassuidae). *Journal of Mammalogy*, 92(4), 828–839. <https://doi.org/10.1644/10-MAMM-A-336.1>
- Sowls, L. K. (1997). Javelinas and Other Peccaries: Their Biology, Management, and Use (2nd ed.). Tucson: Texas A&M University Press.
- Team, R. C. (2014). R: A language and environment for statistical computing. Vienna, Austria: R Foundation for Statistical Computing.
- Venables, W. N., & Ripley, B. D. (2002). Modern Applied Statistics with S (Fourth). New York: Springer.
- Wiley, R. H., & Richards, D. G. (1978). Physical constraints on acoustic communication in the atmosphere: Implications for the evolution of animal vocalizations. *Behavioral Ecology and Sociobiology*, 3, 69–94.

Tongue adaptations of suckling babirusa (*Babyrousa celebensis*) and other Suiformes

Alastair A. Macdonald¹ and Steven Mitchell²

¹Royal (Dick) School of Veterinary Studies

The University of Edinburgh

Easter Bush Campus

Midlothian EH25 9RG

Scotland

²Institute of Molecular Plant Science

School of Biological Science

The University of Edinburgh

Edinburgh EH9 3JF

Scotland

Email: Alastair.Macdonald@ed.ac.uk

Key words: anatomy, tongue, fetus, neonatal, pig, bushpig, warthog, peccary, pygmy hippopotamus

Introduction

Following a pregnancy of about 157 days the babirusa (*Babyrousa celebensis*) produces one, two or more rarely three piglets (Macdonald, 2018). The neonatal babirusa are small in size and weigh less than 800g at birth. There are usually four functioning mammary glands available to them, two located on the sow inguinally and the second pair on her abdomen; an additional pair of non-functional teats, slightly cranial to the others, has sometimes been reported (Leus et al. 1995; Alexander et al., 2015).

The teat begins to enlarge about three weeks before the birth of the piglets and becomes quite prominent in the week before parturition (Bowles, 1986; Leus et al, 1992). It is an elongated structure (Figure 1). The initial two thirds of the length of the teat from the teat base is slightly



Physiology and Anatomy

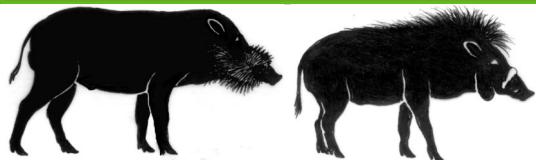


Fig.1: Rear view of a lactating babirusa in North Sulawesi illustrating her udder and teats.

Photo: M. Patry

conical in shape and its epithelium has an irregular, cobbled appearance; these irregularities appear as a series of three to six 'rings' encircling the teat. The epithelial surface of the remaining third of the teat is smoother and has a narrower diameter, which rounds off to a somewhat flattened disc around the orifices of the teat canals. The variability in the number of milk canals draining through the teat remains unknown. The composition of the milk has been reported as: total solids=23%; fat=13%; protein=7.8%; sugars=2.7% (Bowles, pers. comm. cited by Macdonald, 2000). The biochemical composition of the cholesterol remains to be investigated.

Various aspects of babirusa nursing behaviour have been described (Leus et al., 1992; Patry et al., 1995; MacLaughlin et al., 2000). Babirusa piglets have been filmed in north Sulawesi suckling, and obtaining milk from both abdominal and inguinal teats (Figure 2). They have also been observed using tongue movements with the teat, and occasionally pulling on the teat (Patry et al., 1995). The anatomical adaptations of the tongue of the neonatal babirusa piglet which may contribute to this aspect of suckling behaviour form the bases of this report.



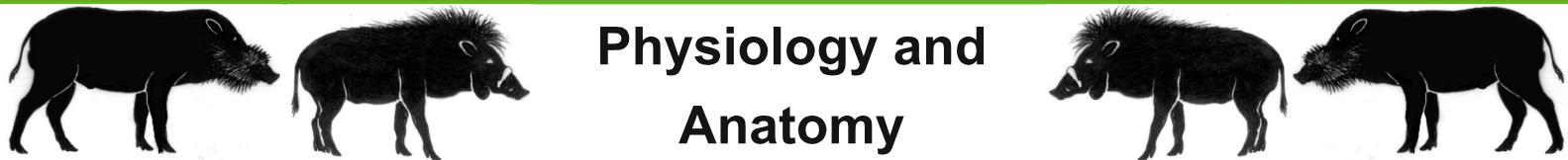
Fig. 2: Female babirusa piglet in North Sulawesi suckling from the inguinal teats. Photo: M. Patry

Materials and Methods

The tongues of twelve babirusa piglets aged between birth and 14 days postnatal, and 17 other fetal and neonatal suiformes conserved in museum and zoological collections were studied (Table 1). Several were collected for photography and scanning electron microscopic examination. The latter had been fixed in alcohol or formalin and were either secondarily fixed in 3% glutaraldehyde in 0.1m sodium cacodylate buffer for 45 minutes, or they were prepared by a modification of the procedure described by Murakami et al (1977). This involved rinsing the tissues first in distilled water containing 2% guanidine hydrochloride and 2% tannic acid for 8 hours and then in distilled water for 30 minutes. Post fixation of these tissues was carried out in a solution of 2% osmium tetroxide in distilled water for 8 hours. After post fixation, all tissues were dehydrated through a graded series of acetones, dried in a critical point drier



Physiology and Anatomy



using carbon dioxide, and then sputter coated with 20um gold/palladium. They were viewed with a scanning electron microscope (Philips 505).

Tab. 1: The identification number, species, sex, age and institution of origin of the fetal and neonatal suiform tongues studied.

ID	Species	Sex	Age	Institution
aam218	<i>Babyrousa celebensis</i>	female	2 days	Jersey Wildlife Preservation Trust
aam219	<i>Babyrousa celebensis</i>	male	6.5 days	Jersey Wildlife Preservation Trust
aam228	<i>Babyrousa celebensis</i>	male	12 days	Jersey Wildlife Preservation Trust
aam387	<i>Babyrousa celebensis</i>	female	neonate	Blijdorp Zoo, Rotterdam
aam419	<i>Babyrousa celebensis</i>	male	neonate	Blijdorp Zoo, Rotterdam
aam420	<i>Babyrousa celebensis</i>	?	neonate	Blijdorp Zoo, Rotterdam
aam584	<i>Babyrousa celebensis</i>	male	neonate	Blijdorp Zoo, Rotterdam
aam586	<i>Babyrousa celebensis</i>	female	neonate	Blijdorp Zoo, Rotterdam
aam587	<i>Babyrousa celebensis</i>	male	1 day	Wilhelma Zoo Stuttgart
aam591	<i>Babyrousa celebensis</i>	male	14 days	Marwell Zoo
aam747	<i>Babyrousa celebensis</i>	female	neonate	Zoo Berlin
aam748	<i>Babyrousa celebensis</i>	male	neonate	Zoo Berlin
aam213a	<i>Sus scrofa</i>	?	~50 days gestation	The University of Edinburgh
aam213b	<i>Sus scrofa</i>	?	~50 days gestation	The University of Edinburgh
aam215	<i>Sus scrofa</i>	?	85 days gestation	The University of Edinburgh
aam241	<i>Sus scrofa</i>	?	105 days gestation	The University of Edinburgh
aam256	<i>Sus scrofa</i>	female	1 day	The University of Edinburgh
aam257	<i>Sus scrofa</i>	male	2 days	The University of Edinburgh
aam749	<i>Potamochoerus porcus</i>	female	1 day	Museum für Naturkunde Berlin
aam751	<i>Potamochoerus larvatus</i>	female	near term fetus	Museum für Naturkunde Berlin
aam756	<i>Phacochoerus africanus</i>	?	neonate	Museum für Naturkunde Berlin
aam758	<i>Phacochoerus africanus</i>	male	neonate	The University of Edinburgh
aam759	<i>Phacochoerus africanus</i>	female	neonate	The University of Edinburgh
aam221	<i>Pecari</i> spp.	?	neonate	unknown
aam753	<i>Pecari</i> spp.	female	near term fetus	Museum für Naturkunde Berlin
aam754	<i>Pecari</i> spp.	male	near term fetus	Museum für Naturkunde Berlin
aam755	<i>Pecari</i> spp.	female	near term fetus	Museum für Naturkunde Berlin
aam223	<i>Choeropsis liberiensis</i>	?	neonate	unknown
aam77	<i>Choeropsis liberiensis</i>	?	neonate	National Museum of Scotland

Results

Neonatal babirusa (*Babyrousa celebensis*)

Marginal papillae were observed on the tongues of all the neonatal babirusa (Figures 3&4). They were present on the lateral edges of the rostral section of the tongue, extending caudally from close to, but not on, the apex of the tongue (Figure 4). Rostrally they were often simple, thin,



Fig. 3: Left lateral view of the open mouth of a babirusa neonate (aam586) showing the marginal papillae on the edge of the curled tongue and the round fungiform papillae on the tongue's dorsal surface. (scale=1mm).

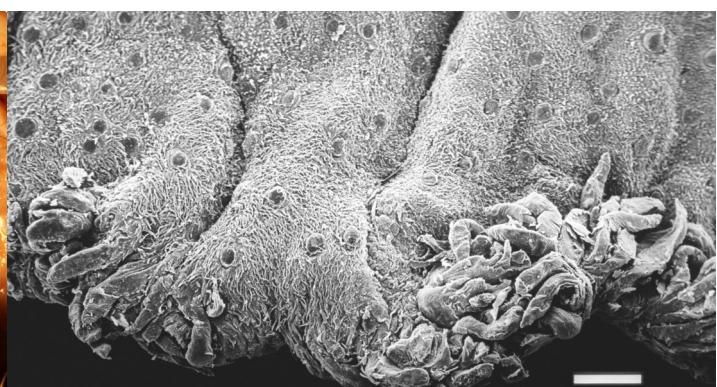
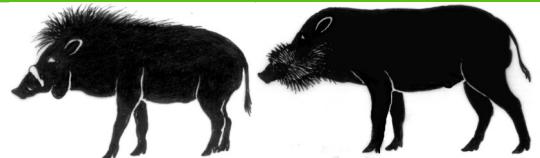
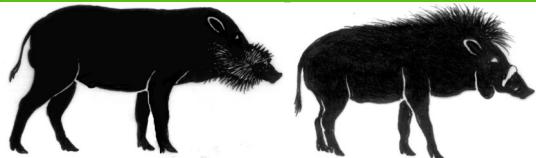


Fig. 4: Apex of the tongue of a 2-day old babirusa neonate (aam218) with marginal papillae on the edges and round-shaped fungiform papillae surrounded by slender filiform papillae on the tongue's dorsal surface. (scale=1mm).



Physiology and Anatomy



flexible, rod-like structures, clustered in two or three rows along the edge of the tongue. Caudally they were more closely bunched, five to seven rows deep. Many, more caudal, papillae were longer (>2cm) and thicker, sometimes paddle-shaped. Some papillae branched in a variable way near their tips (Figures 3&4).

The filiform papillae on the apex of the tongue, although present in large numbers, were spaced apart from one another (Figure 4&6). They formed a ‘carpet’ of thin, keratinised structures extending about five millimetres caudally from the apex of the tongue. Thereafter on the dorsum of the tongue their lengths were much reduced (Figure 4).

The fungiform papillae were present as slightly domed, round (~150-300µm diameter) structures over the dorsal surface of the tongue (Figures 3-5).

*12-14 day-old babirusa (*Babyrousa celebensis*)*

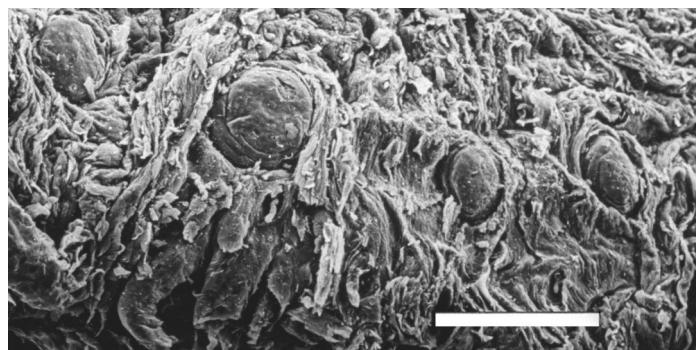


Fig. 5: Apex of the tongue of a 2-day old babirusa neonate (aam218) illustrating four round-shaped fungiform papillae surrounded by slender filiform papillae on the tongue's dorsal surface. (scale=500µm).

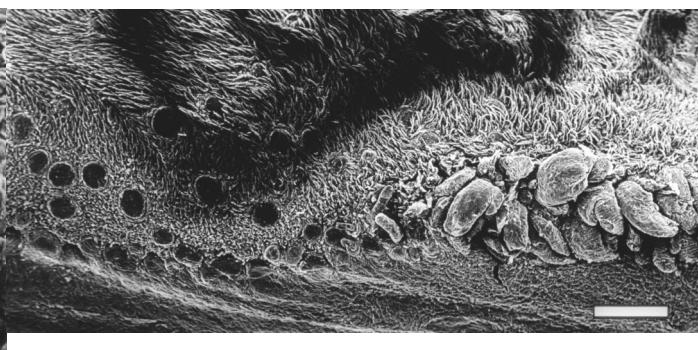


Fig. 6: Left lateral view of the tongue of a 12-day old babirusa neonate (aam228) illustrating elongated marginal papillae (on right), round fungiform papillae (on left) and large numbers of filiform papillae on the medial dorsal surface. (scale=1mm).

At 12-14 days of age the marginal papillae were present on the lateral edges of the tongue. They were absent from about 1.5cm of the rostral edge of the tongue. The few, most rostrally positioned papillae were simple, thin, rod-like structures, about 500µm in length. Caudally the marginal papillae were variable in size (~1mm) and shape (rod-like to paddle-like) and formed less than four rows on the edge of the tongue (Figure 6).

The filiform papillae were short in length on the apical surface of the tongue (Figure 6). However, they were present in large numbers on the dorsal surface of the tongue and reached up to 1mm in length (Figures 6&7).

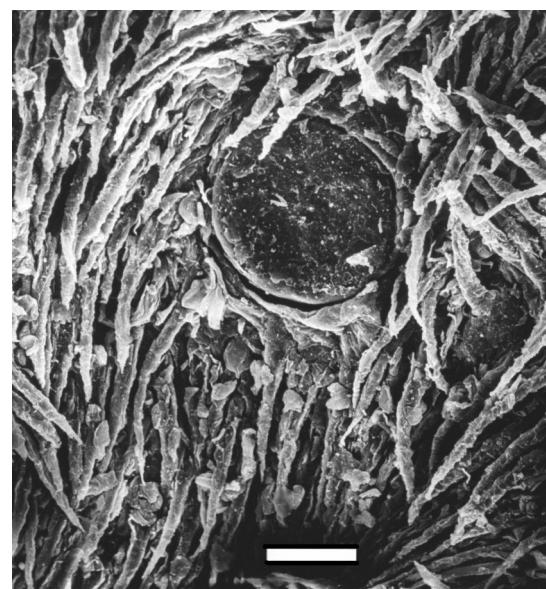


Fig. 7: Close-up view of a single fungiform papilla surrounded by many simple filiform papillae on the tongue of a 12-day old babirusa (aam228) (scale=100µm).



Physiology and Anatomy

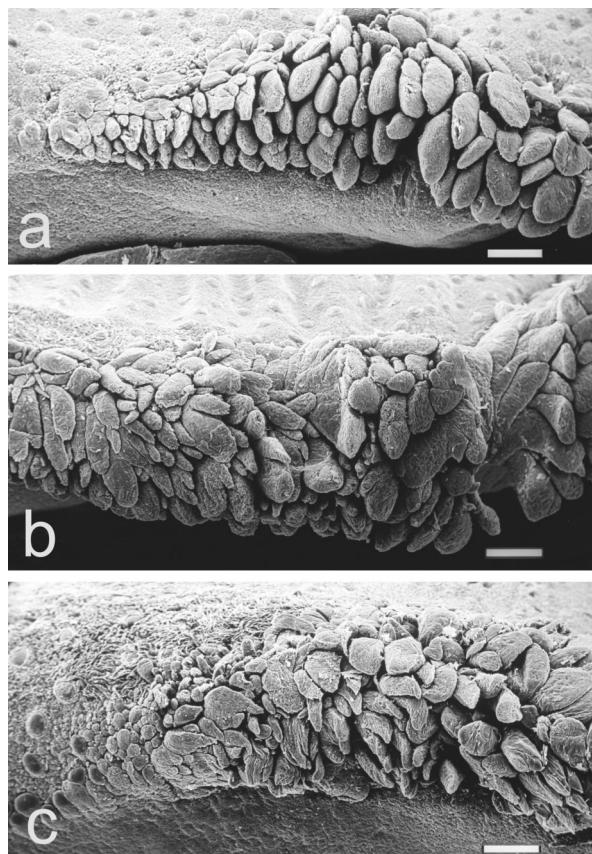
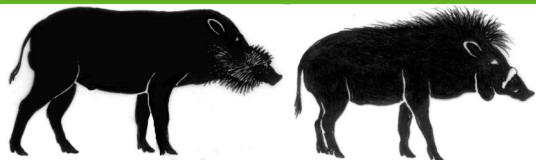


Figure 8a: Left lateral view of the largely paddle-shaped marginal papillae on the tongue of a domestic pig fetus (aam215) at 85 days of gestation. Small dome-shaped fungiform papillae are visible on the dorsal surface of the tongue. (scale=1mm).

Figure 8b: Left lateral view of the variously-sized and shaped marginal papillae on the tongue of a domestic pig fetus (aam241) at 105 days of gestation. Small fungiform papillae are visible on the dorsal surface of the tongue. (scale=1mm).

Figure 8c: Left lateral view of the variously-sized and shaped marginal papillae on the tongue of a 3-day old domestic pig neonate (aam257). Round, flattened fungiform papillae and thin filiform papillae are visible on the dorsal mid and rostral surfaces of the tongue. (scale=1mm).

the three neonatal warthogs (*Phacochoerus africanus*). They were arranged 1-3 papillae deep, with the middle and caudal papillae being larger than the rostral papillae. Almost all papillae were rod-like, of variable diameter, and many had pointed tips. Some were branched. Marginal papillae were not present on the apex of the tongue (Figure 9).

Filiform papillae were thin, thread-like structures and were almost inconspicuous.

Small fungiform papillae were present in large numbers on the dorsal surface of the tongue (Figure 9). They were relatively flat, oval to round structures, approximately 400µm in diameter.

The fungiform papillae were present as flat, round (~150-600µm diameter) structures scattered over the dorsal surface of the tongue (Figures 6&7).

Fetal and neonatal domestic pig (Sus scrofa)

Marginal papillae were not observed on the tongues of fetal pigs aged about 50 days (gestation length 114 days). However, at 85 days of gestation they were present (Figures 8a). The number of the papillae increased from near the apex of the tongue caudally. The villi were paddle-shaped and increased in length to over 1mm. Approximately ten days before birth and three days after birth the layer of marginal papillae along the edge of the tongue was approximately 4mm thick (Figure 8b&c).

The filiform papillae in fetal and neonatal pigs were short in length (Figure 8).

The fungiform papillae in fetal pigs were small, round domed structures (Figures 8a&b). After birth they were flat and up to 400µm in diameter (Figure 8c).

Neonatal red river hog and bushpig Potamochoerus spp.

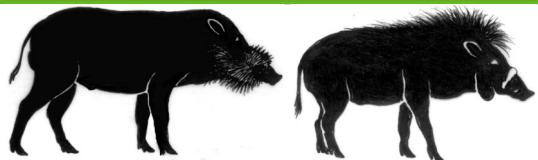
Prominent marginal papillae were observed on the lateral edges of the tongue of a neonatal Red river hog (*Potamochoerus porcus*) and a neonatal bushpig (*Potamochoerus larvatus*).

Neonatal common warthog (Phacochoerus africanus)

Small marginal papillae (0.5-2mm in length) were present along a length of approximately 12mm of the rostral, lateral edges of the tongues (Figure 9) of the three neonatal warthogs (*Phacochoerus africanus*). They were arranged 1-3 papillae deep, with the middle and caudal papillae being larger than the rostral papillae. Almost all papillae were rod-like, of variable diameter, and many had pointed tips. Some were branched. Marginal papillae were not present on the apex of the tongue (Figure 9).



Physiology and Anatomy



Fetal and neonatal Collared peccaries (*Pecari* spp.)

No marginal papillae were found on the tongues of fetal and neonatal collared peccaries (*Pecari* spp.).

Neonatal Pygmy hippotamus (*Choeropsis liberiensis*)

The tongue of the neonatal pygmy hippopotamus (*Choeropsis liberiensis*) had a few small, isolated papillae on its lateral surface (Figure 10).

The filiform papillae were present in large numbers and were very short in size.

Flat and domed fungiform papillae, round in shape, were scattered over the dorsal surface of the tongue.

Large numbers of long, conical papillae covered the oral mucosal surfaces of the lips and cheeks.

Discussion

The discovery of marginal papillae on the tongues of neonatal babirusa, red river hogs, bushpigs and common warthogs expands our knowledge of the presence of these papillae among the suidae. A number of years ago Habermehl (1952) drew attention to the presence of 'Randpapillen' along the edges of the neonatal tongues of fetal and neonatal Eurasian wild pigs and domestic pigs (*Sus scrofa*). He referred to them as 'Saugpapillen' because of their proposed functional relationship to suckling. The blood vessel supply to each papilla in *Sus scrofa* is arranged in such a way as enables erection of the marginal papillae during the process of suckling (Schlechta et al, 1996). If present in each of the pig species studied, this would permit the curled tongue of the neonatal piglet to more completely grasp the teat. The variety of shapes of these papillae in the domestic pig, described by Schneider et al (1996) as predominantly leaf-like, tongue-like finger-like and conical in appearance, implied variability in the structural requirement for teat attachment. Their relatively early fetal development, seen in *Sus scrofa*, was of some interest, and raised questions of function one month before the end of gestation (Habermehl, 1952; Ates et al, 2013; current study).

The external morphology of the babirusa teat is comparable to that of *Sus scrofa* (Farmer et al, 2017). For the first approximately two thirds of its length from the teat base it has a rough,



Fig. 9: View of the dorsal surface of the tongue of a female neonatal warthog (aam758). The apex of the tongue carries no marginal papillae, these being restricted to a restricted region on the lateral edges of the tongue. Thread-like filiform papillae are present. Round fungiform papillae are visible over the surface of the tongue. (scale=1mm).



Physiology and Anatomy

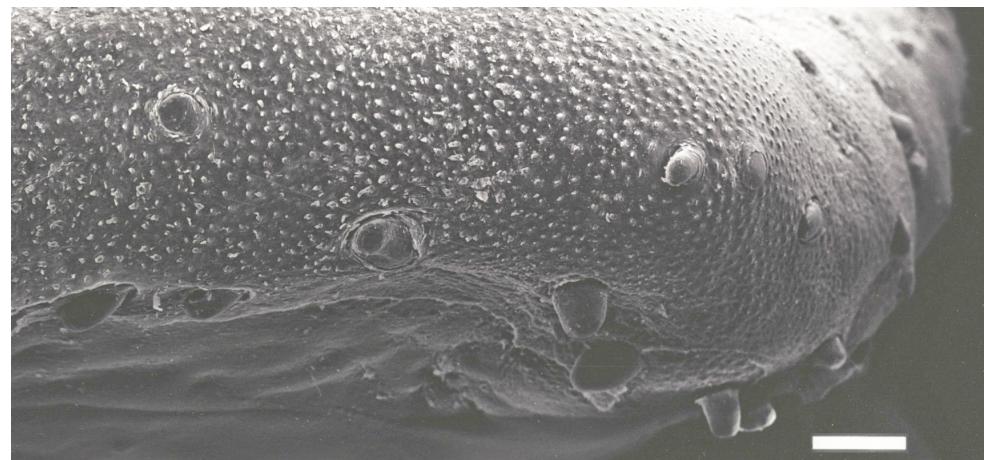


Fig. 10: Right lateral view near the apex of the tongue of a neonatal pygmy hippopotamus tongue (aam223); a few, widely distributed, finger-like marginal papillae projected from the lateral and rostral surfaces. Several round fungiform papillae are visible on the dorsal surface of the tongue. Filiform papillae appear to be very short in size. (scale=1mm).

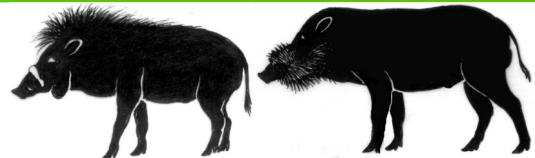
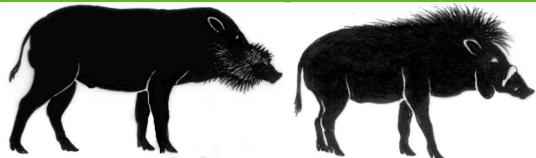
'cobbled' appearance. The gnarled structure of the teat's external epithelium in this region offers an appropriately knobbly area for piglet tongue attachment. Movement by the marginal papillae may also act as some sort of tactile stimulus to the nipple to eject milk. Erection of the teat following piglet stimulated oxytocin release (Ellendorff et al, 1982), would further expand this surface area. Teat length and teat diameter are larger in multiparous compared to primiparous domestic pig sows (Ocepek et al, 2016). The teats of the lactating pygmy hippopotamus are small and conical in shape (Lang, 1975). Unlike in the pigs, they appeared to have a fairly smooth external epithelial structure. This difference suggests that there is a different form of neonatal suckling attachment to the teat in the pygmy hippopotamus.

The nerve fibres and terminals in the marginal papillae of new-born *Sus scrofa* suggest that these papillae have a sensory function and act as mechanoreceptors (Sommer et al, 1997). Although the current investigation did not seek to identify similar structures in the marginal papillae of the babirusa, the structural similarities of these papillae in babirusa, domestic pig, red river hog and bushpig genera may be instructive. The absence of marginal papillae on the tongue of the peccary and the small number seen on the tongue of the neonatal pygmy hippopotamus were both note-worthy. Conical papillae were observed on the lower lip of the latter. It would appear from veterinary reports that there should be sufficient research material available naturally to study the papillae on the tongue and lips of the neonatal peccaries and pygmy hippopotamus in more depth (Sutherland-Smith, 2015; Flacke et al, 2016).

In *Sus scrofa*, piglet olfaction plays a critical role in teat attachment. The odours from the sow's ventrum influence teat attachment. Studies have shown that washing the sow's ventrum with organic solvents virtually eliminated teat attachment in *Sus scrofa* piglets (Morrow-Tesch and McGlone, 1990). It would appear that specific substances, probably volatile and lipid in nature, were produced ventrally by the sow, and that these compounds modulated teat attachment. Comparable studies have yet to be carried out on the babirusa and other suids. However, perhaps the known nesting behaviour of babirusa, bushpig, red river hog and common warthog contribute sufficient neonatal confinement to enable piglet access to olfactory and other stimuli from the sow (Macdonald, 2000). What these studies also demonstrated was that the *Sus* piglet's senses of olfaction, gustation and touch each influenced teat attachment.



Physiology and Anatomy



In the babirusa the filiform papillae development after birth created a relatively thick and dense mat of connective tissue protrusions (Figures 6&7). The mechanical function that this mat may have been to help maintain the close attachment of the growing tongue to the teat; perhaps they increased the friction of the neonatal tongue's surface. At 92 days of gestation the tongue of *Sus scrofa* was covered in short, densely packed, filiform papillae (Tichý, 1992). Similarly, short filiform papillae were present on the tongue of the neonatal pygmy hippopotamus (Figure 10). These were much smaller than the elongated filiform papillae of the adult common hippopotamus (*Hippopotamus amphibius*) (Yoshimura et al, 2009). In the adult wild and domestic *Sus scrofa* two types of long filiform papillae, simple and compound, are present, the latter having a body and a variable number (2-10) of papillary hairs (Chamorro et al, 1994; Kumar and Bate, 2004). The filiform papillae of the 12-day old babirusa appeared to be of the simple type.

The slightly dome-shaped fungiform papillae of the neonatal babirusa (Figure 3) resembled the fungiform papillae found in *Sus scrofa* at 85 days (Figure 8a), 92 days, 94 days and 105 days (Figure 8b) of gestation (Tichý, 1991). Taste buds had been found in the fungiform papillae of *Sus scrofa* at 94 days of prenatal development. There was insufficient clarity in the scanning electron micrographs of the present study to identify gustatory pores on the surfaces of the fungiform papillae of the babirusa, warthogs or pygmy hippopotamus.

Finally, it is important to point out that marginal papillae have also been described on the tongues of a number of other cetartiodactyl species – aquatic mammals that are distant relatives of the suidae: young harbour porpoise (*Phocoena phocoena*), bottlenose dolphin (*Tursiops truncatus*) and Commerson's dolphin (*Cephalorhynchus commersonii*) (Kastelein and Dubbeldam, 1990). They are also present on the tongues of young estuarine dolphin (*Sotalia guianensis*) (Guimarães et al, 2011), striped dolphin (*Stenella coeruleoalba*) (Yamasaki et al, 1978), Stejneger's beaked whale (*Mesoplodon stejnegeri*) (Shindo et al, 2008) and the gray whale (*Eschrichtius robustus*) (Kienle et al, 2015).

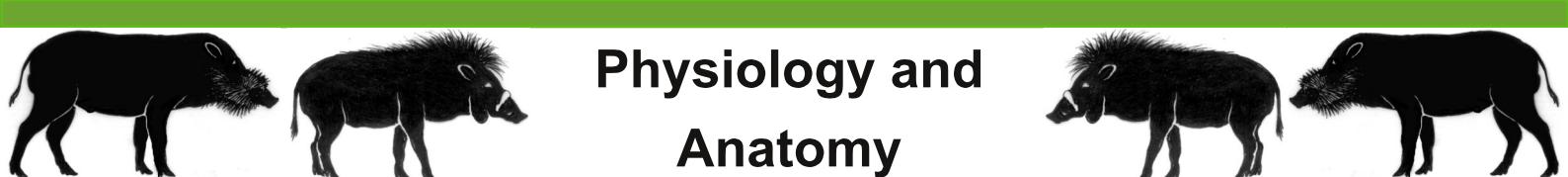
Conclusions

This study has partially expanded awareness of one part of the biology of suckling by neonatal suiformes, the marginal papillae on the tongues of neonatal babirusa, Eurasian wild pig, bushpig, red river hog, warthog, collared peccary and pygmy hippopotamus has been described. Some notes have also been made concerning the filiform and fungiform papillae of these genera. There is much that is still unknown. The anatomy of the teat during lactation and suckling in pigs, peccaries and hippopotamidae is one such area deserving of research. Similarly, there is much still to be learned about the morphological changes occurring within the mouths of the fetuses and neonates of these animals, and how neonatal growth affects the morphology and function of the tongue.

Acknowledgements

The authors would like to thank the directors and staff of the following institutions for access to biological material in their collections: Blijdorp Zoo, Rotterdam, The Netherlands; Jersey Wildlife Preservation Trust (now Durrell Wildlife Conservation Trust), Channel Islands; Museum für Naturkunde Berlin, Germany; Marwell Zoo, Winchester, England; The National Museum of Scotland, Edinburgh, Scotland; The University of Edinburgh, Scotland; Wilhelma Zoo Stuttgart,



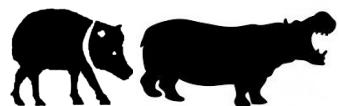


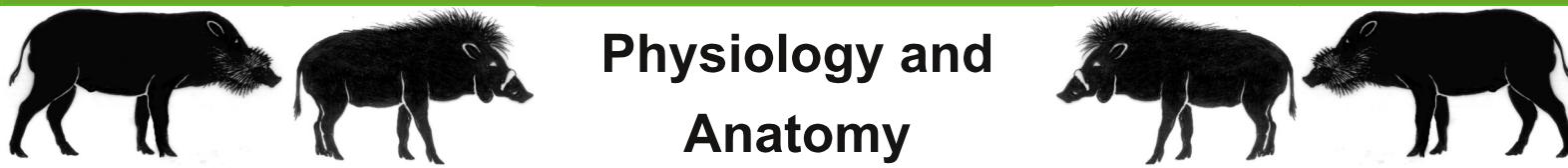
Physiology and Anatomy

Germany. Financial support for this study was kindly provided by the University of Edinburgh and the Balloch Trust.

References

- Alexander, A.B., Hanley, C.S., Fischer, M.T. and Luis R. Padilla, L.R. 2015. Management of toxic mastitis in a babirusa (*Babyrousa celebensis*). *Journal of Zoo and Wildlife Medicine*, 46, 949–952.
- Ates, S., Akaydin Bozkurt, Y., Kozlu, T., Alan, A. and Düzler, A. 2013. Light and scanning electron microscopic studies on the lingual papillae of 80-day-old wild pig fetal siblings. *Turkish Journal of Veterinary and Animal Sciences*, 37, 664-671.
- Bowles, D. 1986. Social behaviour and breeding of Babirusa (*Babyrousa babyrussa*) at the Jersey Wildlife Preservation Trust. *Dodo, Journal of the Jersey Wildlife Preservation Trust*, 23, 86-94.
- Chamorro, C.A., Fernández, J.G., de Paz, P., Pelaez, B. and Anel, L. 1994. Scanning electron microscopy of the wild boar and pig lingual papilla. *Histology and Histopathology*, 9, 657-667.
- Ellendorff, F., Forsling, M.L. and Poulain, D.A. 1982. The milk ejection reflex in the pig. *Journal of Physiology*, 333, 577-594.
- Farmer, C., Fortin, É. and Méhot, S. 2017. In vivo measures of mammary development in gestating gilts. *Journal of Animal Science*, 95, 5358-5364.
- Flacke, G.L., Tkalcic, S., Steck, B., Warren, K. and Martin, G.B. 2016. A retrospective analysis of mortality in captive pygmy hippopotamus (*Choeropsis liberiensis*) from 1912-2014. *Zoo Biology*, 35, 556-569.
- Guimarães, J.P., Mari, R. de B., Marigo, J., Rosas, F.C.W. and Watanabe, I-S. 2011. Light and scanning electron microscopic study of the tongue in the estuarine dolphin (*Sotalia guianensis* van Bénéden, 1864). *Zoological Science*, 28, 617–622.
- Habermehl, K.H. 1952. Über besondere Randpapillen an der Zunge neugeborener Säugetiere. *Zeitschrift für Anatomie und Entwicklungsgeschichte*, 116, 355-372.
- Kastelein RA, Dubbeldam JL. 1990. Marginal papillae on the tongue of the harbour porpoise (*Phocoena phocoena*), bottlenose dolphin (*Tursiops truncatus*) and commerson's dolphin (*Cephalorhynchus commersonii*). *Aquatic Mammals*, 15, 158–170.
- Kienle, S.S., Ekdale, E.G., Reidenberg, J.S. and Demere, T.A. 2015. Tongue and hyoid musculature and functional morphology of a neonate gray whale (Cetacea, Mysticeti, *Eschrichtius robustus*). *The Anatomical Record*, 298, 660-674.
- Kumar, S. and Bate, L.A. 2004. Scanning electron microscopy of the tongue papillae in the pig (*Sus scrofa*). *Microscopy Research and Technique*, 63, 253-258.
- Lang, E.M. 1975. Das Zwergflüßpferd. *Die Neue Brehm-Bücherei*. A. Ziems Verlag: Wittenberg Lutherstadt.
- Leus, K., Bland, K.P., Dhondt, A.A. and Macdonald, A.A. 1995. Ploughing behaviour of the babirusa (*Babyrousa babyrussa*) suggests a scent marking function. *Journal of Zoology*, 238, 209-219.
- Leus, K., Bowles, D., Bell, J. and Macdonald, A.A. 1992. Behaviour of the babirusa (*Babyrousa babyrussa*) with suggestions for husbandry. *Acta Zoologica et Pathologica Antverpiensia*, 82, 9-27.
- Macdonald, A.A. 2000. Comparative anatomy, physiology and ecology of pregnancy and lactation





Physiology and Anatomy

- in wild pigs: a review. In (Nijboer, J., Hatt, J.M., Kaumans, W. Beijnen, A. & Gansloßer, U., eds.) Zoo Animal Nutrition, Filander: Fürth, pp. 213-236.
- Macdonald, A.A. 2018. Sulawesi Babirusa *Babirousa celebensis* (Deninger, 1909). Chapter 6, In (M. Melletti & E. Meijaard, Eds). Ecology, conservation and management of wild pigs and peccaries. Cambridge University Press: Cambridge, pp. 76-84.
- MacLaughlin, K., Ostro, L.E.T., Koontz, C. and Koontz, F. 2000. The ontogeny of nursing in *Babirousa babyrussa* and a comparison with domestic pigs. *Zoo Biology*, 19, 253-262.
- Morrow-Tensch, J. and McGlone, J.J. 1990. Sensory systems and nipple attachment behaviour in neonatal pigs. *Physiology and Behavior*, 47, 1-4.
- Murakami, T., Yamamoto, K., Itoshima, T. and Iriwo, S. 1977. Modified tannin osmium conductive staining method for non-coated scanning electron microscope specimens. Its application to microdissection scanning, electron microscopy of the spleen. *Archivum Histologicum Japonicum*. 40, 35-40.
- Ocepek, M., Andersen-Ranberg, I., Edwards, S.A. and Andersen, I.L. 2016. Udder characteristics of importance for teat use in purebred and crossbred pigs. *Journal of Animal Science*, 94, 780-788.
- Patry , M., Leus, K. and Macdonald, A.A. 1995. Group structure and behaviour of babirusa (*Babirousa babyrussa*) in North Sulawesi. *Australian Journal of Zoology*, 43, 643-655.
- Schlechta C, Kressin M, Schnorr B, Krebs C. 1996. Architektur und Feinstruktur der terminalen Blutgefäße der Zungenrandpapillen neugeborener Ferkel. *Annals of Anatomy*, 178: 137–143.
- Schneider C, Kressin M, Schnorr B. 1996. Zur Morphologie der Zungenrandpapillen neugeborener Ferkel. *Anatomia Histologia Embryologia*, 25, 95–100.
- Shindo J, Yamada TK, Yoshimura K, Kageyama I. 2008. Morphology of the tongue in a newborn Stejneger's beaked whale (*Mesoplodon stejnegeri*). *Okajimas Folia Anatomica Japonica*. 84, 121–124.
- Sommer, U., Schlechta, C., Kressin, M. and Schnorr, B. 1997. Intraepithelial Nervenendigungen in den Zungenrandpapillen neugeborener Ferkel. *Anatomia Histologia Embryologia*, 26, 121-126.
- Sutherland-Smith, M. 2015. Suidae and Tayassuidae (Wild pigs, peccaries). In (R.E. Miller and M.E. Fowler, eds.) Fowler's Zoo and Wild Animal Medicine. Saunders, Volume 8, Chapter 58, pp. 568-584.
- Tichý, F. 1991. The morphogenesis of circumvallate papillae and the differentiation of taste buds in the porcine fetus from day 76 till birth and in the adult pig. *Acta Veterinaria Brno*, 60, 307-315.
- Tichý, F. 1992. The morphogenesis of selected lingual papillae in ovine and porcine foetuses observed by scanning electron microscopy *Acta Veterinaria Brno*, 61, 3-10.
- Yamasaki F, Komatsu S, Kamiya T 1978. Papillary projections at the lingual margin in the striped dolphin, *Stenella coeruleoalba*, with special reference to their development and regression. *Journal of Morphology*, 157, 33–48.
- Yoshimura, K., Hama, N., Shindo, J., Kobayashi, K. and Kageyama, I. 2009. Light and scanning electron microscopic study on the tongue and lingual papillae of the common hippopotamus, *Hippopotamus amphibius amphibius*. *The Anatomical Record*, 292, 921-934.





New literature on Suiformes

Veterinary, Genetic and Physiological Studies

First Identification of Porcine Parvovirus 3 in a Wild Boar in Italy by Viral Metagenomics - Short Communication.

Amoroso, M. G., F. Cerutti, N. D'Alessio, M. G. Lucibelli, A. Cerrone, P. L. Acutis, G. Galiero, G. Fusco, and S. Peletto. 2019.

Acta Veterinaria Hungarica 67, no. 1 (Mar): 135-139. <https://dx.doi.org/10.1556/004.2019.015>.

Metagenomic analysis revealed the presence of porcine parvovirus 3 (PPV3) in the pool of the internal organs of a wild boar found dead in Southern Italy. Phylogenetic analysis based on the complete coding sequences showed that the newly detected virus is most closely related to those found also in wild boars in Romania during 2010-2011. Even though the death could not be associated with this virus, PPV3 could have contributed to lowering the host's immunological defences.

Evolution of Mhc Class II Sla-Drb1 Locus in the Croatian Wild Boar (*Sus Scrofa*) Implies Duplication and Weak Signals of Positive Selection.

Arbanasic, H., D. Konjevic, L. Vrankovic, M. Bujanic, S. Stipoljev, M. Balazin, N. Srem, D. Skoric, and A. Galov. 2019.

Animal Genetics 50, no. 1 (Feb): 33-41. <https://dx.doi.org/10.1111/age.12734>.

The wild boar is an ancestor of the domestic pig and an important game species with the widest geographical range of all ungulates. Although a large amount of data are available on major histocompatibility complex (MHC) variability in domestic pigs, only a few studies have been performed on wild boars. Due to their crucial role in appropriate immune responses and extreme polymorphism, MHC genes represent some of the best candidates for studying the processes of adaptive evolution. Here, we present the results on the variability and evolution of the entire MHC class II SLA-DRB1 locus exon 2 in 133 wild boars from Croatia. Using direct sequencing and cloning methods, we identified 20 SLA-DRB1 alleles, including eight new variants, with notable divergence. In some individuals, we documented functional locus duplication, and SLA-DRB1*04:10 was identified as the allele involved in the duplication. The expression of a duplicated locus was confirmed by cloning and sequencing cDNA-derived amplicons. Based on individual genotypes, we were able to assume that alleles SLA-DRB1*04:10 and SLA-DRB1*06:07 are linked as an allelic combination that co-evolves as a two-locus haplotype. Our investigation of evolutionary processes at the SLA-DRB1 locus confirmed the role of intralocus recombination in generating allelic variability, whereas tests of positive selection based on the dN/dS (non-synonymous/synonymous substitution rate ratio) test revealed atypically weak and ambiguous signals.

First Oral Vaccination of Eurasian Wild Boar against African Swine Fever Virus Genotype II.

Barasona, J. A., C. Gallardo, E. Cadenas-Fernandez, C. Jurado, B. Rivera, A. Rodriguez-Bertos, M. Arias, and J. M. Sanchez-Vizcaino. 2019.

Frontiers in Veterinary Science 6 (Apr). <https://dx.doi.org/10.3389/fvets.2019.00137>.

African swine fever (ASF), the most significant threat to the pig industry worldwide, has spread to more than 55 countries on three continents, and it affects more than 77% of the world swine population. In the European Union, wild boar (*Sus scrofa*) is the most severely affected host. The





New literature on Suiformes

main reasons for the unprecedented and constant spread of ASF in Europe are the trade activities, the continuous movement of infected-wild boar populations among regions and the lack of vaccine to prevent ASF infection. In this study, we demonstrate that oral immunization of wild boar with a non-hemadsorbing, attenuated ASF virus of genotype II isolated in Latvia in 2017 (Lv17/WB/Rie1) conferred 92% protection against challenge with a virulent ASF virus isolate (Arm07). This is, to our knowledge, the first report of a promising vaccine against ASF virus in wild boar by oral administration. Further studies should assess the safety of repeated administration and overdose, characterize long-term shedding and verify the genetic stability of the vaccine virus to confirm if Lv17/WB/Rie1 could be used for free-ranging wild boar in ASF control programs.

The Architecture of the Lymph Nodes in the Abdominal and Thoracic Cavities of Wild Boar.

Bozkurt, Y. A., S. Ates, T. Kozlu, and F. Basak. 2019.

Indian Journal of Animal Research 53, no. 5 (May): 609-615. <https://dx.doi.org/10.18805/ijar.B-759>.

The distribution of lymph nodes located in the abdominal and thoracic cavities of ten wild boars, and their structure were determined anatomically, histologically and immunohistochemically, to be the first detailed investigation on the wild boar. Though general localization and distribution were similar, the number of lymph nodes showed small differences from those of domestic pig. Histological investigations did not reveal a significant hilus. Besides, T lymphocytes with anti-CD3, CD4, CD8, B lymphocytes with anti-CD79a, macrophages with anti-macrophage monoclonal antibodies, and follicular dendritic cells using anti-S100 polyclonal antibody and their distribution in the lymph nodes were detected. Many CD3 positive T lymphocytes were observed in the germinal center of the lymph follicles, in the cortical area and in the medulla. CD8 positive T lymphocytes were few, and CD4 positive T lymphocytes were not seen. CD79 positive cells were scanty.

Lactobacilli Isolated from Wild Boar (*Sus Scrofa*) Antagonize *Mycobacterium Bovis* Bacille Calmette-Guerin (Bcg) in a Species-Dependent Manner.

Bravo, M., T. Combes, F. O. Martinez, R. Cerrato, J. Rey, W. Garcia-Jimenez, P. Fernandez-Llario, D. Risco, and J. Gutierrez-Merino. 2019.

Frontiers in Microbiology 10 (Jul). <https://dx.doi.org/10.3389/fmicb.2019.01663>.

Background: Wildlife poses a significant burden for the complete eradication of bovine tuberculosis (bTB). In particular, wild boar (*Sus scrofa*) is one of the most important reservoirs of *Mycobacterium bovis*, the causal agent of bTB. Wild boar can display from mild TB lesions, usually found in head lymph nodes, to generalized TB lesions distributed in different anatomical regions; but rarely clinical signs, which complicates the diagnosis of *Mycobacterium bovis* infection and bTB control. Among the possibilities for this variability in lesion distribution is the influence of the host-beneficial commensal-primed immune barrier. In this respect, beneficial microbes may delay bTB dissemination as a consequence of an antagonistic competition for nutrients and phagocytes. In order to explore this possibility, we have tested whether typical commensals such as lactobacilli have the capacity to reduce the survival rate of the surrogate *M. bovis* strain Bacillus Calmette-Guerin (BCG); and to modulate its phagocyte intake. **Results:** Three *Lactobacillus* species, *L. casei*, *L. plantarum*, and *L. salivarius*, isolated from wild boar feces displayed a pH-dependent inhibitory activity against BCG and influenced its intake by





New literature on Suiformes

porcine blood phagocytes in a species-dependent manner. All lactobacilli showed a very significant bactericidal effect against BCG at low pH, but only isolates of *L. plantarum* and *L. casei* displayed such antimycobacterial activity at neutral pH. The genomes of these isolates revealed the presence of two-peptide bacteriocins whose precursor genes up-regulate in the presence of BCG cells. Furthermore, *L. plantarum* reduced significantly the BCG phagocytic intake, whereas *L. casei* had the opposite effect. *L. salivarius* had no significant influence on the phagocytic response to BCG. Conclusions: Our in vitro results show that lactobacilli isolated from wild boar antagonize BCG as a consequence of their antimycobacterial activity and a competitive phagocytic response. These findings suggest that commensal bacteria could play a beneficial role in influencing the outcome of bTB dissemination. Further work with lactobacilli as a potential competitive pressure to control bTB will need to take into account the complex nature of the commensal microbiome, the specific immunity of the wild boar and the in vivo infection context with pathogenic strains of *M. bovis*.

Risk of Exposure of Farms and Subsistence Nurseries to Contact with Wild Boar in Southern Mato Grosso Do Sul.

Braz, P. H., M. R. Oliveira, V. S. Silva, W. M. Tomas, R. S. Juliano, T. A. Moreira, N. P. Zimmermann, and A. O. Pellegrin. 2019.

Pesquisa Veterinaria Brasileira 39, no. 2 (Feb): 148-154. <https://dx.doi.org/10.1590/1678-5150-pvb-5888>.

With the advancement of wild boar distribution in the rural environment, its impacts are not limited to health in the pig sector, but the requirements for monitoring and control of the species are requirements laid down by the OIE for the recognition of classical swine fever free zone status. The construction of ecological models of favorability or suitability for the occurrence of pest species are necessary tools for the decision making on priority areas of management aiming at risk management. This work aims to map the level of suitability for the occurrence of wild boar in the southern state of Mato Grosso do Sul, as well as to identify the main risk variables for contact with the wild boar and evaluate the biosecurity measures adopted by commercial farms integrated in the south of the State of Mato Grosso do Sul. To evaluate the risk potential of wild boar for commercial and subsistence swine farming in southern Mato Grosso do Sul, a model of environmental suitability was constructed for this species in the swine producing region. This model considered different environmental strata, being the selection of the layers considered the physiological and behavioral characteristics of the species. In parallel, interviews were carried out in a sample of commercial farms integrating the region to survey the perception of the presence of the invasive species and the biosafety measures adopted. The results of this work indicate that the risk of contact among wild boars and animals reared in closed production systems may be high in the study area and only establishment of appropriate biosecurity measures that consider the characteristics and habits of the boar may prevent the intrusion of this species and contact with domestic swine. The built model can be considered of high reliability and it is recommended to apply it to other areas of the state, being a useful tool for the productive sector, environmental agencies and decision makers.

Helminths of Wild Boar (*Sus Scrofa*) in the Calabrian Region of Southern Italy.

Castagna, F., V. Musella, L. Esposito, A. Poerio, L. Rinaldi, A. Bosco, G. Cringoli, and D. Britti. 2019.





New literature on Suiformes

Journal of Wildlife Diseases 55, no. 2 (Apr): 416-420. <https://dx.doi.org/10.7589/2018-02-028>.
In Calabria, as in other Italian regions, the wild boar (*Sus scrofa*) population has increased considerably in the last few years. The presence of this wild ungulate, a huntable species, was detected throughout this region. Wild boars are a host for many endoparasites, some of which are zoonotic. Our aim was to acquire data on the prevalence endoparasites in wild boar in the region of Calabria, Italy, where such information is limited. We used 60 wild boars culled during the 2014-15 hunting season. We used FLOTAC dual techniques for fecal microscopic exams, as well as qualitative and quantitative microscopic examination with a sensitivity level of 2 eggs/g of feces. The research has underlined the remarkable diffusion of gastrointestinal helminths, particularly *Ascaris suum*, in wild boar of the areas of Sila and Presila in the province of Catanzaro, Calabria.

Epidemiological Investigation of Tick Species from near Domestic Animal Farms and Cattle, Goat, and Wild Boar in Korea.

Chae, J. B., Y. S. Cho, Y. K. Cho, J. G. Kang, N. S. Shin, and J. S. Chae. 2019. Korean Journal of Parasitology 57, no. 3 (Jun): 319-324.
<https://dx.doi.org/10.3347/kjp.2019.57.3.319>.

This study aimed to investigate the tick species and give background for tick-borne investigations in Korea. Ticks were collected from the area within 2 km radius of the 4 domestic animal farms, where they were located in mountainous areas and raising animals on pasture, and from animal bodies in 2014 and 2015. In total, 7,973 nymphal and adult ticks were collected from the farms - 7,758 *Haemaphysalis longicomis*, 198 *Haemaphysalis flava*, and 17 *Ixodes nipponensis*, and 1,763 were collected from animals - 729 *H. longicomis* from cattle; 569 *H. longicomis* from goats; and 297 *H. longicomis*, 118 *H. flava*, 1 *I. nipponensis*, and 49 *Amblyomma testudinarium* from wild boars. As more species of ticks were collected from wild boars than domesticated animals and their habitats, various animal hosts should be considered while investigating tick species.

Malignant Peritoneal Mesothelioma in a Boar Who Lived in Calabria (Italy): Wild Animal as Sentinel System of Human Health.

Colombino, E., S. Capella, F. Casalinoovo, R. Racco, F. Pruitt, M. Volante, V. D. Lo Presti, E. Belluso, and M. T. Capucchio. 2019.

Science of the Total Environment 683 (Sep): 267-274.
<https://dx.doi.org/10.1016/j.scitotenv.2019.05.254>.

Mesothelioma is a tumor of the serosal membranes described both in human and veterinary medicine. While in humans the relationship between mesothelioma and exposure to asbestos and some other asbestiform minerals is well known, in animals it is still difficult to establish. In this paper a case of malignant peritoneal mesothelioma probably related to asbestos exposure in a wild boar is described. At post-mortem evaluation the peritoneum, diaphragm and serosal surface of liver and kidneys showed isolated to coalescent multiple nodular lesions. Samples from diaphragm, liver and lung were collected to perform microbiological and histological investigations. To assess the presence of asbestos and/or other asbestiform minerals, SEM-EDS investigations were performed on organs and soil samples collected from the area where the wild boar lived. Microbiological investigations were negative for *Mycobacterium* species. Gross and histological examination were compatible with a biphasic mesothelioma, with nodules composed of epithelioid and sarcomatoid elements with high pleomorphism. Immunohistochemistry revealed





New literature on Suiformes

only multifocal scattered positivity for WT-1 and D2-40. Asbestos fibres were detected in all samples (organs and soil) by SEM-EDS, demonstrating a potential relationship between the neoplasia and the exposure to naturally occurring asbestos (NOA). In conclusion, the results of the present study are further confirmation that wild animals, such as the boar, are suitable sentinels to indicate the risk of environmental exposure to asbestos for human populations.

Prevalence and Intensity of Digestive and Pulmonary Parasites in Wild Boars in Romania.

Darabus, G., F. S. Hora, N. Mederle, S. Morariu, M. Ilie, T. Suici, and M. Imre. 2019.

Journal of Zoo and Wildlife Medicine 50, no. 1 (Mar): 270-273. <https://dx.doi.org/10.1638/2018-0040>.

The prevalence and intensity of infection with digestive, liver, and pulmonary parasites in wild boars in Romania was determined by examination of 280 cadavers from 26 hunting grounds during the period 2012-2016. Eleven genera of parasites were recovered: nine within the digestive system (*Eimeria*, *Ascaris*, *Globocephalus*, *Gongylonema*, *Hyostrongylus*, *Oesophagostomum*, *Phyocephalus*, *Trichuris*, and *Macracanthorinchus*); and two (*Dicrocoelium*, *Metastrongylus*) located in the hepatic and pulmonary systems. The overall prevalence of infection was 80.7% (n = 280). Polyparasitism was found in 82.8% of positive cases. The mean intensity of parasitism was highest for pulmonary parasites (*Metastrongylus salmi*, 25.95). Regarding gastrointestinal parasites, the highest mean intensity occurred in the case of *Oesophagastomum dentatum* infections (22.14), whilst the lowest was that of *Macracanthorhynchus hirudinaceus* (1.66). Wild boars are an important source of infection for domestic pigs in Romania and neighboring countries where extensive breeding systems occur.

Interaction of Historical and Modern Sardinian African Swine Fever Viruses with Porcine and Wild-Boar Monocytes and Monocyte-Derived Macrophages.

Dei Giudici, S., G. Franzoni, P. Bonelli, D. Bacciu, G. Sanna, P. P. Angioi, M. Ledda, G. Pilo, P. Nicolussi, and A. Oggiano. 2019a.

Archives of Virology 164, no. 3 (Mar): 739-745. <https://dx.doi.org/10.1007/s00705-018-04140-6>.

African swine fever (ASF) is a contagious viral disease of wild and domestic pigs that is present in many parts of Africa, Asia and Europe, including Sardinia (Italy). Deletions in the EP402R and B602L genes have been found in almost all ASF virus (ASFV) strains circulating in Sardinia from 1990 onwards, and modern Sardinian strains (isolated after 1990) might have acquired some selective advantage compared to historical ones (isolated before 1990). Here, we analysed the host cell responses of wild boars and domestic pigs upon infection with virus variants. Higher intracellular levels of the late protein p72 were detected after infection with the modern strain 22653/14 compared to the historical strain Nu81.2, although both isolates grew at the same rate in both monocytes and monocyte-derived macrophages. Higher cytokine levels in the supernatants of ASFV-infected pig monocytes compared to pig macrophages and wild-boar cells were detected, with no differences between isolates.

Phylogenetic Analysis of Porcine Circovirus Type 2 in Sardinia, Italy, Shows Genotype 2d Circulation among Domestic Pigs and Wild Boars.

Dei Giudici, S., A. Lo Presti, P. Boneili, P. P. Angioi, G. Sanna, S. Zinelli, F. Balzano, F. Sails, M. Ciccozzi, and A. Oggiano. 2019b.

Infection Genetics and Evolution 71 (Jul): 189-196.





New literature on Suiformes

<https://dx.doi.org/10.1016/j.meegid.2019.03.013>.

Porcine circovirus type 2 (PCV2) is associated with multi-factorial syndromes, commonly known as porcine-circovirus-associated diseases, which cause severe economic losses in the swine industry worldwide. Four genotypes (PCV2a, PCV2b, PCV2c, and PCV2d) have been identified. Lately, the prevalence of PCV2d has been increasing in many countries, thereby prefiguring a global replacement of PCV2b. Wild boars are also susceptible to PCV2 infection, with virus prevalence similar to that of domestic pigs. This work was aimed at expanding the knowledge about the molecular epidemiology of PCV2 in Italy. For this purpose, we analysed 40 complete ORF-2 sequences from PCV2 strains isolated from domestic pigs and wild boars in Sardinia (Italy) over a period of 5 years (2009-2013). Phylogenetic and Bayesian analyses were performed on three data sets compiled from DNA sequences over a large geographical area. PCV2b was found to be dominant in Sardinia, whereas no PCV2a and PCV2c were found. This study indicates the presence of genotype PCV2d-2 infecting both domestic and wild pigs, thus confirming its circulation in Italy. Sardinian sequences clustered mostly with Italian isolates and with strains from China, Belgium, Croatia, Taiwan, Korea, and Portugal. Genetic variability of PCV2 in Sardinia appears to be a result of both local viral evolution and different epidemic introduction events.

Quantification and Genetic Diversity of Hepatitis E Virus in Wild Boar (*Sus Scrofa*) Hunted for Domestic Consumption in Central Italy.

Di Pasquale, S., P. De Santis, G. La Rosa, K. Di Domenico, M. Iaconelli, G. Micarelli, E. Martini, S. Bilei, D. De Medici, and E. Suffredini. 2019.

Food Microbiology 82 (Sep): 194-201. <https://dx.doi.org/10.1016/j.fm.2019.02.005>.

Hepatitis E is an emerging disease in industrialized countries. The food-borne transmission of hepatitis E virus (HEV) is associated principally with products derived from the domestic pig, the wild boar, and deer; however, few quantitative data are available on HEV loads in animals used in food production. This study assessed HEV occurrence, viral load and genetic variability in wild boar hunted for domestic consumption in the district of Viterbo (Central Italy) where high anti-HEV IgG seroprevalence values are reported in humans. A total of 332 liver and 69 intestine samples were obtained from wild boar hunted between 2011 and 2014. The liver tissue in 54 of the animals (16.3%) was HEV-positive. Viral loads in quantifiable liver samples (n=29) ranged between 3.2×10^2 and 3.8×10^5 genome copies (g.c.)/g with a mean value of 1.85×10^4 g.c./g. A statistically significant positive correlation was found between viral concentration in liver and intestinal tissue, though mean viral load in the intestines was lower (3.13×10^3 g.c./g). Twenty-six samples were characterized molecularly as genotype 3 (G3) and four subtypes (a, c, f and l) were detected. Finally, twelve samples with near identical sequences were identified as G3 but could not be assigned to any of the known subtypes, and could therefore represent a potentially new subtype.

Molecular Detection of *Mycoplasma suis* in Captive White-Lipped Peccaries (*Tayassu pecari*) and Wild Boars (*Sus scrofa*) in Brazil.

Dias, G. B., R. B. do Amaral, I. R. H. Gatto, I. M. Lapera, L. G. de Oliveira, E. G. L. Hoppe, R. Z. Machado, and M. R. Andre. 2019.

Comparative Immunology Microbiology and Infectious Diseases 63 (Apr): 94-96.

<https://dx.doi.org/10.1016/j.cimid.2019.01.013>.





New literature on Suiformes

Mycoplasma suis, the etiological agent of swine hemoplasmosis, is an epicellular bacterium that adheres to the surface of pig erythrocytes leading to deformations of the target cells. Little is known about the occurrence of *M. suis* in wild swine populations around the world, its economic impact on swine herds, and the risk of human infection. The aim of this study was to investigate, by quantitative real-time PCR (qPCR) based on the 16S rRNA gene, the occurrence of *M. suis* in a captive population of white-lipped peccaries (100 *Tayassu pecari*) and in free-living wild boars (14 *Sus scrofa*) in Brazil. None of the white-lipped peccaries were positive for *M. suis*, whereas seven (50%) wild boars were positive in qPCR assays. The quantification of *M. suis*-16S rRNA copies/mu L ranged from 1.42×10 degrees to $3.906 \times 10(1)$ in positive animals, indicating a low bacteremia and a chronic carrier status in free-living wild boars. In conclusion, *M. suis* might be a non-frequent pathogen in wild suids maintained in captivity. Despite the low bacteremia, the prevalence of *M. suis* in wild boar population in Brazil seems to be high.

Systematization and Description of the Arterial Blood Supply of the Paleopallia Areas in the Brain Surface of the Wild Boar (*Sus Scrofa Scrofa*).

do Nascimento, P. B., J. C. D. Oliveira, and R. Campos. 2019.

Acta Scientiae Veterinariae 47 (Feb). <https://dx.doi.org/10.22456/1679-9216.90141>.

Background: The study was performed on wild boar (*Sus scrofa scrofa*) which is a wild ancestor of the domestic pig and is not part of Brazilian fauna. The arterial blood supply of the encephalus has been studied by some researchers, who have systematized the cerebral blood supply from the rostral' and caudal epidural rete mirabile and its sources in wild boar until the blood supply of the base of the brain. The objective was to improve the understanding of the arterial blood supply of the brain, particularly the paleopallium, of the wild boar and to provide a reference for comparative anatomy studies. **Materials, Methods & Results:** A total of 30 brains were obtained from an officially authorised slaughterhouse and approved by Brazilian Institute of Environment and Natural Renewable Resources. The animals were desensitized, followed by bleeding of the jugular veins and common carotid arteries near the entrance of the thorax, according to the slaughter procedure. Finally, the animals were decapitated at the level of axis vertebra. The cerebral arterial system of each animal was rinsed (cooled saline containing 2500 IU of heparin) and drained by the jugular veins, and vessels were filled with latex 603 stained with specific red dye. The heads were submerged for one hour in running water immersed in 20% formaldehyde for fixation; the brains were removed along with a cervical segment of the spinal cord. The duramater was removed, and the arteries were dissected. Schematic drawings of the ventral view of the all preparations were made using magnifying glasses and photographic records. The Nomina Anatomica Veterinaria was used to name the cerebral arteries and their branches, and calculation of percentages was applied in the statistical analysis. The cerebral carotid artery originating from the rostral' epidural rete mirabile emitted a rostral branch and a caudal branch on the side of the hypophysis gland. The rostral' branch emitted one to three middle cerebral arteries and continued as rostral cerebral artery. The latter emitted the superficial and perforating central arteries, lateral rhinal artery, ethmoidal artery, medial branch and medial rhinal artery. **Discussion:** Wild boar is a macrosmatic animal, it presents well-developed areas of the paleopallium that are exclusively olfactory. Its extensive paleopallium was nourished by branches of the rostral' cerebral artery and its collateral branches, including the lateral rhinal, ethmoidal, and medial branch and the medial rhinal artery. The rostral' cerebral arteries and their collateral branches supplied blood to the olfactory bulb, olfactory peduncle, two-thirds of the lateral olfactory tract, medial olfactory tract and rostral' two-thirds of the olfactory trigone. The medial cerebral arteries within the lateral





New literature on Suiformes

fossa of the brain, emitted superficial rostral central branches to the paleopallium, perforating central branches (striated) to the lateral fossa of the brain and caudal third of the olfactory trigone and caudal central branches to the piriform lobe. The rostral most two-thirds of a small medial band of the piriform lobe was vascularised by central branches originating mainly from the rostral branch of the cerebral carotid artery. The paleopallium in the wild boar was nourished by branches of the cerebral rostral, middle and caudal arteries and by the central branches of the cerebral carotid artery. The arterial blood supply of the paleopallium in the wild boar was compared to the chinchilla, nutria, rabbit and pampas fox. Three cerebral vessels were mainly responsible for the emission of the central branches that supplied blood to the paleopallium, namely the middle, rostral, and caudal cerebral arteries. The differences or variations among these species were due to the type of cerebral blood supply in the formation of the cerebral arterial circle.

A Wild Circulation: High Presence of Porcine Circovirus 3 in Different Mammalian Wild Hosts and Ticks.

Franzo, G., L. Grassi, C. M. Tucciarone, M. Drigo, M. Martini, D. Pasotto, A. Mondin, and M. L. Menandro. 2019.

Transboundary and Emerging Diseases 66, no. 4 (Jul): 1548-1557.

<https://dx.doi.org/10.1111/tbed.13180>.

Porcine circovirus 3 (PCV-3) has emerged as a potential threat for swine industry, being consistently reported in the presence of several clinical signs all around the world. Recently, its presence in wild boar has been demonstrated at high prevalence. This evidence is surprising since the lower density of wild populations might not be expected to sustain such efficient viral transmission. Porcine circoviruses were proven to exhibit a certain plasticity in the host tropism and were detected in unrelated species, like mice, dogs and ruminants. However, if this scenario applies also to wild animals remains to be established. Therefore, this study aimed to investigate the presence of PCV-3 in wild ungulates other than wild boar and in related hematophagous ectoparasites. One hundred and nine animals were sampled from different hilly and mountain areas of Friuli Venezia Giulia, including 9 chamois (*Rupicapra rupicapra*), 17 red deer (*Cervus elaphus*), 4 mouflons (*Ovis musimon*), 50 roe deer (*Capreolus capreolus*) and 29 wild boars (*Sus scrofa*). Additionally, host-matched ectoparasites were collected when present. Porcine circovirus 3 was diagnosed using molecular techniques and sequencing. This study results confirmed the high PCV-3 occurrence in wild boar and reported for the first time its presence, at low prevalence, in chamois and roe deer. Moreover, two ticks (*Ixodes ricinus*), one of which non-engorged, collected from PCV-3 negative roe deer, tested PCV-3 positive. The genetic characterization of some of the strains collected from non-swine hosts allowed to prove that, albeit clearly part of PCV-3 species, they were genetically unique, demonstrating the absence of among-samples contamination and thus confirming the actual presence of PCV-3 genome in these new hosts. Therefore, this study highlights an unexpected broad PCV-3 distribution and circulation in the wild, rising further questions on porcine circoviruses infectious cycle, epidemiology and origin, which will deserve additional investigations.

Prevalence and Molecular Characterisation of *Sarcocystis Miescheriana* and *Sarcocystis Suihominis* in Wild Boars (*Sus Scrofa*) in Italy.

Gazzonis, A. L., B. Gjerde, L. Villa, S. Minazzi, S. A. Zanzani, P. Riccaboni, G. Sironi, and M. T.





New literature on Suiformes

Manfredi. 2019.

Parasitology Research 118, no. 4 (Apr): 1271-1287. <https://dx.doi.org/10.1007/s00436-019-06249-2>.

A sample of the diaphragm was collected from each of 100 wild boars legally hunted in the Val Grande National Park in north-western Italy and examined for the presence of *Sarcocystis* infection by histological and molecular methods. In histological sections, thick-walled sarcocysts consistent with those of *Sarcocystis miescheriana* were detected in 32 wild boars. Genomic DNA extracted from diaphragm samples was initially subjected to PCR amplification of the internal transcribed spacer 1 (ITS1) region, and 97 wild boars were found to harbour a *Sarcocystis* infection at this screening. Selected DNA samples were then subjected to PCR amplification and sequencing of the ITS1 region and the 18S and 28S ribosomal RNA (rRNA) genes of the nuclear ribosomal DNA unit, while all positive samples were subjected to PCR amplification of the mitochondrial cytochrome c oxidase subunit I (cox1) gene. *S. miescheriana* was identified in 97 wild boars (97%), while the zoonotic *Sarcocystis suisominis* was identified in one wild boar (1%), which also harboured *S. miescheriana*. Intra-specific sequence variation was found in all four DNA regions of *S. miescheriana* examined and in the 18S rRNA gene and ITS1 region of *S. suisominis*. The partial cox1 gene was amplified and sequenced from 72 isolates of *S. miescheriana*, yielding 43 haplotypes with pairwise sequence identities of 97.6-99.9%. These haplotypes were 79.1-79.8% identical with the cox1 sequence of *S. suisominis*. Phylogeny based on cox1 sequences placed *S. miescheriana* and *S. suisominis* as sister species within a clade comprising mainly *Sarcocystis* spp. of ruminants with felids as known or presumed definitive hosts. The same was true for the phylogeny based on 18S rRNA gene sequences.

Simulation of Transmission and Persistence of African Swine Fever in Wild Boar in Denmark.

Halasa, T., A. Boklund, A. Botner, S. Mortensen, and L. J. Kjaer. 2019.

Preventive Veterinary Medicine 167 (Jun): 68-79.

<https://dx.doi.org/10.1016/j.prevetmed.2019.03.028>.

African swine fever (ASF) is caused by ASF virus (ASFV) and is currently circulating in the eastern part of Europe posing a serious risk regarding transmission to western European countries. Wild boar is a main driver of the transmission and persistence of ASFV in the endemic infected countries in Europe. Some European countries free from ASF, such as Denmark and the Netherlands, have limited population sizes of wild boar, but have large swine productions. In these countries, the patterns of transmission and persistence of ASFV in the existing wild boar population, in case of introduction of ASFV, are unknown. It is important to get a better understanding of ASFV in these wild boar populations, in order to better manage the existing wild boar population and thereby minimize the risk of virus introduction and transmission to domestic pigs, in case of an ASFV incursion. We created an agent-based spatio-temporal model and simulated the transmission of ASFV within Danish wild boar populations, using actual landscape data. The model was run with 50 and 100 wild boar groups used as initial population sizes, respectively, either distributed across the southern part of the mainland (Jutland) or across both the southern and middle parts of Jutland, where wild boar groups are believed to exist. At first, the model was run without ASFV for 25 years to assess wild boar population dynamics in both regions. Thereafter, ASFV was added to the model 1 year after initiation and run for up to another 4 years. The model predicted that wild boar populations may increase drastically over the next 25





New literature on Suiformes

years, if wild boar groups were distributed across both southern and middle Jutland and no mitigation actions were taken, while the population sizes will be restricted, if groups were distributed only across the southern part of Jutland. The density of the population is an important factor affecting the transmission and persistency of the disease. Model results indicated that ASF epidemics in the simulated populations would generally persist for few months. However, due to the high stochasticity of the process, in certain situations the epidemics may last for more than one year, posing a serious risk of ASFV introduction to domestic pigs.

Level of Endoparasite Infection in Free-Living Wild Boars in Relation to Carcass Weight and Sex.

Jankowska-Makosa, A., D. Knecht, J. Nicpon, and K. Duzinski. 2019.

Medycyna Weterynaryjna-Veterinary Medicine-Science and Practice 75, no. 4 (Apr): 232-237.

<https://dx.doi.org/10.21521/mw.6144>.

Research into the determination of intestinal parasitic levels in free-living animals can provide knowledge enabling action to be taken to improve their health status. The aim of the study was to determine the relationship between the carcass weight of wild boars and the degree of endoparasite infection. The research was performed on 165 culled wild boars, from which a representative group ($n = 50$) was separated and divided according to sex (males $n = 24$, females $n = 26$) and age (2-3 years). Separate weight groups were defined for males (< 70 kg, $n = 6$; 70-80 kg, $n = 9$; > 80 kg, $n = 9$) and females (< 45 kg, $n = 10$; 45-60 kg, $n = 10$; > 60 kg, $n = 6$). *Oesophagostomum* spp., *Ascaris suum*, *Trichuris suis*, *Eimeria* spp. and *Strongyloides ransomi* were observed and defined in the study population. A statistically significant effect of the overall infection on carcass weight was obtained ($F = 9.96$; $P \leq 0.01$). In the case of overall infection, a more than 7 kg lower carcass weight was observed in infected males. A carcass weight over 15 kg lower was noted for overall infection of females ($F = 38.47$; $P \leq 0.01$), for which average EPG was 2946.67 ± 6485.31 with a median of 400 (50-25 300). Correlations were proven between sex and the average number of *Eimeria* spp. oocysts, and carcass weight for males ($r = -0.84$, $P \leq 0.05$). In the case of females, correlations were noted between carcass weight and infection by nematodes ($r = -0.63$, $P \leq 0.05$). Studies have shown that there is a need to monitor the environment in order to improve the condition of free-living animals.

Genetic Diversity of Hepatitis E Virus (Hev) Strains Derived from Humans, Swine and Wild Boars in Croatia from 2010 to 2017.

Jemersic, L., J. Prpic, D. Brnic, T. Keros, N. Pandak, and O. D. Rode. 2019.

Bmc Infectious Diseases 19 (Mar). <https://dx.doi.org/10.1186/s12879-019-3906-6>.

Background To fulfill epidemiological data and investigate possible interspecies transmission, this study shall attempt to sequence representative HEV strains of human, swine and wild boar origin collected from 2010 to 2017 in Croatia. **Methods** In total, 174 anti-HEV antibody positive human sera samples; 1419 blood or faeces samples of swine, as well as 720 tissue and/or blood samples of wild boar originating from different counties (18 in total) in Croatia were tested for the presence of HEV RNA. **Results** HEV RNA was detected in 26 human sera samples (14.9%; 95% CI 10.4-21.0%). HEV RNA was detected in 216 tested swine (15.2%; 95% CI 13.5-17.1%), regardless of age, farm breeding system or geographical origin. Viral RNA was also detectable in faeces samples which prove that swine actively participate in shedding HEV into the environment. Of the total of 720 tested wild boar samples, 83 were HEV RNA positive (11.5, 95%





New literature on Suiformes

CI 9.4-14.1%) originating from six counties. According to the sequence analysis all strains have shown to be members of Orthohepevirus A genotype HEV-3, regardless of host. The genotyping results confirm grouping of sequences into four subtypes of HEV strains of which subtypes 3a and 3c belong to the general cluster 3abchij, and were predominately detected during the study, while subtypes 3e and 3f fall within cluster 3efg. Strains within subtypes 3a and 3e were found in humans, swine and wild boars; subtype 3c strains were derived from humans and swine, whereas subtype 3f strains were found only in humans. Strains belonging to subtypes 3a and 3c were derived during the entire investigated period and may be considered endemic in Croatia, whereas strains within subtypes 3e and 3f were detected sporadically indicating the possibility of newly imported infections. Conclusions All detected strains show to be genetically highly related to strains found in humans and/or animals from other European Countries, indicating that trade of live animals or wild boar movement increases the risk of HEV infection spread. Furthermore, homologous strains found in different investigated species within this study indicate interspecies transmission of HEV and/or an existence of an accessible mutual source of infection.

Differentiation between Wild Boar and Domestic Pig in Food by Targeting Two Gene Loci by Real-Time Pcr.

Kaltenbrunner, M., W. Mayer, K. Kerkhoff, R. Epp, H. Ruggeberg, R. Hochegger, and M. Cichnawski. 2019.

Scientific Reports 9 (Jun). <https://dx.doi.org/10.1038/s41598-019-45564-7>.

Studies indicate that many meat products are not authentic, most frequently because the meat species differ from those given on the food labels. At present, DNA based methods play the most important role in meat species authentication. Discrimination of wild boar and domestic pig meat in food is challenging because it is differentiation on the subspecies level. We developed and validated two singleplex real-time PCR assays targeting SNP rs81416363 on chromosome 9 and a duplex real-time PCR assay targeting SNP g.299084751C > T in the NR6A1 gene located on chromosome 1. The singleplex real-time PCR assays led to some ambiguous results for Mangalica and Krskopolje pig breeds and wild boar individuals from Germany, the duplex real-time PCR assay particularly for the Turopolje pig breed. We demonstrate that the probability of misclassification can be substantially reduced if the results of both the singleplex real-time PCR assays and the duplex real-time PCR assay are taken into consideration. 86 (91.5%) of a total of 94 individuals, comprising 64 domestic pigs (14 different breeds and 6 cross-breeds) and 30 wild boars (from Austria, Germany, Romania, USA and Estonia), were classified correctly.

Genetic Variability of Porcine Pegivirus in Pigs from Europe and China and Insights into Tissue Tropism.

Kennedy, J., V. M. Pfankuche, D. Hoeltig, A. Postel, O. Keuling, M. Ciurkiewicz, W. Baumgartner, P. Becher, and C. Baechlein. 2019.

Scientific Reports 9 (Jun). <https://dx.doi.org/10.1038/s41598-019-44642-0>.

Pegiviruses belong to the family Flaviviridae and have been found in humans and other mammalian species. To date eleven different pegivirus species (Pegivirus A-K) have been described. However, little is known about the tissue tropism and replication of pegiviruses. In 2016, a so far unknown porcine pegivirus (PPgV, Pegivirus K) was described and persistent infection in the host, similar to human pegivirus, was reported. In this study, qRT-PCR, phylogenetic analyses and fluorescence in situ hybridization (FISH) were implemented to detect





New literature on Suiformes

and quantify PPgV genome content in serum samples from domestic pigs from Europe and Asia, in tissue and peripheral blood mononuclear cell (PBMC) samples and wild boar serum samples from Germany. PPgV was detectable in 2.7% of investigated domestic pigs from Europe and China (viral genome load $2.4 \times 10(2)$ to $2.0 \times 10(6)$ PPgV copies/ml), while all wild boar samples were tested negative. Phylogenetic analyses revealed pairwise nucleotide identities >90% among PPgVs. Finally, PPgV was detected in liver, thymus and PBMCs by qRT-PCR and FISH, suggesting liver- and lymphotropism. Taken together, this study provides first insights into the tissue tropism of PPgV and shows its distribution and genetic variability in Europe and China.

Ticks and Serosurvey of Anti-Rickettsia Spp. Antibodies in Wild Boars (*Sus Scrofa*), Hunting Dogs and Hunters of Brazil.

Kmetiuk, L. B., F. S. Krawczak, F. P. Machado, I. A. D. Paploski, T. F. Martins, P. I. Teider, M. C. A. Serpa, A. R. M. Barbieri, R. V. W. Bach, I. R. Barros, L. C. Lipinski, A. P. dos Santos, M. B. Labruna, and A. W. Biondo. 2019.

Plos Neglected Tropical Diseases 13, no. 5 (May).

<https://dx.doi.org/10.1371/journal.pntd.0007405>.

Background Rickettsia bacteria are responsible for diseases in humans and animals around the world, however few details are available regarding its ecology and circulation among wild animals and human populations at high transmission risk in Brazil. The aim of this study was to investigate the occurrence of ticks and *Rickettsia* spp. in wild boars, corresponding hunting dogs and hunters. Methods: Serum samples and ticks were collected from 80 free-range wild boars, 170 hunting dogs and 34 hunters from southern and central-western Brazil, from the Atlantic Forest and Cerrado biomes, respectively, between 2016 and 2018. Serum samples were tested by indirect immunofluorescent-antibody assay (IFA) to detect IgG antibodies against *Rickettsia rickettsii*, *Rickettsia parkeri*, *Rickettsia bellii*, *Rickettsia rhipicephali* and *Rickettsia amblyommatis*. Tick species were identified by morphological taxonomic keys, as previously described. A total of 164 ticks including *A. sculptum*, *A. brasiliense* and *A. aureolatum* were tested in PCR assays for Spotted Fever Group (SFG) *Rickettsia* spp. Results A total of 58/80 (72.5%) wild boars, 24/170 (14.1%) hunting dogs and 5/34 (14.7%) hunters were positive (titers 64) to at least one *Rickettsia* species. A total of 669/1,584 (42.2%) ticks from wild boars were identified as *Amblyomma sculptum*, 910/1,584 (57.4%) as *Amblyomma brasiliense*, 4/1,584 (0.24%) larvae of *Amblyomma* spp. and 1/1,584 (0.06%) nymph as *Amblyomma dubitatum*. All 9 ticks found on hunting dogs were identified as *Amblyomma aureolatum* and all 22 ticks on hunters as *A. sculptum*. No tested tick was positive by standard PCR to SFG *Rickettsia* spp. Conclusions The present study was the concomitant report of wild boar, hunting dog and hunter exposure to SFG rickettsiae agents, performed in two different Brazilian biomes. Wild boar hunting may increase the risk of human exposure and consequently tick-borne disease. Wild boars may be carrying and spreading capybara ticks from their original habitats to other ecosystems. Further studies can be required to explore the ability of wild boars to infect ticks and be part of transmission cycle of *Rickettsia* spp. Author summary The present study reported serological findings and molecular assays of *Rickettsia* spp and ticks of wild boars, simultaneous to their correspondent hunting dogs and hunters. Seropositivity for *Rickettsia* spp. was higher in wild boars when compared to dogs and humans but was similar between dogs and humans. Despite *Rickettsia* spp. prevalence was statistically higher in southern than central-western Brazil for wild boars, no significance was observed in hunting dogs and hunters. For the first time, *A. sculptum* ticks were founded in wild





New literature on Suiformes

boars from the subtropical climate of southern Brazil. Despite human beings have been considered less exposed to ticks (and therefore rickettsiae) than animals, specific human activities such as wild boar hunting may increase the risk of exposure and consequently tick-borne disease. Wild boars may be carrying and spreading capybara ticks from their original habitats to other ecosystems. These results may provide important findings for public action planning to prevent neglected vector-borne diseases in overlapping areas of wild boars, hunting dogs and hunters. Further studies can be required to explore the ability of wild boars to infecting ticks and be part of transmission cycle of *Rickettsia* spp.

Cross-Border Transmission of *Salmonella Choleraesuis* Var. Kunzendorf in European Pigs and Wild Boar: Infection, Genetics, and Evolution.

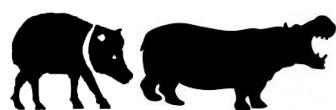
Leekitcharoenphon, P., G. Sorensen, C. Lofstrom, A. Battisti, I. Szabo, D. Wasyl, R. Slowey, S. H. Zhao, A. Brisabois, C. Kornschober, A. Karssin, J. Szilard, T. Cerny, C. A. Svendsen, K. Pedersen, F. M. Aarestrup, and R. S. Hendriksen. 2019.

Frontiers in Microbiology 10 (Feb). <https://dx.doi.org/10.3389/fmicb.2019.00179>.

Salmonella enterica subspecies *enterica* serotype *Choleraesuis* is a swine adapted serovar. *S. Choleraesuis* variant Kunzendorf is responsible for the majority of outbreaks among pigs. *S. Choleraesuis* is rare in Europe, although there have been serious outbreaks in pigs including two outbreaks in Denmark in 1999-2000 and 2012-2013. Here, we elucidate the epidemiology, possible transmission routes and sources, and clonality of European *S. Choleraesuis* isolates including the Danish outbreak isolates. A total of 102 *S. Choleraesuis* isolates from different European countries and the United States, covering available isolates from the last two decades were selected for whole genome sequencing. We applied a temporally structured sequence analysis within a Bayesian framework to reconstruct a temporal and spatial phylogenetic tree. MLST type, resistance genes, plasmid replicons, and accessory genes were identified using bioinformatics tools. Fifty-eight isolates including 11 out of 12 strains from wild boars were pan-susceptible. The remaining isolates carried multiple resistance genes. Eleven different plasmid replicons in eight plasmids were determined among the isolates. Accessory genes were associated to the identified resistance genes and plasmids. The European *S. Choleraesuis* was estimated to have emerged in similar to 1837 (95% credible interval, 1733-1983) with the mutation rate of 1.02 SNPs/genome/year. The isolates were clustered according to countries and neighbor countries. There were transmission events between strains from the United States and European countries. Wild boar and pig isolates were genetically linked suggesting cross-border transmission and transmission due to a wildlife reservoir. The phylogenetic tree shows that multiple introductions were responsible for the outbreak of 2012-2013 in Denmark, and suggests that poorly disinfected vehicles crossing the border into Denmark were potentially the source of the outbreak. Low levels of single nucleotide polymorphisms (SNPs) differences (0-4 SNPs) can be observed between clonal strains isolated from different organs of the same animal. Proper disinfection of livestock vehicles and improved quality control of livestock feed could help to prevent future spread of *S. Choleraesuis* or other more serious infectious diseases such as African swine fever (ASF) in the European pig production system.

Infection of African Swine Fever in Wild Boar, China, 2018.

Li, L., Z. W. Ren, Q. H. Wang, S. Q. Ge, Y. T. Liu, C. J. Liu, F. X. Liu, Y. X. Hu, J. M. Li, J. Y. Bao, W. J. Ren, Y. Q. Zhang, T. G. Xu, C. Y. Sun, S. J. Wang, X. X. Fan, Z. B. Wu, B. X. Huang, H. C.





New literature on Suiformes

Guo, X. D. Wu, and Z. L. Wang. 2019.

Transboundary and Emerging Diseases 66, no. 3 (May): 1395-1398.

<https://dx.doi.org/10.1111/tbed.13114>.

On 16 November 2018, a wild boar infected with African swine fever was reported in China. The phylogenetic analysis showed that its causative strain belonged to the p72 genotype II, CD2v serogroup 8 and contained no additional tandem repeat sequences between the I73R and the I329L protein genes, which was different from previously reported strains in China.

High Frequency of Coagulase-Positive Staphylococci Carriage in Healthy Wild Boar with Detection of Mrsa of Lineage St398-T011.

Mama, O. M., L. Ruiz-Ripa, R. Fernandez-Fernandez, D. Gonzalez-Barrio, J. F. Ruiz-Fons, and C. Torres. 2019.

Fems Microbiology Letters 366, no. 4 (Feb). <https://dx.doi.org/10.1093/femsle/fny292>.

The objective of this study was to determine the frequency and diversity of coagulase-positive staphylococci (CoPS) in nasal samples of healthy wild boar, to study their resistance phenotypes/genotypes and to check the occurrence of the MRSA-ST398. Nasal samples of 371 wild boars were collected in Spain for staphylococci and MRSA recovery. Staphylococci identification was performed by matrix-assisted laser desorption/ionization time of flight mass spectrometry (MALDI-TOF). The susceptibility to 11 antimicrobials was tested by disc-diffusion and the presence of resistance genes by PCR. Molecular typing and virulence factors determination were carried out by PCR and sequencing. The rate of CoPS carriage (*Staphylococcus aureus*, *Staphylococcus hyicus* and *Staphylococcus pseudintermedius*) in wild boar was of 17.8% (13.7%, 2.7% and 1.6%, respectively). Susceptibility to all tested antimicrobials was shown in 74.5% of *S. aureus* and one strain was MRSA [lineage ST398-t011-agrl, carrying blaZ, mecA, tet(M) and tet(K) genes]. A total of 22 spa-types and 17 STs were detected among *S. aureus*, including: ST398/CC398 (n=1), ST2328-ST133/CC133 (n=20), ST425/CC425 (n=7), ST5/CC5 (n=5), ST1/CC1 (n=3), ST130/CC130 (n=2) and ST88/CC88 (n=1). Two spa-types (t02, t15) and four STs (ST455, ST796, ST797, ST798) were detected among the six *S. pseudintermedius* isolates recovered, and all of them carried the lukF/S-I and siet virulence genes. All *S. hyicus* isolates were susceptible to antimicrobials tested.

Isolation and Molecular Characterization of a Variant of Chinese Gc-Genotype II Pseudorabies Virus from a Hunting Dog Infected by Biting a Wild Boar in Japan and Its Pathogenicity in a Mouse Model.

Minamiguchi, K., S. Kojima, K. Sakumoto, and R. Kirisawa. 2019.

Virus Genes 55, no. 3 (Jun): 322-331. <https://dx.doi.org/10.1007/s11262-019-01659-x>.

We isolated a variant of Chinese pseudorabies virus from a hunting dog with symptoms similar to Aujeszky's disease and designated the isolate MY-1 strain. The dog developed symptoms 6 days after hunting and biting a wild boar and died the day after onset. The Bam HI restriction profile of MY-1 DNA was different from those of the Japanese reference strain Yamagata-S81 and two vaccine strains, Bartha and Begonia, and resembled Bam HI-RFLP (restriction fragment length polymorphism) type IV. Complete nucleotide sequences were determined, and phylogenetic analyses revealed that MY-1 belonged to the same cluster of old Chinese strains and variant strains isolated recently in China, but most of the open reading frames of MY-1 were located on a different branch from those of these Chinese strains. Based on a gC phylogenetic analysis, MY-1





New literature on Suiformes

belonged to gC-genotype II composed of those Chinese strains. In mice, the 50% lethal dose (LD50) of MY-1 (10(3.0) TCID50) was almost the same as those of Yamagata-S81 and Bartha. The LD50 value of Begonia was 10(4.5) TCID50. The mean survival periods of mice after infection with 10(4) TCID50 of MY-1, Yamagata-S81 and Bartha were 3.9days, 2.3days, and 8.0days, respectively. The results suggested that the variant of Chinese PRV with slightly weaker pathogenicity than that of wild virulent viruses might be maintained in wild boars in Japan. Furthermore, we would like to propose that old Chinese strains, recent Chinese variant strains, and MY-1 should be grouped as an Asian type PRV.

Prevalence of *Salmonella* Spp. in Tonsils, Mandibular Lymph Nodes and Faeces of Wild Boar from Spain and Genetic Relationship between Isolates.

Molino, M. G., A. G. Sanchez, D. R. Perez, P. G. Blanco, A. Q. Molina, J. R. Perez, F. E. M. Cano, R. C. Horrillo, Jhdm Salcedo, and P. F. Llario. 2019.

Transboundary and Emerging Diseases 66, no. 3 (May): 1218-1226.

<https://dx.doi.org/10.1111/tbed.13140>.

The importance of wild boars as game species in Spain is well known. Their feeding habits and intrusive behaviour, together with a progressively wider spreading of populations, increases the interactions of these animals with livestock and humans. Considering that wild boars could have a potential role in the transmission of certain pathogens as salmonellae, the aims of this study were to determine the prevalence of *Salmonella* spp. in wild boars hunted in central-western Spain, the occurrence of this pathogen in tonsils, mandibular lymph nodes and faeces (as markers for transmission risk), and to define the phylogenetic relationships among isolated strains, in order to investigate the circulation pathways of bacteria among tissues, animals and estates. Samples from 1,041 hunted wild boars were analysed for the presence of *Salmonella* spp. by bacteriological culture. Isolates were confirmed by PCR and serotyped in the Spanish national reference laboratory. The genetic relationships between strains were determined by PFGE. The results showed a 7.7% of positive animals (81 wild boars), being tonsils the organ most frequently colonised by *Salmonella* spp. (18.7%), followed by lymph nodes (5.1%) and faecal samples (2.9%). Serovars Enteritidis and Newport were the most frequent amongst the 34 different serovars obtained. The pulsed-field gel electrophoresis (PGFE) analysis showed a great genetic diversity, with serovars that exhibited different pulsotypes when isolated from different estates and multiple serovars in the same estate. In conclusion, this study reveals the importance of wild boars as carriers and possible transmitters of virulent and/or antimicrobial-resistant clones of *Salmonella* spp. to livestock and humans.

Symmetric Undivided Diplopagus with Cardiac Malformation in a Japanese Wild Boar (*Sus Scrofa Leucomystax*).

Nakamura, T., Y. Sunden, T. Imagawa, T. Tsuka, K. Shiraishi, and T. Morita. 2019.

Journal of Veterinary Medical Science 81, no. 5 (May): 657-659.

<https://dx.doi.org/10.1292/jvms.18-0765>.

A captured Japanese wild boar (*Sus scrofa leucomystax*) fetus was dicephalic. The fetus had two heads, but one body from the cranial neck region. Computed tomography imaging revealed that the two crania merged at the occipital bone, and the vertebral bodies between the atlas and the seventh thoracic vertebra were deformed. The fetus was found to have two tongues and laryngopharynges, but its esophagus and trachea were not duplicated. Each head contained a





New literature on Suiformes

cerebrum and cerebellum, but the brains merged at the obex of the medulla oblongata, and the cervical spinal cord had duplicated ventral clefts. The heart was composed of three atria and four ventricles. This is the first report of a dicephalus with cardiac malformation in a wild boar.

The Genetics of Life and Death: Virus-Host Interactions Underpinning Resistance to African Swine Fever, a Viral Hemorrhagic Disease.

Netherton, C. L., S. Connell, C. T. O. Benfield, and L. K. Dixon. 2019.

Frontiers in Genetics 10 (May). <https://dx.doi.org/10.3389/fgene.2019.00402>.

Pathogen transmission from wildlife hosts to genetically distinct species is a major driver of disease emergence. African swine fever virus (ASFV) persists in sub-Saharan Africa through a sylvatic cycle between warthogs and soft ticks that infest their burrows. The virus does not cause disease in these animals, however transmission of the virus to domestic pigs or wild boar causes a hemorrhagic fever that is invariably fatal. ASFV transmits readily between domestic pigs and causes economic hardship in areas where it is endemic. The virus is also a significant transboundary pathogen that has become established in Eastern Europe, and has recently appeared in China increasing the risk of an introduction of the disease to other pig producing centers. Although a DNA genome mitigates against rapid adaptation of the virus to new hosts, extended epidemics of African swine fever (ASF) can lead to the emergence of viruses with reduced virulence. Attenuation in the field leads to large deletions of genetic material encoding genes involved in modulating host immune responses. Therefore resistance to disease and tolerance of ASFV replication can be dependent on both virus and host factors. Here we describe the different virus-host interfaces and discuss progress toward understanding the genetic determinants of disease outcome after infection with ASFV.

Mitochondrial Diversity of the East Balkan Swine (*Sus Scrofa F. Domestica*) in South-Eastern Bulgaria.

Palova, N., I. Yankova, B. Neov, P. Hristov, and G. Radoslavov. 2019.

Acta Veterinaria-Beograd 69, no. 2 (Jun): 229-236. <https://dx.doi.org/10.2478/acve-2019-0018>.

The East Balkan Swine (EBS) is the only preserved local swine breed in Bulgaria and one of the few indigenous pig breeds in Europe. The EBS is distributed in the region of Eastern Balkan Mountains and the Strandja Mountain. To reveal the breed's genetic profile, we analyzed 50 purebred individuals according to mitochondrial DNA (D-loop region, HVR1) and sequence analysis in the Scientific Center of Agriculture (Sredets region) in the country. The obtained results show the presence of four haplotypes: three Asian specific haplotypes (H1, H2, and H3) and the European specific E1a1. The haplotypes H2 (6 %) and H3 (2 %) were newly described and were branched from the basic clade H1 (90 %). All haplotypes belong to the Asiatic clade A (98 %), except one sample assigned to the European haplogroup E1 (2 %) in contrast to samples from East North Bulgaria where Asiatic and European clades were with almost equal distribution. The coexistence of two mtDNA clades in EBS in Bulgaria may be related to the source of the pig populations and/or the historical crossbreeding with imported pigs. In conclusion, due to its native origin, the East Balkan Swine may be the only possible option for a solution to the exhaustion of the beneficial genetic variation of available cultural breeds. With its participation, high-productive populations can be restored and established after a long and purposeful selection.

Pathomorphological Studies on Wild Boars Infected with *Metastrongylus* Spp., *Ascarops Strongylina*, and *Macracanthorhynchus Hirudinaceus*.





New literature on Suiformes

Panayotova-Pencheva, M., K. Todorova, and V. Dakova. 2019. Journal of Veterinary Research 63, no. 2 (Jun): 191-195. <https://dx.doi.org/10.2478/jvetres-2019-0037>.

Introduction: Pathomorphological changes in the lungs, stomach, and small intestines of wild boars infected with *Metastrongylus* spp., *Ascarops strongylina*, and *Macracanthorhynchus hirudinaceus* were investigated. **Material and Methods:** Dissection of 11 wild boars was performed, and parasitised organs were histologically investigated by common techniques. **Results:** Macroscopic lesions in the lungs infected with *Metastrongylus* spp. were seen within the apical parts of the large lobes, irregular in form, pale greyish in colour, and compact in consistency. The main pathohistological findings were: the presence of parasite forms, and lymphocytes and neutrophils in the lumen of bronchi and bronchioles, desquamation of the bronchial and bronchiolar epithelium, emphysema, thickening of alveolar septa, hyperaemia, alveolitis, infiltration of the interstitial tissue with giant cell, monocytes and eosinophils, and peribronchial and disseminated lymphoid hyperplasia. The principal observations accompanying infection with *A. strongylina* were inflammation and focal mucosal damage in the stomach, the latter clearly demarcated from the surrounding tissues. Severe injuries in the place of attachment of *M. hirudinaceus* to the wall of the small intestine were seen. Intestinal villi, underlying mucosa, and submucosa were destroyed, and an intense inflammatory reaction was present. **Conclusion:** The histopathological lesions showed wide diversity, varying from mild to severe; but none of them were lethal.

Assessment of Microbial Communities on Freshly Killed Wild Boar Meat by MalDI-ToF Ms and 16s Rrna Amplicon Sequencing.

Peruzy, M. F., N. Murru, Z. Yu, P. J. Kerkhof, B. Neola, M. Joossens, Y. T. R. Proroga, and K. Houf. 2019.

International Journal of Food Microbiology 301 (Jul): 51-60.

<https://dx.doi.org/10.1016/j.ijfoodmicro.2019.05.005>.

Wild boars (*Sus scrofa*) are the most widely distributed large mammals and recent increase in consumption of wild boar meat urges the need of microbiological quality criteria. The aim of the study was to characterize the initial bacterial contamination on freshly-killed wild boar meat using a culture-dependent approach with ISO-methods combined with matrix-assisted laser desorption/ionization time-of-flight mass spectrometry identification and 16S rRNA amplicon sequencing. Moreover, the presence of foodborne pathogens was examined using Real-Time-PCR and confirmed by classical isolation. Analysing 22 unrelated wild boar meat samples showed a higher bacterial contamination level compared to pork, with *Salmonella* present in almost one third of the samples. A great variability of the microbial contamination between the samples was recorded, as well as complementary results between culturing and 16S rRNA amplicon sequencing as frequently isolated genera were not always detected, and vice versa. Furthermore, the foodborne pathogen *Salmonella* was never detected with 16S rRNA amplicon sequencing, demonstrating the necessity for a cautious approach in the implementation of new analysis techniques in food safety. The present work determines that attention should be paid to the trade of non-inspected meat directly to retail or consumers.





New literature on Suiformes

Signatures of De-Domestication in Autochthonous Pig Breeds and of Domestication in Wild Boar Populations from Mc1r and Nr6a1 Allele Distribution.

Ribani, A., V. J. Utzeri, C. Geraci, S. Tinarelli, M. Djan, N. Velickovic, R. Doneva, S. Dall'Olio, L. N. Costa, G. Schiavo, S. Bovo, G. Usai, M. Gallo, C. Radovic, R. Savic, D. Karolyi, K. Salajpal, K. Gvozdanovic, I. Djurkin-Kusec, M. Skrlep, M. Candek-Potokar, C. Ovilo, and L. Fontanesi. 2019. Animal Genetics 50, no. 2 (Apr): 166-171. <https://dx.doi.org/10.1111/age.12771>.

Autochthonous pig breeds are usually reared in extensive or semi-extensive production systems that might facilitate contact with wild boars and, thus, reciprocal genetic exchanges. In this study, we analysed variants in the melanocortin 1 receptor (MC1R) gene (which cause different coat colour phenotypes) and in the nuclear receptor subfamily 6 group A member 1 (NR6A1) gene (associated with increased vertebral number) in 712 pigs of 12 local pig breeds raised in Italy (Apulo-Calabrese, Casertana, Cinta Senese, Mora Romagnola, Nero Siciliano and Sarda) and south-eastern European countries (Krskopolje from Slovenia, Black Slavonian and Turopolje from Croatia, Mangalitsa and Moravka from Serbia and East Balkan Swine from Bulgaria) and compared the data with the genetic variability at these loci investigated in 229 wild boars from populations spread in the same macro-geographic areas. None of the autochthonous pig breeds or wild boar populations were fixed for one allele at both loci. Domestic and wild-type alleles at these two genes were present in both domestic and wild populations. Findings of the distribution of MC1R alleles might be useful for tracing back the complex genetic history of autochthonous breeds. Altogether, these results indirectly demonstrate that bidirectional introgression of wild and domestic alleles is derived and affected by the human and naturally driven evolutionary forces that are shaping the *Sus scrofa* genome: autochthonous breeds are experiencing a sort of 'de-domestication' process, and wild resources are challenged by a 'domestication' drift. Both need to be further investigated and managed.

Seasonal and Dietary Effects on Vitamin D Deficiencies Detected in Wild Boar from Mid-Western Spain.

Risco, D., P. Goncalves, M. Bravo, W. Garcia-Jimenez, R. Cerrato, J. H. de Mendoza, and P. Fernandez-Llario. 2019.

Journal of Animal Physiology and Animal Nutrition 103, no. 2 (Mar): 668-674.
<https://dx.doi.org/10.1111/jpn.13058>.

Vitamin D (VitD) is involved in important mammalian physiological mechanisms, such as Ca-P metabolism, bone development and immunological response. VitD deficiencies are frequently detected in domestic animals and related to various health problems (e.g., rickets, bone deformation). However, knowledge about the status of VitD in wildlife species, such as the wild boar, is scarce. The aims of this work were to explore VitD status in wild boar populations from mid-western Spain and to elucidate the influence of daylight exposure and food supplementation in levels of VitD. Serum concentration of VitD (measured as 25-hydroxyvitaminD) was assessed in 276 wild boar from 27 game estates located in mid-western Spain using a commercial ELISA kit. In 19 out of 27 estates, the staff supplied a specific VitD-enriched food (2,000UI/Kg) ad libitum throughout the year, while in the remaining estates (8), no food was supplied. Blood samples were extracted from hunted animals (198) between October and February of hunting seasons 2016/2017 and 2017/2018, and from live wild boar (78) that were captured, sampled and released (March-September of 2017). The percentage of animals with VitD deficiency (<20ng/ml), VitD insufficiency (20-30ng/ml) and VitD sufficiency (>30ng/ml) was estimated, and the





New literature on Suiformes



relationship of these levels to factors like sex, age and season was assessed using chi-square tests. Furthermore, associations between daylight exposure and supplemental food with VitD levels were explored using linear models. Of the studied wild boar population, 82.2% showed a VitD deficiency or insufficiency. VitD deficiencies were more frequent in animals sampled in winter and spring. Furthermore, levels of VitD positively correlated with daylight exposure and supplemental food intake. Ad libitum supplementation with VitD-enriched food was insufficient to prevent VitD deficiencies in wild boar from November to April, probably because food consumption is lower during this period.

Real-Time Pcr Detection of *Toxoplasma Gondii* in Tissue Samples of Wild Boars (*Sus Scrofa*) from Southern Italy Reveals High Prevalence and Parasite Load.

Santoro, M., M. Viscardi, G. Sgroi, N. D'Alessio, V. Veneziano, R. Pellicano, R. Brunetti, and G. Fusco. 2019.

Parasites & Vectors 12 (Jul). <https://dx.doi.org/10.1186/s13071-019-3586-5>.

Background Toxoplasmosis is a zoonotic parasitic disease caused by *Toxoplasma gondii*, a widespread protozoan in the phylum Apicomplexa. In Europe, several studies have demonstrated the presence of the parasite in tissues of wild boars (*Sus scrofa*), but no data exists on the *T. gondii* load in tissues which in turn may be an useful way to assess the infection risk for the consumer of wild boar meat. **Methods** We sampled and tested a total of 472 tissue samples of brain, heart and masseter muscle from 177 wild boars from the Campania region of southern Italy by real-time PCR analyses for detection and quantification of *T. gondii*. The sensitivity and specificity of the method were calculated by ROC analysis curves. **Results** PCR analysis revealed the presence of *T. gondii* in tissue samples of 78 out of 177 (44%) wild boars. In general, the brain presented the highest PCR prevalence (31%), followed by the heart (28.3%) and the masseter muscle (24.2%), with the highest estimated parasite numbers observed in the brain followed by the heart and masseter muscle. The PCR method showed an excellent discriminating ability for each of the examined tissues. According to the ROC analysis curves, the respective sensitivity and specificity were 99 and 100% for masseter muscle, 98 and 98% for brain and 96 and 98% for heart samples. **Conclusions** The high prevalence of infection here detected suggests a widespread distribution of the parasite in the wildlife of the Campania region of southern Italy. The *T. gondii* burdens detected may potentially represent a source of infection for humans.

Epidemiological Evaluation of Latvian Control Measures for African Swine Fever in Wild Boar on the Basis of Surveillance Data.

Schulz, K., E. Olsevskis, C. Staubach, K. Lamberga, M. Serzants, S. Cvetkova, F. J. Conraths, and C. Sauter-Louis. 2019a.

Scientific Reports 9 (Mar). <https://dx.doi.org/10.1038/s41598-019-40962-3>.

A wild boar population infected with African Swine Fever (ASF) constitutes a constant threat to commercial pig farms and therefore to the economy of the affected country. Currently, ASF is still spreading in several countries and the implementation of intensive measures such as reducing wild boar population densities seems not to be able to stop the further spread of the disease. In addition, there are still substantial knowledge gaps regarding the epidemiology of the disease. To identify risk factors for a higher probability of a wild boar sample being virological or serological positive, comprehensive statistical analyses were performed based on Latvian surveillance data. Using a multivariable Bayesian regression model, the effects of implemented control measures on





New literature on Suiformes

the proportion of hunted or found dead wild boar or on the estimated virus prevalence were evaluated. None of the control measures applied in Latvia showed a significant effect on the relevant target figure. Also, the estimated periodic prevalence of wild boar that had tested ASF positive by PCR appeared to remain unaffected over time. Therefore, there is an urgent need to reconsider the implemented control measures. The results of this study and the course of ASF in other affected countries, raise the question, whether an endemic situation of ASF in wild boar is reversible.

Analysis of Estonian Surveillance in Wild Boar Suggests a Decline in the Incidence of African Swine Fever.

Schulz, K., C. Staubach, S. Blome, A. Viltrop, I. Nurmoja, F. J. Conraths, and C. Sauter-Louis. 2019b.

Scientific Reports 9 (Jun). <https://dx.doi.org/10.1038/s41598-019-44890-0>.

African swine fever (ASF) in wild boar populations is difficult to control. In affected areas, samples from all wild boar shot and found dead are investigated. The use of laboratory tests allows estimating the duration of the infection in affected animals. The study aimed to test the hypothesis that the stage of the epidemic in different areas of Estonia can be assessed on the basis of prevalence estimates. ASF surveillance data of Estonian wild boar were used to estimate prevalences and compare them between the East and West of Estonia. The temporal trend of the estimated prevalence of ASF virus positive animals and of the estimated seroprevalence of wild boar showing antibodies against ASFV was analyzed. Due to the potential influence of population density on the course of ASF in wild boar, also population density data (number of wild boar/km²) were used to investigate the relationship with laboratory test results. In areas, where the epidemic had already lasted for a long time, a small number of new cases emerged recently. The prevalence of samples that were only seropositive was significantly higher in these regions as compared to areas, where the epidemic is in full progress. The observed course of the disease could be the beginning of an ASF endemicity in this region. However, the results may also indicate that ASF has started to subside in the areas that were first affected in Estonia.

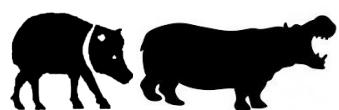
Cystic Echinococcosis in Wild Boars (*Sus Scrofa*) from Southern Italy: Epidemiological Survey and Molecular Characterization.

Sgroi, G., A. Varcasia, G. Dessi, N. D'Alessio, C. Tamponi, U. Saarma, T. Laurimae, L. Kinkar, M. Santoro, V. Caputo, P. Sarnelli, G. Fusco, P. Varuzza, A. Fioretti, A. Scala, and V. Veneziano. 2019.

International Journal for Parasitology-Parasites and Wildlife 9 (Aug): 305-311.

<https://dx.doi.org/10.1016/j.ijppaw.2019.04.013>.

Cystic Echinococcosis (CE) caused by *Echinococcus granulosus* sensu lato (s.l.) is one of the most important parasitic zoonotic diseases in the world and it represents an important public health and socio-economic concern. In the Mediterranean basin, CE is widespread and it is endemic in Italy, with major prevalence in southern areas. Several studies have investigated CE in domestic pigs, however, such data in wild boars are scant. In the last decades the wild boar population in Italy has increased and this ungulate could play an important role in the spreading of CE in the wild. Here we report on the prevalence and fertility rate of hydatid cysts in wild boars that were shot during two hunting seasons (2016-2017) in the Campania region of southern Italy. For each animal, a detailed inspection of the carcass and organs (lungs, liver and spleen) was





New literature on Suiformes

performed and when cysts were found, their number, morphology and fertility were determined by visual and microscopic examination. Cysts were classified morphologically as fertile, sterile, caseous and calcified. Protoscoleces and germinal layers were collected from individual cysts and DNA was extracted to identify different strains/genotypes of *E. granulosus* s.l. Out of a total of 2108 wild boars 93 (4.4%) were found positive for CE. Infected animals were 45 males and 48 females, aged between 1 and 8 years. The average number of cysts per wild boar was 1.3 (min 1 - max 13). The total number of cysts collected was 123, of which 118 (95.9%) in the liver, 4 (3.3%) in the lungs and 1 (0.8%) in the spleen. Of all analyzed cysts, 70 (56.9%) were fertile and 53 (43.1%) sterile/acephalous. The presence of fertile cysts in 19.4% of CE-positive animals is noteworthy. Overall, molecular diagnosis showed 19 wild boars infected with the pig strain (G7).

Pathogenic Potential to Humans of Shiga Toxin-Producing *Escherichia Coli* Isolated from Wild Boars in Poland.

Szczerba-Turek, A., P. Socha, A. Bancerz-Kisiel, A. Platt-Samoraj, K. Lipczynska-Ilczuk, J. Siemionek, K. Konczyk, E. Terech-Majewska, and W. Szweda. 2019. International Journal of Food Microbiology 300 (Jul): 8-13. <https://dx.doi.org/10.1016/j.ijfoodmicro.2019.04.004>.

The aim of the study was to investigate the presence of Shiga toxin-producing *Escherichia coli* (STEC) in the wild boar population of north-eastern Poland, and to evaluate the potential health risk associated with wild boars carrying STEC/AE-STEC strains. In Poland, the African Swine Fever (ASF) virus has been a growing problem in domestic pigs and wild boars, one of the main reservoirs of the virus, because of this hunters, veterinary practitioners and foresters thus face a greater risk of coming into contact with animals. Rectal swabs samples were obtained from 152 wild boars hunter-harvested in the 2017/2018 season (autumn-winter) in north-eastern Poland. The samples were enrichment in modified buffered peptone water. Polymerase chain reaction (PCR) assays were conducted to determine the virulence profile of stx1, stx2 and eae and aggR genes, identify subtypes of stx1 and stx2 genes, and perform O and H serotyping. STEC/AE-STEC virulence genes were detected in 43 isolates (28.29%): STEC in 17 isolates (11.18%) and AE-STEC in 26 isolates (17.11%), respectively. None of the tested isolates carried the aggR gene. The most dangerous AE-STEC virulence profile associated with HUS was found in 2 isolates (1.32%): stx1NS/stx2a/d/eae serotype ONT:H7 and stx2a/eae serotype O146:H7. Six of the 152 tested samples belonged to serogroup O157 (3.95%), including one AE-STEC isolate with virulence profile stx2g/eae and five EPEC isolates. The results of this study suggest that wild boars in north-eastern Poland can carry STEC/AE-STEC strains that are potentially pathogenic for humans. This is the first report documenting the virulence of STEC and AE-STEC isolates from wild boars in Poland.

Relationship among Ovarian Follicular Status, Developmental Competence of Oocytes, and Anti-Mullerian Hormone Levels: A Comparative Study in Japanese Wild Boar Crossbred Gilts and Large White Gilts.

Tanihara, F., M. Hirata, S. Iizuka, S. Sairiki, M. Nii, N. T. Nguyen, Q. A. Le, T. Hirano, and T. Otoi. 2019.

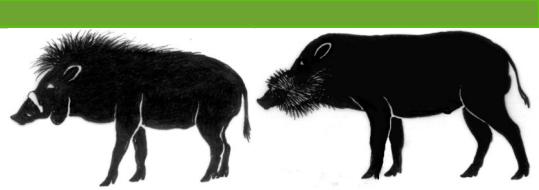
Animal Science Journal 90, no. 6 (Jun): 712-718. <https://dx.doi.org/10.1111/asj.13200>.

The aim of this study was to investigate the ovarian follicular development, developmental competence of oocytes, and plasma anti-Mullerian hormone (AMH) levels of Japanese wild boar





New literature on Suiformes



crossbred (wild hybrid) gilts, whose litter size is inferior to that of European breeds. Ovary and plasma samples were collected from two different breeds of gilts (wild hybrid and Large White breeds). The ovaries from the wild hybrid gilts had a lower average numbers of secondary follicles and vesicular follicles in ovarian cross-sections and of good quality oocytes collected from ovarian follicles as compared with those from Large White gilts ($p < 0.05$). The development rate to the blastocyst stage of good quality oocytes after in vitro maturation, fertilization and culture was also lower ($p < 0.05$) in wild hybrid gilts than in Large White gilts. Plasma AMH levels with >0.16 ng/ml were detected in 8.3% of the examined wild hybrid gilts and 33% of the Large White gilts. These results indicate that the low reproductive performance of wild hybrid breed may result in part from low numbers of vesicular follicles and good quality oocytes, and low developmental competence of oocytes. Moreover, plasma AMH levels may support low number of vesicular follicles in ovaries of wild hybrid gilts.

Genetically Similar Hepatitis E Virus Strains Infect Both Humans and Wild Boars in the Barcelona Area, Spain, and Sweden.

Wang, H., R. Castillo-Contreras, F. Saguti, J. R. Lopez-Olvera, M. Karlsson, G. Mentaberre, M. Lindh, J. Serra-Cobo, and H. Norder. 2019.

Transboundary and Emerging Diseases 66, no. 2 (Mar): 978-985.

<https://dx.doi.org/10.1111/tbed.13115>.

Hepatitis E virus (HEV) is a hepatotropic virus, endemic in Europe where it infects humans and animals, with domestic pigs and wild boars as main reservoirs. The number of HEV-infected cases with unknown source of infection increases in Europe. There are human HEV strains genetically similar to viruses from domestic pigs, and zoonotic transmission via consumption of uncooked pork meat has been shown. Due to continuous growth of the wild boar populations in Europe, another route may be through direct or indirect contacts with wild boars. In the Collserola Natural Park near Barcelona, Spain, the wild boars have spread into Barcelona city. In Sweden, they are entering into farmlands and villages. To investigate the prevalence of HEV and the risk for zoonotic transmissions, the presence of antibodies against HEV and HEV RNA were analysed in serum and faecal samples from 398 wild boars, 264 from Spain and 134 from Sweden and in sera from 48 Swedish patients with HEV infection without known source of infection. Anti-HEV was more commonly found in Spanish wild boars (59% vs. 8%; $p < 0.0001$) while HEV RNA had similar prevalence (20% in Spanish vs. 15% in Swedish wild boars). Seven Swedish and three Spanish wild boars were infected with subtype 3f, and nine Spanish with subtype 3c/i. There were three clades in the phylogenetic tree formed by strains from wild boars and domestic pigs; another four clades were formed by strains from humans and wild boars. One strain from a Spanish wild boar was similar to strains from chronically infected humans. The high prevalence of HEV infections among wild boars and the similarity between wild boar HEV strains and those from humans and domestic pigs indicate that zoonotic transmission from wild boar may be more common than previously anticipated, which may develop into public health concern.

Toxoplasma Gondii and Trichinella Infections in Wild Boars (*Sus Scrofa*) from Northeastern Patagonia, Argentina.

Winter, M., S. D. Abate, M. I. Pasqualetti, F. A. Farina, M. E. Ercole, L. Pardini, G. More, M. C. Venturini, N. Perera, M. J. Corominas, S. Mancini, B. Alonso, A. Marcos, R. Veneroni, M. Castillo, D. E. Birochio, and M. M. Ribicich. 2019.

Preventive Veterinary Medicine 168 (Jul): 75-80.





New literature on Suiformes

<https://dx.doi.org/10.1016/j.prevetmed.2019.04.014>.

Wild boar (*Sus scrofa*) was introduced in many countries of the world and is recognized as carrier of many infectious diseases. Wild game meat consumption is recognized as a source of transmission of *Toxoplasma gondii* and *Trichinella* spp. The aim of the present study was to evaluate the prevalence of antibodies to *T. gondii* and *Trichinella* spp. in free-range wild boars in Northeastern Argentine Patagonia. Between 2014 and 2018, 144 blood samples and 423 muscle samples from 423 carcasses were collected. To detect *T. gondii* IgG, 144 sera were processed by an immunofluorescent antibody test, and to detect anti-*Trichinella* IgG, 125 sera and 304 muscle juice samples were processed by ELISA. Detection of first stage larvae in muscle was performed by artificial digestion. A total of 423 wild boars muscle samples were negative to *Trichinella* spp. by artificial digestion. Antibodies to *Trichinella* spp. were detected in 2.4% (3/125) of serum samples and in 1.64% (5/304) of meat juice samples. Antibodies to *T. gondii* infection were detected in 12.5% (18/144) of the serum samples. This is the first study to reveal the presence of antibodies to *T. gondii* in wild boars from Argentina. The present results suggest that consumption of raw or undercooked wild boar meat could represent a potential source risk for toxoplasmosis in humans and that *Trichinella* spp. is infrequent and/or that it circulates in low burdens among wild boars in Northeastern Patagonia.

The Mutations within Mc1r, Tyrp1, Asip Genes and Their Effects on Phenotypes of Coat Color in Wild Pigs (*Sus Scrofa Ussuricus*).

Yang, G. L., C. X. Shi, D. L. Fu, and Z. Q. Li. 2019.

Indian Journal of Animal Research 53, no. 3 (Mar): 288-293. <https://dx.doi.org/10.18805/ijar.B-804>.

Animal coloration is a powerful model for studying the genetic mechanisms that determine animal phenotypes. But, there has not been comprehensive characterization of the molecular basis of the complex patterns of coat color phenotype variation in wild boars. This study results indicated that the wild-type allele E+ of the MC1R gene was a dominant allele in wild boars and was not responsible for black, brown or other coat color phenotypes. A novel mutation c.695 T > C was identified in the 3'-UTR of the ASIP gene. The association analysis showed that the C mutation allele was highly significantly associated with wild-type coat colors between wild boars and Western pig breeds ($P=1.35E-33$). A non-synonymous g.2254 G > A substitution was found in exon 2 of the TYRP1 gene (p.143His>Arg). The association analysis demonstrated that the G mutation allele was also significantly associated with wild-type coat colors between wild boars and Western pig breeds ($P = 5.09E-10$). In short, a few mutation sites in MC1R, ASIP, and TYRP1 genes were identified and surveyed several polymorphisms molecular variations in Chinese wild boars. In our identified mutations have caused the morphological diversity in wild boars, but did not influence coat color phenotype variation in some domesticated pig breeds. The conclusion was obtained that some mutations in color-associated genes were associated with wild-type coat colors in wild boar population, and that similar coat colorations observed in domesticated pig and wild boars can be the product of underlying differences in the genetic basis of color variants.

Distinguishing Domestic Pig Femora and Tibiae from Wild Boar through Microscopic Analyses.

Zedda, M., D. Brits, S. Giua, and V. Farina. 2019.

Zoomorphology 138, no. 1 (Mar): 159-170. <https://dx.doi.org/10.1007/s00435-018-0426-7>.





New literature on Suiformes

Pigs are the only species where the geographical distribution of the domestic type overlaps with that of its wild ancestors. Therefore, distinction between domestic pig and wild boar remains are important to better understand the roles of these animals. The aim of this study was to distinguish domestic pig and wild boar femora and tibiae based on bone microstructure. Midshaft cross sections were prepared from femora ($n=15$) and tibiae ($n=12$) belonging to domestic pigs and wild boars. The bone tissue was classified and 300 osteons per animal were measured. Measurements included the perimeter, area, minimum and maximum diameters of osteons and Haversian canals, osteon density and lamellae count. Comparisons were made using a Kruskal-Wallis test. Domestic pig bone was mainly characterized by plexiform bone sandwiching a layer of irregular Haversian tissue, whereas wild boars exhibited a tissue transition from plexiform to irregular to dense Haversian tissue towards the subendosteal zone. A greater number of osteon lamellae were noted in the wild boars, with an increased number in tibiae compared to femora. Similarly, all metric parameters including osteon density were significantly larger in wild boars compared to domestic pigs except for the minimum diameter of the Haversian canal. Domestic pigs had more circularly shaped osteons and Haversian canals compared to the more elliptical shapes found in wild boars. Our results support the idea that a strong correlation exists between lifestyle and bone structure.

African Swine Fever Virus.

Sánchez Vizcaíno, J. M., Laddomada, A., Arias, M. L.

Book Editor(s): Zimmerman, J. J., Karriker, L. A., Ramirez, A., Schwartz, K. J., Stevenson, G. W., Zhang, J.

First published: 29 March 2019; <https://doi.org/10.1002/9781119350927.ch25>

African swine fever is a large, icosahedral, linear double stranded DNA virus and the only member of the family Asfarviridae, genus Asfivirus. African swine fever virus (ASFV) is maintained in Africa via a complex transmission cycle involving African wild suid species, soft ticks, and domestic pigs. ASFV is transmitted within Europe most often directly via contact between sick and healthy animals, including domestic pigs and wild boar. The sites of primary ASFV replication are the monocytes and macrophages of the lymph nodes nearest the point of virus entry. The most convenient, safe, and frequently used techniques to detect and identify ASFV are the polymerase chain reaction. The serological diagnosis of ASF plays an important role in the surveillance program due to the fact that no vaccine is currently available against ASFV and, therefore, the presence of anti-ASFV antibodies in an animal indicates infection.

Development of semi dry sausages (cabanossi) with warthog (*Phacochoerus africanus*) meat: physicochemical and sensory attributes.

Mahachi, L. N., Rudman, M., Arnaud, E., Muchenje, V., Hoffman, L. C.

Food Science and Technology

The use of warthog meat to produce cabanossi (cured, smoked and semi-dried sausages) with different fat levels (10%, 20% and 30% by weight) were investigated. Weight loss during drying and smoking significantly increased as fat level decreased. Despite this, in the end products, the 10% pork backfat cabanossi had a slightly higher moisture content compared to the 30% treatment due to its higher initial moisture content. However, this did not result in any differences ($P > 0.05$) in water activity between all treatments. Water activity was sufficiently low (≤ 0.94) to ensure shelf stability coupled to pH lower than 5.2. The 10% fat warthog cabanossi showed a





New literature on Suiformes

better nutritional composition in terms of higher protein, lower fat content, higher amounts of n-3 fatty acids, lower n-6:n-3 ratio and lower thrombogenic index among the three treatments while there was no difference in lipid oxidation. The 10% pork backfat treatment was scored higher ($P \leq 0.01$) for overall aroma intensity and smoky aroma, followed by the 20% and 30% treatments, respectively and generally scored better for most sensory attributes.

Genetic and biological aspects of teats in Suidae - a review.

Rekiel, A., Batorska, M., Więcek, J.

Animal Science Papers & Reports . 2019, Vol. 37 Issue 1, p5-18. 14p.

The objective of the study was to show the breeding and production importance of the number of teats, their growth and development, morphology and function in pigs. Domestication gave rise to efforts to improve performance traits, including a moderate heritable number of teats. This polygenic trait can be improved using both classical methodology (the BLUP under an animal model) and a molecular approach. It was shown that the main QTL affecting teat number in pigs is found on chromosome 7. This trait is also influenced by the dam, fetal number and the sex ratio. The present study characterises the trait of teat quality and its determinants, indicating that some abnormalities may be genetically determined. A normally developing and functioning mammary gland provides piglets with colostrum and milk, which offer immune protection, provide nutrients and maintain the dam-offspring bond. No definitive relationships were observed between teat number and fertility. From the genetic point of view the relationship between teat number and weight of weaned piglets appears low, but position along the milk line and fostering of piglets may well contribute to rearing performance. The use of teats by piglets depends on teat position in the upper and lower rows. Their accessibility is determined by teat pair distance (TPD), a trait that is still not being selected for. It should be stated that at present morphological characteristics (including TPD) appear to be of equal importance in breeding programmes as the number of functional teats.

Epidemiology of African swine fever in Africa today: Sylvatic cycle versus socio' economic imperatives.

Penrith, M.-L., Duarte Bastos, A., Etter, E. M. C., Beltrán Alcrudo, D.

Transboundary and Emerging Diseases

African swine fever (ASF) is believed to have evolved in eastern and southern Africa in a sylvatic cycle between common warthogs (*Phacochoerus africanus*) and argasid ticks of the *Ornithodoros moubata* complex that live in their burrows. The involvement of warthogs and possibly other wild suids in the maintenance of ASF virus means that the infection cannot be eradicated from Africa, but only prevented and controlled in domestic pig populations. Historically, outbreaks of ASF in domestic pigs in Africa were almost invariably linked to the presence of warthogs, but subsequent investigations of the disease in pigs revealed the presence of another cycle involving domestic pigs and ticks, with a third cycle becoming apparent when the disease expanded into West Africa where the sylvatic cycle is not present. The increase in ASF outbreaks that has accompanied the exponential growth of the African pig population over the last three decades has heralded a shift in the epidemiology of ASF in Africa, and the growing importance of the pig husbandry and trade in the maintenance and spread of ASF. This review, which focuses on the ASF situation between 1989 and 2017, suggests a minor role for wild suids compared with the domestic cycle, driven by socio-economic factors that determine the ability of producers to implement the control measures needed for better management of ASF in Africa.





New literature on Suiformes

Gastrointestinal helminths from the common warthog, *Phacochoerus africanus* (Gmelin) (Suidae), in KwaZulu-Natal Province, South Africa, with comments on helminths of Suidae and Tayassuidae worldwide

Junker, K., Spickett, A., Swanepoel, M., Krasnov, B. R. et al.

Parasitology

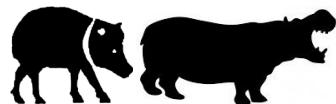
Thirty warthogs, *Phacochoerus africanus*, were collected in the Pongola Game Reserve, South Africa and examined for helminths. Gastrointestinal helminth assemblages comprised *Gastrophilus aegyptiacus*, the cestode genus *Moniezia* and seven species of nematodes. A single warthog harboured a metacestode of *Taenia hydatigena* in the mesenteries. No helminths were found in the heart, lungs or liver of the warthogs. *Probstmayria vivipara* and *Murshidia* spp. were the most prevalent as well as abundant helminth species, followed by *Physocephalus sexalatus*. The incidence of *Moniezia* did not differ between hosts of different sex or age. Numbers of *Murshidia* spp. were not affected by host sex, but were higher in adults than in juveniles. Conversely, burdens of *Trichostrongylus thomasi* were not affected by host age, but were higher in males than in females. While not highly significant, helminth assemblages in male warthogs were more species rich than in females. Helminth communities in the three genera of wild sub-Saharan suids are largely unique, but *Ph. africanus* and *Hylochoerus meinertzhageni* share more worm species with each other than with *Potamochoerus larvatus*, possibly because the former two are more closely related. Overlap between helminth communities of African wild suids and those of other suids and Tayassuidae worldwide is limited.

Reproductive monitoring of collared peccary females (*Pecari tajacu*) by analysis of fecal progesterone metabolites.

Mayor, P., Guimaraes, D. A., da Silva, J., Jori, F., Lopez-Bejar, M.

Theriogenology, 134, August 2019, Pages 11-17

The measurement of fecal progesterone metabolites (fPM) by enzyme immunoassay analysis is a non-invasive technique that permits gathering reproductive information from wildlife without the stress associated with restraint. In the collared peccary (*Pecari tajacu*), a high correlation between serum progesterone and fPM levels ($r^2 = 0.783$) suggests that fPM can be used to monitor their reproductive function. We monitored fPM during the estrous cycle of 15 collared peccary females. Estrous cycles averaged 27.9 ± 4.5 days ($n = 28$), ranging from 21 to 36 days. The luteal phase was 22.2 ± 4.8 days and the inter-luteal phase was 4.3 ± 1.4 days. Mean concentration of fPM across pregnancy were not different from those found during the luteal phase (1230 ± 718 and 1265 ± 584 ng/100 mg dried feces, respectively), however, significant differences were found when luteal phase concentrations were compared only against fPM concentrations during late pregnancy. In addition, late pregnancy fPM concentrations (1893 ± 551 ng/100 mg) were also significantly higher than those in the early (639 ± 339 ng/100 mg) and mid (1134 ± 449 ng/100 mg) pregnancy. For females during the early post-partum period, fPM concentrations were significantly increased (243 ± 118 ng/100 mg) than those of non-cycling females (103 ± 89 ng/100 mg). The analysis of fPM is a simple, non-invasive methodology to detect the ovarian activity in the collared peccary; moreover, it provides a husbandry tool, which may be used to help understand how social structure may impact reproduction.





New literature on Suiformes

Anti-influenza A virus antibodies in Tayassuidae from commercial rearing farms in Brazil

Baraldi, T. G., de Souza, H. M., Bonalume, A. A., de Morais, C., Yuri, G., Hélio, S., Montassier, J., Motta, R. G., Ribeiro, M. G., de Oliveira, L. G.

Ciencia Rural

Family Tayassuidae in the suborder Suina include two species of peccaries in Brazil: the white-lipped peccary (*Tayassu pecari*) and the collared peccary (*Pecari tajacu*). These animals share common pathogens with domestic swine (*Sus scrofa*); however, their role as potential carrier remains unclear. This study focused on detecting the prevalence of influenza A antibodies in *Tayassu pecari* and *Pecari tajacu* from commercial rearing farms from two states in Brazil. A set of 50 blood samples from *Pecari tajacu* and 55 from *Tayassu pecari* were analyzed using a commercial indirect ELISA in order to investigate anti influenza A antibodies. *Pecari tajacu* samples presented 22% (11/50) of seropositivity for the virus. Serological surveillance is an important tool to identify the presence and the spread of the influenza virus in feral pigs.

Effect of cryoprotectant type and concentration on the vitrification of collared peccary (*Pecari tajacu*) ovarian tissue.

Lima, G. L., Luz, V. B., Lunardi, F. O., Souza, A. L. P., Peixoto, G. C. X., Rodrigues, A. P. R., Oliveira, M. F., Santos, R. R., Silva, A. R.

Animal Reproduction Science, 205, June 2019, 126-133

The aim of the present study was to establish a protocol for solid surface vitrification of peccary ovarian tissue by using different cryoprotectants. Ovarian pairs from five adult females were fragmented and two fragments (fresh control group) were immediately subjected to morphological evaluation using classical histology, transmission electron microscopy, and viability analysis using fluorescent probes. The remaining fragments ($n = 18$) were vitrified using a solid surface method with different concentrations (3 or 6 M) of ethylene glycol (EG), dimethyl sulfoxide(DMSO) or dimethyl formamide (DMF). After 2 weeks, samples were re-warmed and evaluated. A decrease in the percentage of morphologically normal preantral follicles (PFs) was verified for all the groups in comparison to the fresh control ($92.0 \pm 2.8\%$); however, if only the primordial follicles are considered, the most effective preservation ($P < 0.05$) was achieved with the use of EG at 3 M ($74.2 \pm 7.3\%$) or DMSO at 6 M ($75.0 \pm 4.2\%$). Ultrastructural analysis indicated there were well-preserved PFs in all the groups evaluated, having well-defined membranes, a few vacuoles, and organelles that were uniformly distributed throughout the cytoplasm, mainly round and elongated mitochondria in close association with lipid droplets. Viability was preserved ($P < 0.05$) with the use of EG at 3 (97%) or 6 (97%) M, DMSO at 3 (100%), and DMF at 6 (97%) M. Solid surface vitrification, therefore, is an effective method for conservation of peccary female germplasm, especially with the use of EG at 3 M, which was highly effective for preservation of both the morphology and viability of PFs.

Embryonic and fetal development of the collared peccary (*Pecari tajacu*).

Mayor, P., Silva, G. P., dos Santos deAndrade, R., BarrosMonteiro, F. O., El Bizri, H. R.

Animal Reproduction Science, 208, 2019, 106-123

The relative timing of the main fetal development events in species determine the extent of fetal development at birth, which range along a gradient of having altricial and precocial traits. The results from this study allow for description of important fetal developments in collared peccary (*Pecari tajacu*) using data from 118 embryo/fetuses from 68 pregnant peccaries obtained over a





New literature on Suiformes

period of 15 years through collaborative methods with local hunters in the Amazon. The chronological order of emergence of external characteristics in relation to the total dorsal length (TDL) was: differentiated genitalia, limbs and eyelid buds ($TDL \geq 4.5$ cm), fused eyelids and outer ear ($TDL \geq 5.6$ cm), dorsal gland ($TDL \geq 7.3$ cm), skin ($TDL \geq 9.2$ cm), tactile pelage ($TDL \geq 12.9$ cm), coverage pelage ($TDL \geq 17.0$ cm), opened eyelids ($TDL \geq 21.5$ cm) and tooth eruption ($TDL \geq 24.5$ cm). The formula of fetal age was $W = 0.079(t - 27.6)$, with a linear relationship between TDL and gestational age. The relative weight of tubular gastrointestinal organs, lungs, spleen and thymus increased during fetal development. In contrast, the relative weight of kidneys and liver consistently decreased during the fetal development period. Results of this study indicate the collared peccary is a precocial species and that changes during fetal development are very similar to those in other Suiform species.

Single injection of eCG/hCG leads to successful estrous synchronization in the collared peccary (*Pecari tajacu* Linnaeus, 1758).

Peixoto, G. C. X., Lima, G. L., Maia, K. M., Souza, A. L. P., Castelo, T. S., Paiva, A. L. C., Paula, V. P., Oliveira, M. F., Brito, A. B., Domingues, S. F. S., Viana, A. C. N. P. C. S., Melo, L. M., Comizzoli, P., Silva, A. R.

Animal Reproduction Science, 208, September 2019, 106-112

The establishment of protocols for the control of the ovarian function of collared peccaries is recommended for the development of assisted reproductive techniques. The goals were to (1) compare a gonadotropin combination with prostaglandin analogue to synchronize timing of onset of estrus among animals, and (2) elucidate the effects of the most desirable protocol for performing an artificial insemination study and macroscopic evaluation of the ovaries. Three of five females treated with a double administration of 120 µg prostaglandin (cloprostenol) at a 9-day interval expressed symptoms of estrus 9 days after the second injection. One female presented estrus after 6 days, whereas other did not respond to the treatment. All females (5/5) treated with a single dose containing 400 IU eCG and 200 IU hCG manifested estrus 6 days after the hormone injection. In a second experiment, ten females that were estrous synchronized using eCG/hCG, were artificially inseminated with fresh semen and monitored for pregnancy every 30 days. Although there was no detection of fetuses by ultrasonic examination, seven females (7/10) had greater than basal progesterone values for 60 days after the treatments were imposed. Ovaries from two females treated with eCG/hCG were collected 6 days post-injection. There was confirmation of an ovarian stimulation as a result of the presence of 88 and 25 antral follicles, as well as three and eight hemorrhagic structures in ovaries of each female, respectively. It, therefore, is proposed that eCG/hCG can be used as an effective treatment for estrous synchronization in collared peccaries.

Postnatal testis development in the collared peccary (*Tayassu tajacu*), with emphasis on spermatogonial stem cells markers and niche.

de Lima, N., Lara, M., Jardim Costa, G. M., Avelar, G. F., Guimarães, D., A., França, L. R., General and Comparative Endocrinology, 273, 1 March 2019, 98-107

Collared peccaries (*Tayassu tajacu*) present a unique testis cytoarchitecture, where Leydig cells (LC) are mainly located in cords around the seminiferous tubules (ST) lobes. This peculiar arrangement is very useful to better investigate and understand the role of LC in spermatogonial stem cells (SSCs) biology and niche. Recent studies from our laboratory using adult peccaries





New literature on Suiformes

have shown that the undifferentiated type A spermatogonia (Aund or SSCs) are preferentially located in ST regions adjacent to the intertubular compartment without LC. Following these studies, our aims were to investigate the collared peccary postnatal testis development, from birth to adulthood, with emphasis on the establishment of LC cytoarchitecture and the SSCs niche. Our findings demonstrated that the unique LC cytoarchitecture is already present in the neonate peccary's testis, indicating that this arrangement is established during fetal development. Based on the most advanced germ cell type present at each time period evaluated, puberty (the first sperm release in the ST lumen) in this species was reached at around one year of age, being preceded by high levels of estradiol and testosterone and the end of Sertoli cell proliferation. Almost all gonocytes and SSCs expressed Nanos1, Nanos2 and GFRA1. The analysis of SSCs preferential location indicated that the establishment of SSCs niche is coincident with the occurrence of puberty. Taken together, our findings reinforced and extended the importance of the collared peccary as an animal model to investigate testis function in mammals, particularly the aspects related to testis organogenesis and the SSCs biology and niche.

Addition of Equex STM to Extender Improves Post-Thawing Longevity of Collared Peccaries' Sperm.

Bezerra, L. G. P., Souza, A. L. P., Lago, A. E. A., Campos, L. B., Nunes, T. L., Paula, V. V., Oliveira, M. F., Silva, A. R.

Biopreservation and Biobanking, 17, No. 2

The effect of Equex STM® paste supplementation on the Tris-extender for collared peccaries' semen cryopreservation was assessed. Semen from 12 mature individuals was obtained by electroejaculation and evaluated for morphology, membrane integrity, osmotic response, and sperm kinetic metrics. Samples were diluted in Tris plus 20% egg yolk and divided into three aliquots. The first aliquot was without any supplementation, the second and third contained 0.5 and 1.0% Equex STM, respectively. The samples were added with 3% glycerol, frozen in liquid nitrogen, thawed, and assessed for the same parameters after a thermal resistance test (TRT) for 120 minutes. Similar values were detected for the different treatments immediately after thawing, except for the amplitude lateral head that was reduced in samples containing Equex ($p < 0.05$). During TRT, samples containing Equex were more efficient in preserving the sperm motility (at 0.5%: $25.5\% \pm 4.4\%$; at 1%: $33.3\% \pm 6.3\%$) at 30 minutes, in comparison with the control group ($16.6\% \pm 6.0\%$), in which sperm motility decreased at 15 minutes ($p < 0.05$). Moreover, Equex, especially at 0.5% concentration, was able to maintain plasma membrane integrity and sperm motility in all the samples after incubation for 60 minutes. In conclusion, we recommend the addition of Equex STM at 0.5% to the Tris-extender to improve post-thawing sperm longevity in collared peccaries.

Skull shape and the demands of feeding: a biomechanical study of peccaries (Mammalia, Cetartiodactyla).

Hendges, C. D., Patterson, B. D., Cáceres, N. C., Gasparini, G. M., Ross, C. F.

Journal of Mammalogy, 100, 2, 24 April 2019, 475–486.

A primary requirement of the mammalian skull is to exert forces on different foods and to resist the forces imposed on it during feeding. Skull shape patterns within and among mammals are generally well known, but the biomechanical relevance of this variation remains limited for some groups. By integrating geometric morphometric and biomechanical analyses, we test the





New literature on Suiformes

hypothesis that skull shape in peccaries reflects biomechanical attributes to generate and dissipate powerful forces, presumably in response to tough foods. We obtained skull shape and size from 213 specimens of the three living peccary species and estimated bite force, bite stress at molars, bending and shear stress on the mandibular corpus, and condylar stress. We found larger estimated bite forces, greater resistance to bending loads, and lower stress emerging from the larger muscle attachment areas and shorter and deeper mandibular corpora for both *Pecari tajacu* and *Tayassu pecari* relative to *Parachoerus wagneri*. Peccaries (*P. tajacu* and *T. pecari*) with more powerful biomechanical attributes feed mainly on tougher foods (e.g., palm fruits). These results support the hypothesis that species eating tough foods tend to have a feeding morphology mechanically adapted to stronger bites and greater biting resistance, which must be closely reflected in their craniomandibular shape.

Reproductive cycle and pregnancy monitoring in the common hippopotamus (*Hippopotamus amphibius*) through salivary steroid analyses and transabdominal ultrasonography.

J. Wojtusik, J. Brandicourt, I. M. C., Rice, W., Roth, T. L.

Reproduction, Fertility and Development

The common hippopotamus (*Hippopotamus amphibius*) is listed as vulnerable to extinction by the IUCN due to a significant decrease in population size, caused by habitat loss and poaching. Ex situ populations can help ensure against species loss, but careful reproductive management is essential to maintain sustainable populations. Hormone monitoring allows for characterisation of the reproductive cycle and gestation, offering insight into timing of receptivity and conception and facilitating pregnancy diagnosis and estimation of parturition date. Fecal steroid analysis has been validated for measuring progestogens in hippos. However, hippos are often housed in groups and frequently defecate in the water, making sample collection and source identification difficult. Salivary steroid analysis has been employed for monitoring reproductive activity in several species, but has not been tested in hippos. Additionally, transabdominal ultrasonography has proven valuable in diagnosing and monitoring pregnancy in many large mammals, but efficacy in the common hippo is unknown. The goals of this project were to (1) validate the use of an enzyme immunoassay to monitor progestogens in hippo saliva, (2) confirm that salivary progestogen profiles accurately reflect reproductive activity, (3) determine if transabdominal ultrasonography can be used to diagnose pregnancy, and, if so, (4) monitor and characterise fetal development via weekly examinations. Saliva (4-7 per week) and fecal (2-7 per week) samples were collected from 7 adult female hippos housed at 3 USA facilities over 3-7 months. Saliva and fecal samples were extracted in ethanol and extracts diluted (1:2 to 1:10 and 1:25 to 1:500, respectively) before evaluation by enzyme immunoassay (Progesterone mini-kit; Arbor Assays). Parallelism was confirmed between serially diluted fecal ($r^2 = 0.993$) and saliva ($r^2 = 0.990$) samples and the standard curve. Inter- and intra-assay coefficients of variation were maintained at <10%. Comparison of fecal and saliva progestogen concentrations revealed a strong correlation between the 2 sample types ($r^2 = 0.848$) and suggested that saliva offers a comparable alternative. Both fecal and saliva extracts exhibited elevated progestogens during luteal phases and gestation. One nulliparous female housed at the Cincinnati Zoo & Botanical Garden (Cincinnati, OH, USA) was trained for voluntary transabdominal ultrasound exams. An Ibex Pro portable ultrasound machine (E.I. Medical Imaging, Loveland, CO, USA) with curvilinear probe (5-2.5 MHz) was used at a scanning depth of 17.8 and 23.4 cm. Intrauterine fluid and possible fetal tissue were observed 79 days following the last confirmed mating. Spine, rib cage,





New literature on Suiformes

and beating heart were clearly visible at ~156 days of gestation. Ultrasound procedures were continued until the premature birth of a calf at ~181 days (normal hippo gestation ~231 days). Salivary progestogen monitoring and transabdominal ultrasonography appear suitable for tracking reproductive activity and diagnosing and monitoring pregnancy in the common hippo.

A Comparison of Common Hippopotamus (Artiodactyla) and Mysticete (Cetacea) Nostrils: An Open and Shut Case.

Maust-Mohl, M., Reiss, D., Reidenberg, J. S.

The Anatomical Record

Hippos are considered the closest living relatives to cetaceans and they have some similar adaptations for aquatic living, such as a modified respiratory tract. Behavioral observations of male and female common hippos (*Hippopotamus amphibius*) at Disney's Animal Kingdom® and the Adventure Aquarium were conducted to describe and examine movements of the nostrils during respiration (inspiration, expiration, and inter-breath interval). The hippo nostril is a crescent shaped opening with lateral and medial aspects that are mobile and can be adducted and abducted to regulate the nostril opening. Notably, the default (resting) position of the nostrils is closed during the inter-breath interval, even when hippos are resting in water and their heads are not submerged. Similar to cetaceans, this aquatic adaptation protects the respiratory tract from an accidental incursion of water that can occur even when the nostrils are above water. Dissection of a deceased captive common hippo suggests there are separate muscles that pull the medial and lateral aspects for abduction. The internal nasal passage has a nasal plug that is similar in shape but less pronounced than the nasal plugs of two baleen whale species studied (minke whale *Balaenoptera acutorostrata*, fin whale *Balaenoptera physalus*). Examination of the musculature suggests fibers attach from the premaxillae and extend caudally to retract the plug to open the nasal passage. We discuss similarities and differences of the nostrils/blowholes of fully aquatic, semi-aquatic, and terrestrial species to assess adaptations related to environmental conditions that may be convergent or derived from a common ancestor.

Taxonomic, Biogeographic and Evolutionary Studies

Maternal Genomic Variability of the Wild Boar (*Sus Scrofa*) Reveals the Uniqueness of East-Caucasian and Central Italian Populations.

Khederzadeh, S., S. Kusza, C. P. Huang, N. Markov, M. Scandura, E. Babaev, N. Sprem, I. V.

Seryodkin, L. Paule, A. Esmailizadeh, H. B. Xie, and Y. P. Zhang.

Ecology and Evolution. <https://dx.doi.org/10.1002/ece3.5415>.

The phylogeography of the European wild boar was mainly determined by postglacial recolonization patterns from Mediterranean refugia after the last ice age. Here we present the first analysis of SNP polymorphism within the complete mtDNA genome of West Russian (n = 8), European (n = 64), and North African (n = 5) wild boar. Our analyses provided evidence of unique lineages in the East-Caucasian (Dagestan) region and in Central Italy. A phylogenetic analysis revealed that these lineages are basal to the other European mtDNA sequences. We also show close connection between the Western Siberian and Eastern European populations. Also, the North African samples were clustered with the Iberian population. Phylogenetic trees and migration modeling revealed a high proximity of Dagestan sequences to those of Central Italy and suggested possible gene flow between Western Asia and Southern Europe which was not directly





New literature on Suiformes

related to Northern and Central European lineages. Our results support the presence of old maternal lineages in two Southern glacial refugia (i.e., Caucasus and the Italian peninsula), as a legacy of an ancient wave of colonization of Southern Europe from an Eastern origin.

Genomic Analysis on Pygmy Hog Reveals Extensive Interbreeding During Wild Boar Expansion.

Liu, L. Q., M. Bosse, H. J. Megens, L. A. F. Frantz, Y. L. Lee, E. K. Irving-Pease, G. Narayan, M. A. M. Groenen, and O. Madsen. 2019.

Nature Communications 10 (Apr). <https://dx.doi.org/10.1038/s41467-019-10017-2>.

Wild boar (*Sus scrofa*) drastically colonized mainland Eurasia and North Africa, most likely from East Asia during the Plio-Pleistocene (2-1Mya). In recent studies, based on genome-wide information, it was hypothesized that wild boar did not replace the species it encountered, but instead exchanged genetic materials with them through admixture. The highly endangered pygmy hog (*Porcula salvania*) is the only suid species in mainland Eurasia known to have outlived this expansion, and therefore provides a unique opportunity to test this hybridization hypothesis. Analyses of pygmy hog genomes indicate that despite large phylogenetic divergence (similar to 2 My), wild boar and pygmy hog did indeed interbreed as the former expanded across Eurasia. In addition, we also assess the taxonomic placement of the donor of another introgression, pertaining to a now-extinct species with a deep phylogenetic placement in the Suidae tree. Altogether, our analyses indicate that the rapid spread of wild boar was facilitated by inter-specific/inter-generic admixtures.

Unexpected evolutionary patterns of dental ontogenetic traits in cetartiodactyl mammals.

Rodrigues, H. G., Lihoreau, F., Orliac, M., Thewissen, J. G. M., Boissarie, J.-R.

Proceeding of the Royal Society Biological Science, 13 February 2019

<https://doi.org/10.1098/rspb.2018.2417>

Studying ontogeny in both extant and extinct species can unravel the mechanisms underlying mammal diversification and specialization. Among mammalian clades, Cetartiodactyla encompass species with a wide range of adaptations, and ontogenetic evidence could clarify longstanding debates on the origins of modern specialized families. Here, we study the evolution of dental eruption patterns in early diverging cetartiodactyls to assess the ecological and biological significance of this character and shed new light on phylogenetic issues. After investigation of the ontogenetic dental series of 63 extinct genera, our parsimony reconstructions of eruption state evolution suggest that the eruption of molars before permanent premolars represents a plesiomorphic condition within Cetartiodactyla. This result substantially differs from a previous study based on modern species only. As a result, the presence of this pattern in most ruminants might represent an ancestral condition contributing to their specialized herbivory, rather than an original adaptation. In contrast, the late eruption of molars in hippopotamoids is more likely related to biological aspects, such as increases in body mass and slower pace of life. Our study mainly shows that eruption sequences reliably characterize higher level cetartiodactyl taxa and could represent a new source of phylogenetic characters, especially to disentangle the origin of hippopotamoids and cetaceans.





New literature on Suiformes

Ecological, Behavioural and Conservation Studies

Seasonal Spatial Ecology of the Wild Boar in a Peri-Urban Area.

Amendolia, S., M. Lombardini, P. Pierucci, and A. Merigli. 2019.

Mammal Research 64, no. 3 (Jul): 387-396. <https://dx.doi.org/10.1007/s13364-019-00422-9>.

The parallel expansion of anthropogenic environments and wild boar *Sus scrofa* populations has favoured the intrusion of the species into many European metropolitan areas, including Rome. In this study, we used Maxent to analyse the seasonal spatial ecology of the wild boar in Marcigiana natural reserve, a rural area located in the northeastern suburbs of Rome. The wild boar avoided urban settlements year-round. In the growing season, it had a higher probability of occurring with an increasing presence of turkey oak *Quercus cerroides* woods, but seemed to be partially adapted to the presence of arable lands, which had a marked negative effect only when very abundant. These results lead us to hypothesise that the species in this part of the year adopts a spatial strategy which optimises the trade-off among the need for thermal cover and food resources. In autumn and winter, the species avoided meadows and pastures. The analysis of wild boar spatial ecology in metropolitan areas is essential to provide important information contributing to the development of effective plans for managing peri-urban populations and mitigating conflicts with humans.

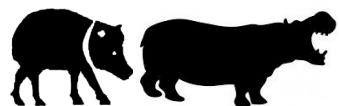
A Comparison of Methods to Derive Aggregated Transfer Factors Using Wild Boar Data from the Fukushima Prefecture.

Anderson, D., K. Okuda, A. Hess, K. Nanba, T. Johnson, T. Takase, and T. Hinton. 2019.

Journal of Environmental Radioactivity 197 (Feb): 101-108.

<https://dx.doi.org/10.1016/j.jenvrad.2018.12.009>.

Aggregated transfer factors (T-ag; m(2) kg(-1)) are often used to predict radionuclide activity concentrations in biota (Bq kg(-1)) from soil contamination levels (Bq m(-2)). Inherently large uncertainties in T-ag values severely limit their predictive power. Many published T-ag values have been derived from radionuclide deposition onto soil following weapons fallout, or the accidents at Chernobyl and Fukushima. In many cases the soil data used to derive a T-ag value were collected for other purposes, and the spatial resolution of the soil data is much less than that of the biota data to which it is paired. We hypothesized that this disassociation and imprecision in pairing deposition density and biota data may contribute to the large variations observed in T-ag values. We tested the hypothesis by deriving T-ag values for Japanese wild boar in two ways. One method used paired deposition density-biota contamination levels, with the soil data collected from each boar trap site. The second method used a soil radioactivity density map, of relatively low spatial resolution, generated by the Japanese government agency MEXT for fallout from the Fukushima accident. We hypothesized that T-ag values derived from the method using paired deposition density-wild boar data would have less variation. Initial statistical test suggested significant differences in the predictive power of the two methods. However, removal of suspected outliers in the MEXT data set decreased the statistical differences and indicated that collecting Cs-137 soil deposition density measurements in the field did not reduce the large variation in our T-ag values. More importantly, both methods revealed that soil contamination levels are a poor predictor of radiocesium concentrations in boar ($r^2 < 0.23$). The inadequacies of T-ag to predict wild boar Cs-137 concentrations is an ominous indication of the lack of applicability of the T-ag





New literature on Suiformes

model as a rigorous research parameter. T-ag values are best suited for their original intended purpose: upper tier, screening level computations. Further studies on how to reduce uncertainty when predicting Cs-137 concentrations in biota are needed to thoroughly understand the transfer of radiocesium within the environment.

Effectiveness of a Calf-Selective Feeder in Preventing Wild Boar Access.

Balseiro, A., A. Oleaga, L. M. A. Morales, P. G. Quiros, C. Gortazar, and J. M. Prieto. 2019. European Journal of Wildlife Research 65, no. 3 (Jun). <https://dx.doi.org/10.1007/s10344-019-1276-4>.

Tuberculosis (TB) transmission between wildlife and domestic animals is usually indirect when they share an interface or visit the same location at different times in order to use the same food and water resources. Preventing aggregation and subsequent contact between domestic and wild animals is a valuable and cheap tool for improving farm biosafety. This study was carried out in a beef cattle farm located in Asturias (Atlantic Spain). Wild boar (*Sus scrofa*) visited the farm facilities every night to feed in the farm's calf feeders. Our aim was to design and test the efficacy of a selective feeder for calves that could hinder its use by wild boar. We analyzed the effectiveness of the design using camera trapping. Pictures showed a reduction of 97.8% and 56.3% in the number of wild boar accessing to the selective feeder and in the number of wild boar around it, respectively. Those data demonstrate that the selective feeder hindered the access of wild boar to the feed and therefore, reduced the feed-mediated indirect interspecies contacts. Biosecurity measures are promising, cheap, and cost-effective tools for preventing TB and other diseases.

Road Hogs: Implications from Gps Collared Feral Swine in Pastureland Habitat on the General Utility of Road-Based Observation Techniques for Assessing Abundance.

Boughton, R. K., B. L. Allen, E. A. Tillman, S. M. Wisely, and R. M. Engeman. 2019. Ecological Indicators 99 (Apr): 171-177. <https://dx.doi.org/10.1016/j.ecolind.2018.12.022>.

Feral swine are among the world's most destructive invasive species, and monitoring their populations is essential for research and management purposes. Observation stations located along primitive roads have been an efficient and effective means to intercept the daily activities of many animal species for collecting data from which abundance indices can be validly calculated. Feral swine are among the many species documented to use primitive (dirt), low-use roads as routes to easily traverse surrounding habitats and thus be well-monitored in various habitats globally by using road-based observation stations such as camera traps or tracking plots. However, there are relatively few assessments of this approach's general utility. Here, we examine whether roadbased observations would be useful in pastureland habitat where roads would be expected to minimally benefit swine as travel pathways. Using GPS collars, we monitored movements of 18 adult feral swine (9 male, 9 female) in a south-central Florida pastureland habitat. We found 17 of 18 swine (94%) were located on roads over half of the days they were monitored. In fact, the average for our sample of swine was road locations on 77% of days they were monitored. Moreover, for days when our monitored swine were located on roads, they averaged 5.3 road crossings/day. For just our combined sample of 18 feral swine, 76 road locations would be expected each day. We concluded that although pastureland habitat offers minimal resistance to overland travel, feral swine are still frequently found on roads, making road-based observation systems likely to be an efficient means to collect population monitoring data in





New literature on Suiformes

this easily traversed habitat, in addition to those habitats where overland travel would be more challenging to swine. This implies a very general utility for a road-based observation system for collecting data from which indices of abundance may be calculated for feral swine.

Risk of Exposure of Farms and Subsistence Nurseries to Contact with Wild Boar in Southern Mato Grosso Do Sul.

Braz, P. H., M. R. Oliveira, V. S. Silva, W. M. Tomas, R. S. Juliano, T. A. Moreira, N. P. Zimmermann, and A. O. Pellegrin. 2019.

Pesquisa Veterinaria Brasileira 39, no. 2 (Feb): 148-154. <https://dx.doi.org/10.1590/1678-5150-pvb-5888>.

With the advancement of wild boar distribution in the rural environment, its impacts are not limited to health in the pig sector, but the requirements for monitoring and control of the species are requirements laid down by the OIE for the recognition of classical swine fever free zone status. The construction of ecological models of favorability or suitability for the occurrence of pest species are necessary tools for the decision making on priority areas of management aiming at risk management. This work aims to map the level of suitability for the occurrence of wild boar in the southern state of Mato Grosso do Sul, as well as to identify the main risk variables for contact with the wild boar and evaluate the biosecurity measures adopted by commercial farms integrated in the south of the State of Mato Grosso do Sul. To evaluate the risk potential of wild boar for commercial and subsistence swine farming in southern Mato Grosso do Sul, a model of environmental suitability was constructed for this species in the swine producing region. This model considered different environmental strata, being the selection of the layers considered the physiological and behavioral characteristics of the species. In parallel, interviews were carried out in a sample of commercial farms integrating the region to survey the perception of the presence of the invasive species and the biosafety measures adopted. The results of this work indicate that the risk of contact among wild boars and animals reared in closed production systems may be high in the study area and only establishment of appropriate biosecurity measures that consider the characteristics and habits of the boar may prevent the intrusion of this species and contact with domestic swine. The built model can be considered of high reliability and it is recommended to apply it to other areas of the state, being a useful tool for the productive sector, environmental agencies and decision makers.

Past Experiences Drive Citizen Perception of Wild Boar in Urban Areas.

Conejero, C., R. Castillo-Contreras, C. Gonzalez-Crespo, E. Serrano, G. Mentaberre, S. Lavin, and J. R. Lopez-Olvera. 2019.

Mammalian Biology 96 (May): 68-72. <https://dx.doi.org/10.1016/j.mambio.2019.04.002>.

Wild boar (*Sus scrofa*) populations in urban environments have increased during the last decades. This has led to a new scenario where humans share the space with this recent colonising species inside urban areas. Citizen perception on wild boar presence must be taken into account to assure the most suitable design, application and acceptance of management measures. In order to advance in the knowledge and comprehension of urban wild boar perception by citizens, we conducted 181 surveys to women and men representing all age classes. Our questions were focused on assessing citizen features, experiences and attitudes regarding wild boar presence in the urban area of La Floresta (Sant Cugat del Valles, Barcelona, Spain). We used a recursive partitioning approach through regression trees to explore the





New literature on Suiformes

relationship between a Wild Boar Perception Score (WBPS) and citizen profile, past and current experiences involving wild boars, contact with wild boars and acceptance of management measures. Our results show that the WBPS is mainly driven by previous incidents suffered by the respondent, independently of citizen profile, current experiences, level of contact and acceptance of management measures. The respondents answered that measures should be taken to minimize wild boar incidents (37%) and to help wild boars to return to their habitat (27%), whereas 16% chose to coexist with wild boars in the current conditions. Culling all the wild boars was not supported at all, even among the citizens with the most negative perception of wild boar. Citizens with positive perception of wild boar presence in urban areas contribute to reinforce the phenomenon by feeding wild boars. Our results verify that socio-demographic variables such as gender, education and public health concern are less important than past experiences to drive citizen perception and explain resident attitudes. Information campaigns on the causes, consequences and effective management options for urban wildlife could help to improve understanding and acceptance of the circumstances and currently non-socially accepted possible solutions. Evaluation of citizen perception and information campaigns should precede wildlife management measures, in order to gain acceptance by residents before being implemented.

Catastrophic Impact of Wild Boars: Insufficient Hunting Pressure Pushes Snakes to the Brink.

Graitson, E., C. Barbraud, and X. Bonnet. 2019.

Animal Conservation 22, no. 2 (Apr): 165-176. <https://dx.doi.org/10.1111/acv.12447>.

Climatic changes, habitat loss and invasive species are important threats for many animal populations. Here, we report rapid declines and extinctions of adder populations monitored during 12 years in Belgium where none of the above causes was involved. This study provides the first large-scale data showing that wild boars represent a major risk for snakes, pushing populations to extinction. Drastic population declines were observed in the sites impacted by wild boars ($N = 14$), while in other sites spared by wild boars populations remained stable ($N = 9$). Wild boars are highly fertile and their main predators have been extirpated from Western Europe; yet, recreational hunting kept populations in check during decades. Hunting pressure is currently insufficient to control the rapid expansion of wild boars, demographic outbreaks are increasingly frequent. Wild boars are omnivorous; they can destroy snakes directly and indirectly through the depletion of snake's preys and via the destruction of key microhabitats. Snakes exhibit limited dispersal capacities; they cannot escape local perturbations and thus are highly vulnerable. Because wild boars have a very eclectic diet, are prolific breeders and are able to devastate a range of habitats their negative impact under relaxed hunting pressure applies to a huge variety of organisms, including reptiles. Policies to limit wild boar populations are urgently needed. Recommendations to target reproductive females and piglets should be generalized and applied.

The Forensic Pathology of Fatal Attacks by the Large Mammals Inhabiting the Nordic Wilderness-a Literature Review.

Gudmannsson, P., and J. Berge. 2019.

Journal of Forensic Sciences 64, no. 4 (Jul): 976-981. <https://dx.doi.org/10.1111/1556-4029.13994>.

Fatalities due to animal attacks are rare in forensic medical work but have been known to pose problems due to their potential to mimic homicide. This review summarizes reported cases of fatal





New literature on Suiformes

attacks by large mammals that inhabit the Nordic wilderness, namely brown bear, moose, wild boar, and wolf, and attempts to elucidate injury patterns that can guide the forensic pathologist to identifying the species and modus operandi of the attacker. A tendency toward a species-specific injury pattern was observed. Injuries by bear and especially wolf are dominated by biting whereas moose and wild boar do not seem to bite their victims. The bear uses its paws, both for hitting, resulting in crush injury and fractures, and clawing with resulting excoriations and possible penetrating injuries. Crush injuries and fractures appear, on the other hand, to be minimal or absent in attacks by wolf and wild boar.

Wild Boar (*Sus Scrofa*) Increases Species Diversity of Semidry Grassland: Field Experiment with Simulated Soil Disturbances.

Horcickova, E., J. Bruna, and J. Vojta. 2019.

Ecology and Evolution 9, no. 5 (Mar): 2765-2774. <https://dx.doi.org/10.1002/ece3.4950>.

Background Foraging activities of wild boar (*Sus scrofa*) create small-scale soil disturbances in many different vegetation types. Rooting alters species composition by opening niches for less-competitive plants and, as a recurrent factor, becomes a part of the community disturbance regime. Vegetation responses to wild boar disturbance have mostly been studied in the boar's non-native range or in native forest, rather than in open habitats in the native range. We investigate the response of open European semidry grassland vegetation dominated by *Brachypodium pinnatum* to native wild boar pressure in an abandoned agricultural landscape. Methods To describe the disturbance regime, we repeatedly mapped rooted patches during a 5-year period. Additionally, to study the vegetation response, we performed an artificial disturbance experiment by creating 30 pairs of simulated disturbances and undisturbed plots. The vegetation composition of the paired plots was repeatedly sampled five times in eight years of the study. Results Based on repeated mapping of disturbances, we predict that if the disturbance regime we observed during the 5-year period were maintained over the long term, it would yield a stable vegetation ratio consisting of 98.7% of the grassland undisturbed, 0.4% with fresh disturbance, and 0.9% in older successional stages. Vegetation composition in the artificially disturbed plots was continuously converging to that of undisturbed vegetation, but these disturbed plots still differed significantly in composition and had higher species number, even after eight years of succession. Synthesis Our results thus show that wild boar disturbance regime in its native range increases heterogeneity and species diversity of semidry grassland vegetation.

Tourist-Wild Boar (*Sus Scrofa*) Interactions in Urban Wildlife Management.

Ikeda, T., N. Kuninaga, T. Suzuki, S. Ikushima, and M. Suzuki. 2019.

Global Ecology and Conservation 18 (Apr). <https://dx.doi.org/10.1016/j.gecco.2019.e00617>.

Wild animals that reach the urban and sub-urban areas have caused various problems in the world. Human-wild boar conflicts have been increasing in these environments since the mid-1990s throughout the world. To manage human-wild boar conflicts in urban environments adequately, it is essential for a culling program to consider the distribution of wild boars and implement an awareness campaign to prevent encounters between human and wild boars. We aimed to visualize the management priority for urban wild boar population from camera trap and a questionnaire survey during August 2017 and November 2018 at Mt. Kinka, Gifu Prefecture, Japan. We investigated distribution and diel activity patterns of wild boar, and the influence of human disturbance on wild boar distribution using camera trap survey. A questionnaire survey





New literature on Suiformes

clarified distribution of tourists. Considering the RAI for each camera, the number of tourists, areas of residential and agricultural lands for each mesh, and photographic rates in day-time for each camera, we described management priority. Wild boars showed mostly nocturnal activity and avoided the human disturbance in urban environment. In addition, we visualized management priority, suggesting that it is necessary for wildlife managers to apply various counterplans according to information on management priority. Consequently, wildlife managers would be able to select high priority management area using various parameters.

When Pigs Fly: Reducing Injury and Flight Response When Capturing Wild Pigs.

Lavelle, M. J., N. P. Snow, C. K. Ellis, J. M. Halseth, M. P. Glow, E. H. VanNatta, H. N. Sanders, and K. C. VerCauteren. 2019.

Applied Animal Behaviour Science 215 (Jun): 21-25.

<https://dx.doi.org/10.1016/j.applanim.2019.03.014>.

Research on the ecology, behavior, and movements of wild pigs (*Sus scrofa*) often involves immobilization of study animals to attach GPS collars or other monitoring devices. In this process, it is important to minimize stress and injury to study subjects. Challenges in handling trapped wild pigs are common because multiple animals are often captured together, wild pigs exhibit intense fight-or-flight responses, large traps provide space for severe trap-related injuries, and immobilization drugs are less effective on excited wild pigs. We trapped and handled 148 wild pigs in corral traps in TX, USA, and evaluated two trap modifications for alleviating these issues, including: 1) using tightly spaced wire mesh for trap walls, and 2) enshrouding traps with a visual barrier prior to handling. We identified that the tightly spaced wire mesh of horse panels (10.2 x 5.1 cm) reduced injuries 88% compared to more widely spaced mesh sizes (10.2 x 10.2 cm or larger). We documented that it took an average of 71.6 s to enshroud traps, which corresponded to a rapid reduction in flight behaviors from wild pigs (i.e., <= 52.6 s until stationary). Enshrouding corral traps facilitated a 28% quicker delivery of chemical immobilization drugs via darting as wild pigs became inactive. We recommend using tightly spaced mesh of horse panels to reduce trap-related injuries and incorporation of trap shrouds to facilitate delivery of chemical immobilization drugs when handling wild pigs.

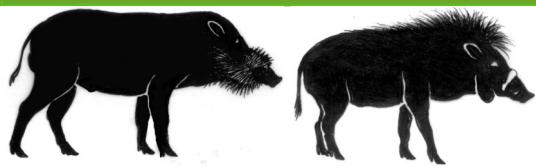
Wildlife Differentially Affect Tree and Liana Regeneration in a Tropical Forest: An 18-Year Study of Experimental Terrestrial Defaunation Versus Artificially Abundant Herbivores.

Luskin, M. S., K. Ickes, T. L. Yao, and S. J. Davies. 2019.

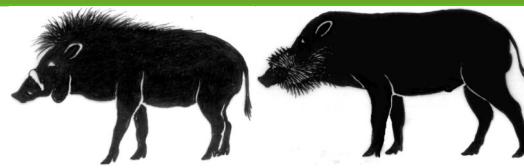
Journal of Applied Ecology 56, no. 6 (Jun): 1379-1388. <https://dx.doi.org/10.1111/1365-2664.13378>.

Hunting and land use change modify native herbivore abundances and cause cascading effects in natural ecosystems. The outcomes for vegetation depend on changes to specific plant-animal interactions, such as seed dispersal or predation, or physical disturbances. We experimentally manipulated terrestrial wildlife populations in a primary lowland forest in Malaysia over an 18-year period (1996-2014) to understand how artificially high or low animal densities affect tree and liana regeneration. Our study site retains a diverse wildlife community and artificially high densities of native wild pigs (*Sus scrofa*) that are sustained by crop raiding in distant oil palm plantations. We used fencing that excluded terrestrial animals >1 kg to experimentally simulate conditions similar to those in defaunated forests. These two treatments - abnormally high pig abundances and megafauna loss from hunting - represent common outcomes in disturbed Southeast Asian forests





New literature on Suiformes



and are characteristic of many forests globally. We focused on trees and lianas because they are the two dominant woody life-forms in tropical forests and crucial determinants of forest structure and function. We found that liana sapling abundances (30-100 cm height) increased by 86% in unfenced control plots with wildlife but were stable in exclosures. In contrast, tree abundances did not change in unfenced control plots but increased by 83% in exclosures without wildlife. Evidence of scaring on surviving stems suggested that these inverted outcomes were driven by selective use of tree saplings for wild pig nests. Lianas may also have greater tolerance to wildlife disturbances like nest building. By the end of the study, lianas comprised 38% of all saplings in unfenced controls but just 14% in exclosures. Synthesis and applications. We conclude that artificially abundant wildlife, such as crop-raiding wild pigs, may shift tropical forest understories towards lianas while defaunation may shift it towards trees. These results highlight that ecological cascades from hunting or land use change can alter plant functional types and reshape long-term patterns of forest succession and change. Managing unnatural wild boar populations may be required to conserve native plant communities in both their native and exotic ranges.

Assessing Caracal-Prey Interactions by Spatial and Temporal Analyses.

Mengulluoglu, D., and H. Ambarli. 2019.

European Journal of Wildlife Research 65, no. 4 (Aug). <https://dx.doi.org/10.1007/s10344-019-1294-2>.

In this study, we assessed habitat preferences and temporal activity patterns of caracal (*Caracal caracal*) and several possible prey species in Koyceiz Wildlife Development Reserve, southwestern Turkey. We investigated whether wild goat (*Capra aegagrus*) is indeed the main prey of caracal and if there is evidence for excessive caracal predation on this ungulate as previously stated by researchers, wildlife wardens and hunters. Results of this 2249 camera trap-day survey revealed a high habitat segregation between caracal and wild goat (Pianka's O=0.2) and very high overlap between caracal and other prey species such as brown hare (*Lepus europaeus*), field mice (*Apodemus* spp.), chukar partridge (*Alectoris chukar*) and wild boar (*Sus scrofa*) (Pianka's O=0.8-1.0). Wild goats preferred steep slopes (Chesson's =0.85) and associated narrow valley bottoms, whereas caracals preferred high flatland forests (Chesson's =0.95). The overlap coefficients in temporal activity patterns of caracal and wild goat ((1)=0.50), and caracal and other prey species were moderate ((1)=0.40-0.59), and did not indicate strict predator-prey relationships based on temporal activities. The results of this study do not support a caracal diet based mainly on wild goat, due to their mostly spatial and partially temporal segregation. Other smaller prey species such as brown hare, rodents and chukar partridge can serve as better prey options due to their continuous presence in caracal habitat throughout the day and year.

Seasonal Competition between Sympatric Species for a Key Resource: Implications for Conservation Management.

Nie, Y. G., W. H. Zhou, K. Gao, R. R. Swaisgood, and F. W. Wei. 2019.

Biological Conservation 234 (Jun): 1-6. <https://dx.doi.org/10.1016/j.biocon.2019.03.013>.

Competition often occurs between two or more sympatric species that use similar ecological niches. During competition, a superior species may exclude the competitor from parts of its fundamental niche or make it go extinct. Determining the potential competition between two sympatric species including an endangered one has important implications for conservation management. We evaluated potential food competition between the wild boar and the giant





New literature on Suiformes

panda in a key national nature reserve established primarily for the giant panda protection. We monitored foraging plots for 9 years, conducted food macronutrient analysis, and combined our analysis with long-term population monitoring results for two species. The wild boar population increased dramatically in the past 18 years, benefiting from conservation policies of the Chinese government, whereas the giant panda population decreased. We found evidence for competition for bamboo shoots, an important seasonally limiting resource. The wild boar had a higher utilization rate at foraging plots than giant panda, which also avoided plots used by wild boar. This study indicates key seasonal food competition may exist between wild boar and giant panda. This competition for a key food resource may have negative impacts on giant panda populations, particularly under the substantial increase of the wild boar, yet this possibility has not figured prominently in conservation planning and policy for panda reserves. We suggest long-term monitoring of this competitive relationship across reserves to determine when and where management intervention is needed. And, we might need more flexible policies instead of the current "one size fits all" one.

Estimating Day Range from Camera-Trap Data: The Animals' Behaviour as a Key Parameter.

Palencia, P., J. Vicente, P. Barroso, J. A. Barasona, R. C. Soriguer, and P. Acevedo. Journal of Zoology. <https://dx.doi.org/10.1111/jzo.12710>.

Day range (DR), the distance travelled by an individual during the day, is an important metric in movement ecology that recently gained interest by its relevance for estimating population density through the random encounter model (REM). Traditionally, DR has been estimated using GPS technology and considering raw straight-line distances between consecutive locations, which is an underestimation of the true path distance. In this work, we tested the accuracy of a new approach based on camera-trap data for the estimation of DR taking into account the animals' behaviour. For this purpose, we considered wild boar (*Sus scrofa*) as a model species. We tagged 18 individuals with telemetry devices and then monitored the population with camera-traps (photo and video mode) to estimate the DR. In the case of telemetry, a straight-line DR was estimated and rescaled with a tortuosity-related correction factor. Using this camera-trap data, we revisited the procedure described by Rowcliffe et al. (Remote Sens. Ecol. Conserv. , 2, 2016, 84) to estimate the DR from the speed and activity information obtained from camera-trapping. A new derivation of this approach was then developed, in which different animal behaviours were weighted to estimate the DR. The analysis showed no significant differences between the DR values obtained using telemetry data (corrected by the tortuosity-related correction factor) and those attained with the weighted approach. However, the original approach used to estimate the DR based on camera-trap data underestimated this parameter. The DR estimated with the weighted approach was $12.74 \text{ km center dot day}^{-1} \pm (se) 1.89$. Here, we showed that animals' behaviour should be taken into account to estimate the DR when working with species that behave differently in front of cameras. These results may be relevant not only for REM, but also for movement ecology, disease dynamics and population monitoring methods.

The Effect of Age and Ultimate Ph Value on Selected Quality Traits of Meat from Wild Boar.

Stanisz, M., A. Ludwiczak, J. Skladanowska-Baryza, and M. Bykowska-Maciejewska. 2019. Canadian Journal of Animal Science 99, no. 2 (Jun): 336-342. <https://dx.doi.org/10.1139/cjas-2018-0090>.





New literature on Suiformes

The meat from hunted wild boar juveniles ($N = 18$) and yearlings ($N = 17$) was analysed to assess the influence of age and the ultimate pH value on selected quality traits. The analysed meat of 55.56% of the juveniles and 64.71% of the yearlings was characterised with normal pH. The pH had been measured 24 and 48 h post mortem. More cases of high ultimate pH ($\text{pH}(u) > 5.8$) and high maximal pH (about 6.2) have been noted in the meat of younger animals compared with older ones. We found no effect of pH_u on the colour coordinates of analysed wild boar meat. A slight effect of age was observed for the lightness (L^*) coordinate. The postmortem time was the most important factor influencing meat colour [L^* , yellowness (b^*), and hue angle]. A high pH_u was related to lower drip loss ($P = 0.001$), lower percentage of free water ($P = 0.036$), lower cooking loss ($P = 0.001$), and lower plasticity ($P = 0.042$). The meat from juveniles showed higher plasticity than meat from yearlings. Summing up, both the pH_u level and the age of wild boars may affect some qualitative patterns of meat, changing the technological usability of this raw animal product.

A Survey of large and medium-sized mammals in Wabe forest fragments, Gurage zone, Ethiopia.

Legese, K., Bekele, A., Kiros, S.

International Journal of Avian and Wildlife Biology, 4,2 - 2019

Mammal inventories are essential tools to effectively direct conservation strategies and management practices. A survey of large and medium-sized mammals was conducted in Wabe Forest fragments near to Wolkite town of Ethiopia to assess their diversity and abundance in the area and to determine their major threats. Transect method and anecdotal interviews were used to collect data for the study. A total of 12 mammal species belonging to seven orders and seven families were recorded by direct and indirect evidences. Porcupine (*Hystrix cristata*), honey badger (*Mellivora capensis*), vervet monkey (*Chlorocebus aethiops*), olive baboon (*Papio anubis*), and colobus guereza (*Colobus guereza*) were among the medium-sized mammals, and spotted hyena (*Crocuta crocuta*), aardvark (*Oryctopus afer*), bohor reedbuck (*Redunca redunca*), Oribi (*Ourebia ourebi*) and common duiker (*Sylvicapra grimmia*) were the large mammals of the study area. Vervet monkey (*C. aethiops*) was the dominant species followed by guereza (*Colobus guereza*), whereas common duiker (*S. grimmia*), spotted hyena (*C. crocuta*) and bush pig (*Pontamochoreus larvatus*) were less common. Mammals were recorded in low population number in the study area. Simpson's Similarity Index (SI) showed a considerable overlap of species between the natural forest and scrubland habitats (0.58%) with reference to species composition. Field observation and interviews indicated illegal logging of trees for fuel wood and charcoal production, domestic dogs, road construction and extraction of construction materials, and agricultural land expansion were the main anthropogenic threats in the area. The study area harbors considerable mammals that are threatened by interacting anthropogenic factors. Urgent conservation program is needed to safeguard these animals. Keywords: abundance, anthropogenic factors, conservation, diversity, ethiopia, mammals, wabe forest fragment

Drought-response strategies of savanna herbivores

Abraham, J. O., Hempson, G. P., Staver, A. C.

1. Climate models predict increases in drought frequency and severity worldwide, with potential impacts on diverse systems, including African savannas. These droughts pose a concern for the conservation of savanna mammal communities, such that understanding how different species respond to drought is vital.





New literature on Suiformes

2. Because grass decreases so consistently during droughts, we predict that grass dependent species (grazers and mixed feeders) will respond strongly to drought, whether by changing diets, seeking drought refugia, or suffering mortality.

3. A recent severe but heterogeneous drought in Kruger National Park, South Africa, afforded a rare opportunity to test these hypotheses *in situ*—crucial, given the central role of landscape scale movement as a potential herbivore strategy. We used herbivore dung as a proxy, integrating spatial distributions (dung counts) with diet composition (carbon isotope analysis of dung).

4. As predicted, browsers showed little response to drought. However, mixed feeders switched their diets to incorporate more C3 trees/forbs, but did not move. Meanwhile, grazers and megaherbivores instead moved toward drought refugia.

5. Synthesis and applications: The responses we observed by savanna herbivores are largely amplifications of typical dry season strategies and reflect constraints imposed by body size and feeding ecology. Grazers may be at particular risk from increased drought frequency and spatial extent if drought refugia become decreasingly available. Conservation strategies should recognize these constraints and work to facilitate the diverse responses of herbivores to drought.

Assessing the Minimum Sampling Effort Required to Reliably Monitor Wild Meat Trade in Urban Markets.

Mayor, P., El Bizri, H. R. Morcatty, T. Q., Moya, K., Solis, S., Bodmer, R. E.

Frontiers in Ecology and Evolution

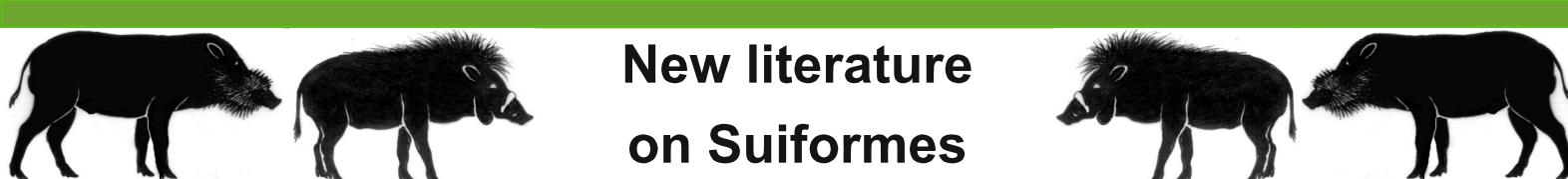
The trade of wild meat generates great economic returns for local communities but at a cost of increasing harvest rates of game species. Monitoring wild meat trade in urban markets is a low-cost method that can be employed to assess impacts of hunting on game populations. Nevertheless, wild meat markets are complex systems to monitor since they often vary over time, are illegal in some countries, and often vendors distrust researchers. We investigated the wild meat trade in the Belén market in Iquitos, Peru, the largest wild meat market in the Amazon, to estimate the minimum sampling effort required to obtain reliable estimates of the amounts and prices of wild meat sold. During two 12-month surveys (Sept. 2006–Aug. 2007, Sept. 2017–Aug. 2018), we conducted a total of 4,524 vendor interviews in 320 sample days. By modeling 10 possible scenarios in which sampling size and amount of meat traded varied, we calculated the accuracy and precision of different survey protocols. We found that in scenarios where the daily amount of wild meat on sale was between 40 and 650 kg, a sampling effort equal to or >2 sampling days per month provided good accuracy (>90%) and precision (>85%). However, in scenarios where wild meat traded was less frequent, or for rarer species, an effort of at least one interview per week is required. Vendor declaration of the daily amounts of meat sold was similar to the quantity on sale (accuracy = 98%), suggesting that sellers are aware of the volume of wildmeat brought to market. To accurately monitor the trade of wild meat in urban markets, we recommend a minimum sampling effort, ranging from two interviews per week to two interviews per month, depending on the amount of wild meat traded; in other occasions, a punctual interview on meat sellers' perception may also be useful.

New altitudinal record for white-lipped peccary *Tayassu pecari* (Link, 1795) in Ecuador, with notes about activity patterns and herd size.

Torres, J., Gavilanez, M. M.

Biodiversity Data Journal





New literature on Suiformes

White-lipped peccaries (*Tayassu pecari*) represent a key element of trophic networks in tropical rainforest ecosystems by playing the dual role of consumer and prey. Despite their importance, pressures on their populations have increased during the last few decades due to hunting and deforestation across its distributional range. These pressures may have led the remaining populations to move into new territories and to change their migratory and gregarious behaviour. In this study, we used photographic records from camera traps to collect data on biogeography of white-lipped peccaries in order to answer some questions about the demography, distribution and population size of the species in Ecuador's western Amazonia. We present new altitudinal records for the species (2,000 metres above sea level), along with some notes on herd size and activity patterns. This information is valuable for obtaining a better understanding of the species distribution and population status in order to achieve better conservation plans.

ESCASEZ DE REGISTROS DE PECARÍ LABIADO (*Tayassu pecari*) EN UN SECTOR DE ALTO VALOR DE CONSERVACIÓN DE LAS YUNGAS AUSTRALES DE ARGENTINA

Bardavid, S., Bustos, S., Natalia Politi, N., Rivera, L. O.

Mastozoología Neotropical, 26(1):167-173

Decline of white-lipped peccary (*Tayassu pecari*) in a high conservation value area in Southern Yungas of Argentina. In Argentina, white-lipped peccary (*Tayassu pecari*) is categorized as Endangered since its distribution was reduced by 63% and its populations are fragmented. Our objectives were to determine group size and to compare camera trapping rate of white-lipped peccary between two areas in the Southern Yungas of Argentina where the species is distributed. In this study, we recorded the smallest group size (10 ± 8 whitelipped peccary/group) compared to other sites in the Neotropics. Camera trapping rate was significantly higher in the southeastern area than in the northern area. The low camera trapping rate of white-lipped peccary in the northern area (214.68 ± 927.39 vs. 0.13 ± 1.69 , $W=5501$, $p < 0.0001$) is striking given that the species was frequent to record in this area a few years ago. The information obtained in this work allows to have a current estimate of the conservation status of white-lipped peccary in the two areas of Southern Yungas of Argentina.

Genetic diversity and population structure of white-lipped peccaries (*Tayassu pecari*) in the Pantanal, Cerrado and Atlantic Forest from Brazil.

Maciel, F. G., AqueuRufo, D. A., Keuroghlian, A. Russo, A. C., Brandt, N. M., Vieira, N. F., Mourada B., Nava, N. A., Nardi, M. S., Jácomo, A. T. A., Silveira, L., Furtado, M. M., Tôrres, N. M., Miyaki, C. Y., Tambosi, L. R., Biondo, C.

Mammalian Biology

<https://doi.org/10.1016/j.mambio.2019.03.001> Get rights and content

In general, habitat fragmentation is associated with a reduction in gene flow that can reduce the genetic diversity, and, consequently, a species ability to survive environmental changes. The white-lipped peccary (*Tayassu pecari*) is a Neotropical ecosystem engineer that is vulnerable throughout its distribution area and under different degrees of threat in the Brazilian Pantanal (near threatened), Cerrado (endangered) and Atlantic Forest (critically endangered). We used 13 microsatellite loci to assess the genetic diversity and population structure of 361 white-lipped peccaries sampled in four areas in the Pantanal, two areas in the Cerrado, and one area in the Atlantic Forest. We found similar levels of genetic diversity in all localities. Bayesian clustering analysis indicated the presence of two ($K = 2$; all Pantanal localities plus the Cerrado locality at





New literature on Suiformes

the Pantanal highlands versus the other Cerrado locality plus the Atlantic Forest one) or three ($K = 3$; with the additional differentiation between the Cerrado locality and the Atlantic Forest) genetically differentiated populations. We found a pattern of isolation by distance (IBD) limited by dispersal events of up to 180 km. This IBD pattern is congruent with gene flow between the geographically closer localities in the Pantanal and the Cerrado in the Pantanal highlands (25–137 km), while dispersal between the other Cerrado locality and the Atlantic Forest, that are 500 km apart, would not be as feasible. Therefore, we considered $K = 3$ as the best scenario to represent the genetic structure of the populations analyzed. As all populations of white-lipped peccary showed moderate levels of genetic diversity, conservation actions are recommended to maintain their diversity, as it is vital to the long-term viability of these populations, especially those in more threatened biomes.

Spatial isotopic dietary plasticity of a Neotropical forest ungulate: the white-lipped peccary (*Tayassu pecari*).

Bradham, J., Jorge, M. L. S. P., Pedrosa, F., Keuroghlian, A., Costa, V. E., Bercê, W., Galetti, M. *Journal of Mammalogy*

White-lipped peccaries (WLPs; *Tayassu pecari*, Tayassuidae, Cetartiodactyla) are forest-dwelling ungulates critical to maintaining healthy Neotropical forest ecosystems through key aspects of their dietary behaviors, including seed predation and dispersal. Land-use change and deforestation threaten WLP access to food resources, and thus knowledge of how WLP diet varies spatially is necessary to frame conservation efforts for the species. Here, we use stable carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) isotopes from WLP hair and food resources to assess whether WLP diet varies among four regions in three Brazilian biomes: the Pantanal, the Cerrado, and the Atlantic Forest (semi-deciduous and ombrophilous), each varying in forest canopy cover, climatic characteristics, and degrees of agricultural impacts. We find that in all regions WLPs are consuming primarily C3 resources, with mean $\delta^{13}\text{C}$ values ranging from $-28.7\text{\textperthousand}$ to $-26.9\text{\textperthousand}$. In the heavily fragmented semi-deciduous Atlantic Forest, $\delta^{13}\text{C}$ values are the highest, and may indicate that some individuals are consuming a small amount of C4 crops or demonstrating increased levels of insectivory. A through-time comparison of WLP hair in the semi-deciduous Atlantic Forest suggests the recorded slight departure from an exclusive C3 diet may be a recent phenomenon, as hairs collected prior to the year 2000 have lower $\delta^{13}\text{C}$ values than those collected in 2016. While some individual WLPs may slightly alter diet in heavily anthropogenically modified areas, C4 crops are not a main component of WLP diet. Our results suggest that WLPs are still highly dependent on forest resources, even in human-altered landscapes, and conservation and management plans for the species must consider these dietary needs in order to be successful.

Comparison of the forage tree species consumption by *Pecari tajacu* in captivity.

Montes-Pérez, R., Canul-Torres, C., Cumi-Martín, J., Castillo-Caamal, J. *Abanico Veterinario* 2019; 9 (1)

The objective was to compare consumption of dry matter (CMS) of Mucuna fruit (*M. deeringiana*), forages of ramón (*B. alicastrum*), jabín (*P. piscipula*), and Moringa (*M. oleifera*) in Collared Peccary male adults (*P. tajacu*). The study was carried out in two parts, the first one was executed with Latin square design (DCL) 4x4 with two repetitions, and three forages with ground Mucuna fruit were offered. In the second part, the preferred forage was eliminated in the first test





New literature on Suiformes

and DCL 3x3 was applied. Variance analysis was used for 4x4 and 3x3 DCL respectively, and Tukey test between means. Linear regression models were adjusted between the CMS and nutrient contents of each forage. The CMS in the first part showed a significant difference between the Moringa forages and the rest of them. In the second test, the CMS presented a significant difference between Ramón and the two remaining forages. Three linear regression models were highly significant, between CMS and crude protein content (PC), neutral detergent fiber (NDF) and total phenols (FT). It is concluded that peccaries have the preference for *M. oleifera*, which has the highest values in PC, FT and the lowest in NDF.

Environmental effects on collared peccaries (*Pecari tajacu*) serum testosterone, testicular morphology, and semen quality in the Caatinga biome.

Maia, K. M., Souza, A. L. P., Silva, A. M., Souza-Jr, J. B. F., Costa, L. L. M., Brandão, F. Z., Oliveira, M. F., Comizzoli, P., Silva, A. R.

Theriogenology, 126, 1 March 2019, 286-294

The objective of the study was to understand the influence of climatic variations in a semiarid environment on serum testosterone, testicular morphology and semen quality in collared peccaries (*Pecari tajacu*). Reproductive metrics (semen quality, testicular morphometry and testosterone serum profiles) of 10 mature males were measured monthly for 18 months. Meteorological data (rainfall, air temperature, relative humidity, wind speed and radiant heat load) also were recorded during the same period. Rainfall regimes were classified in different classes (Class 1: months with no rain; Class 2: months with up to 50 mm of rain; and Class 3: months with >50 mm of rain). Among rainfall classes, average air temperature (°C) and relative humidity (%) were different. Climatic changes between rainfall classes did not lead to overall variations of testicular size, testosterone production, and semen metrics. However, relative humidity recorded before semen collection (one day, one week, or over 51–55 days) was positively correlated ($P < 0.05$) with semen motility metrics (total motility, beat cross frequency and straightness) and sperm subpopulations (medium and static sperm), as well as with volume. Negative correlations ($P < 0.05$) were revealed between air temperature and the same semen motility patterns and volume. Additionally, radiant head load measured on the day of semen collection negatively influenced ($P < 0.05$) sperm straightness. This study demonstrates for the first time that no seasonal changes could be detected over the 18-month period on the serum testosterone, testicular morphology and semen quality of collared peccaries raised in the Caatinga biome; however, it is expected that long term environmental changes will influence the reproductive physiology of species leaving in that habitat.

The paradoxical situation of the white-lipped peccary (*Tayassu pecari*) in the state of Mato Grosso, Brazil.

Lima, M., Peres, C. A., Ilan, M., Abrahams, da Silva Junior, C. A., de Medeiros Costa, G., dos Santos, R. C.

Perspectives in Ecology and Conservation

Populations of white-lipped peccaries, *Tayassu pecari*, have already been extirpated or drastically reduced in much of the Neotropics, but are still relatively abundant in the Brazilian state of Mato Grosso, the country's largest maize and soy producer. This article synthesises over a decade of experience both visiting farms which experienced crop damage and working with hunters, farmers and technicians who live in areas of conflict with *T. Pecari*. These social ungulates feed within





New literature on Suiformes

maize plantations bordering forest fragments during the entire cultivation cycle and farmers in Mato Grosso vociferously protest the severe economic losses they cause. To protect their crops from damage, farmers slaughter white-lipped peccaries using firearms, traps and mass poisoning. We also draw attention to the need to mitigate the damage caused in agricultural frontiers by this ecologically important species, such that it is not decimated as it has been in the Caatinga and Atlantic Forest biomes.

Uso dos diluidores ACP® e BTS para refrigeração a 15°C de sêmen de queixada (*Tayassu pecari*).

Barros, C. H. S. C., Machado, W. M., Vieira, R. L. A., Allaman, A. B., Nogueira-Filho, S. G., Bittencourt, R. F., Snoeck, P. P. N.

Pesquisa Veterinária Brasileira

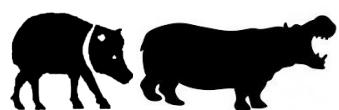
Knowledge about reproduction of white-lipped peccary is of great importance to assist with the conservation of this species and enable its rational use in captivity. This study aimed to evaluate the effect of ACP-103®, ACP-116® and BTS semen extenders on sperm viability during cooling of *Tayassu pecari* semen. Five ejaculates from four adult males were chilled. The animals were submitted to the protocols of sedation and anesthesia for semen collection by the electroejaculation method. After collection, the semen was macro- and microscopically assessed and diluted to reach 35x10⁶ spermatozoa/mL in each of the three different extenders tested. The fresh-extended semen was packed in a BotuFLEX® thermal box to keep samples at 15°C for 24 hours. After cooling, the following semen parameters were analyzed: sperm motility, functional and structural integrity of sperm membranes, mitochondrial activity, chromatin condensation, and the thermoresistance test was performed. The parameters sperm motility, structural and functional integrity of sperm membranes, mitochondrial activity, and chromatin condensation were preserved after use of the extenders tested, and were similar to those of in natura semen ($p>0.05$). Curvilinear velocity (VCL) ($p<0.05$) was the only parameter with reduced values after cooling regardless of the extender used. The percentage of sperm with normal morphology was greater in samples cooled using the BTS extender ($p<0.05$). The ACP-103®, ACP-116® and BTS extenders can be used for the cooling and preservation of white-lipped peccary semen at 15°C for 24 hours.

Drone-based effective counting and ageing of hippopotamus (*Hippopotamus amphibius*) in the Okavango Delta in Botswana.

Inman, V. L., Kingsford, R. T., Chase, M. J., Leggett, K. E. A.

BioRxiv

Accurately estimating hippopotamus (*Hippopotamus amphibius*) numbers is difficult due to their aggressive nature, amphibious lifestyle, and habit of diving and surfacing. Traditionally, hippos are counted using aerial surveys and land/boat surveys. We compared estimates of numbers of hippos in a lagoon in the Okavango Delta, counted from land and video taken from a DJI Phantom 4TM drone, testing for effectiveness at three heights (40 m, 80 m, and 120 m) and four times of day (early morning, late morning, early afternoon, and late afternoon). In addition, we determined effectiveness for differentiating age classes (juvenile, subadult, and adult), based on visual assessment and measurements from drone images, at different times and heights. Estimates in the pool averaged 9.18 ($\pm 0.25\text{SE}$, range 1 – 14, $n = 112$ counts). Drone counts at 40 m produced the highest counts of hippos, 10.6% higher than land counts and drone counts at





New literature on Suiformes

80 m, and 17.6% higher than drone counts at 120 m. Fewer hippos were counted in the early morning, when the hippos were active and most likely submerged, compared to all other times of day, when they tended to rest in shallow water with their bodies exposed. We were able to assign age classes to similar numbers of hippos from land counts and counts at 40 m, although land counts were better at identifying juveniles and subadults. Early morning was the least effective time to age hippos given their active behaviour, increasingly problematic with increasing height. Use of a relatively low-cost drone provided a rigorous and repeatable method for estimating numbers and ages of hippos, but not in the early morning.

Common hippopotamus-human conflicts in Ouémé River area in central Benin Republic.

Dossou, E. M., Houessou, L. G., Lougbegnon, T. O., Codija, J. T. C.

International Journal of Innovation and Applied Studies 25, 2, 2019, 638-644

The common hippopotamus belongs to the threatened species that urgently need conservation programs. In this perspective, a study on the relationships between the species and human was conducted in areas surrounding the Ouémé River in Benin. This study aims to assess the types of damages caused by hippopotamus and conflict mitigation solutions- in order to facilitate pacific cohabitation between hippopotamus and human. A total of 180 people were interviewed in 6 villages using structured and semi-structured interviews. Our results indicated that the main damage caused by common hippopotamus was crops raiding (81.67 % respondents). Most respondents (53.89 %) declared that hippopotamus caused damage to their crops in farmland during the whole year, but period for raids varied significantly between villages ($\chi^2 = 57.926$, $p < 0.0001$). This study highlights the necessity to implement mitigation measures in order to promote pacific cohabitation between hippo and human.

The diversity and conservation of mammals in the Dodo Coastal Forest in southwestern Côte d'Ivoire, western Africa: a preliminary study.

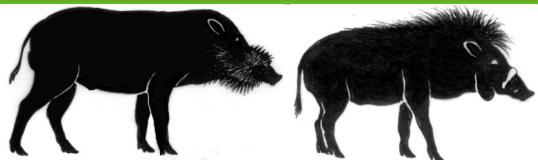
Soiret, S. P. G., Kouakou, C. Y., Koffi, B. J.-C., Kadjo, B., Kouassi, P., Gomez, P. J., Goodwin, R. M., Kone, I.

Journal of Threatened Taxa

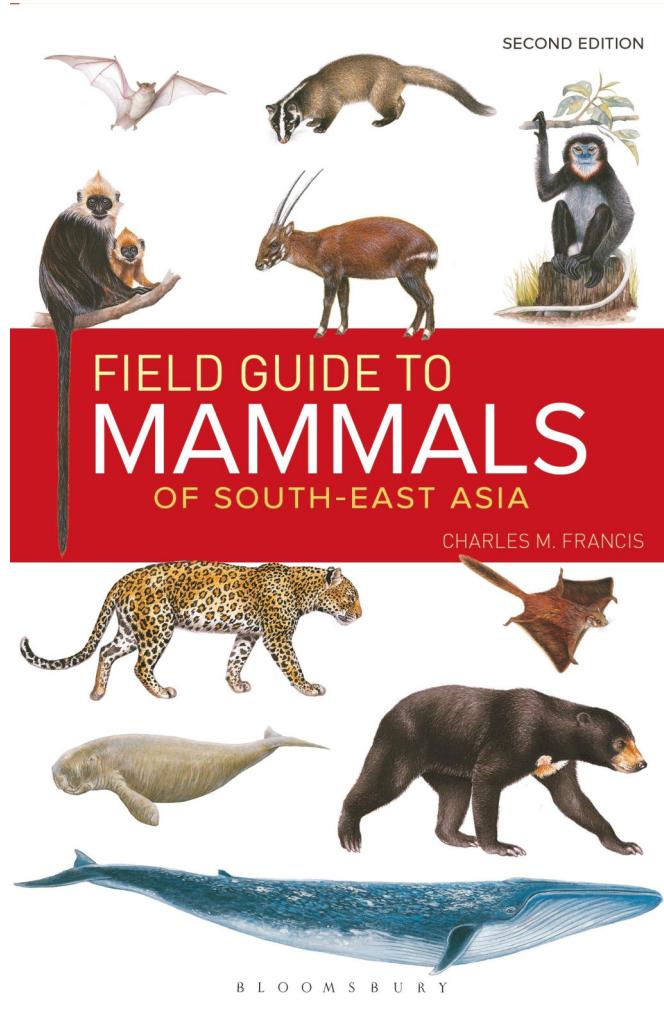
To improve the knowledge of non-volant mammal diversity and conservation prospects in the Dodo Coastal Forest (DCF) in southwestern Côte d'Ivoire, we conducted reconnaissance surveys and interviews, and deployed remote cameras. We calculated visual encounter rates (vER) and sign ER (sER) of mammalian taxa and hunting signs, mapped their locations and tested the hypothesis that sightings and signs of primates occurred closer to the river Dodo in and near the gallery forest. We sighted nine taxa, including threatened King Colobus (Endangered, EN), Olive Colobus (Vulnerable, VU), Lowe's Monkey (VU), the Eastern Lesser Spot-nosed Monkey (VU), and White-bellied Pangolin (VU), with vER of 0.04, 0.12, 0.04, 0.12, 0.04, respectively. We confirmed 14 other taxa with signs including threatened Western Chimpanzee (CR), Pygmy Hippopotamus (Endangered, EN), Bosman's Potto (VU), and Black-bellied Pangolin (VU), with sER of 0.51, 0.04, 0.08, 0.04, respectively. The most frequently encountered signs were of the Red River Hog at 1.73 signs/km, and the Bushbuck at 0.63 signs/km. Remote cameras captured images of these two taxa at image capture rates (ICR) of 0.044 and 0.022, respectively. Images of the African Buffalo were captured at ICR of 0.044. The 23 confirmed taxa include seven primates, four rodents, three carnivores, six even-toed ungulates, two pangolins and a Tree Hyrax. The mean distance from the river Dodo to the sightings and the signs of the primates was



New books about Suiformes



significantly shorter than that of other taxa. This supports our hypothesis. There was a high level of hunting signs ($sER = 0.63$) indicating that intensive hunting pressure is menacing the fauna. We recommend that authorities take actions against poaching, install a surveillance program, and curtail charcoal-making to ensure the conservation of the threatened mammals of the DCF.



South-east Asia is a hotspot of global biodiversity and this is also valid for mammal diversity. The area covered by this book written by Charles M. Francis is mainland South-east Asia and includes Myanmar in the west, Vietnam in the east, Lao People's Democratic Republic and Cambodia in the center and the Malay Peninsula and Singapore in the South. It describes more than 550 mammal species in detail.

After a short introduction about the changes and additions of this second edition of the book the author briefly presents the area covered, the classification of mammals (and the one he follows), how to identify mammals, general notes about the colour plates, the species accounts, finding and studying mammals (including capture techniques, camera traps and bat detectors), where to find mammals and the conservation of mammals.

The following 81 colour plates show the huge diversity of mammals in South-east Asia and even the variation within species. The plates are a cornucopia of very well painted species illustrations. Next to the plates are short

descriptions of each species and up-to-date distribution maps (except for the marine mammals without distribution maps). 23 of the plates with illustrations of species deal with bats and flying foxes, proving how much they contribute to biodiversity.

The section after the plates comprises the species accounts. A few species are not shown in the illustrations on the plates. For this section there is first a short description of the order, then of the family and whenever necessary descriptions of subfamilies or genera. These descriptions help to distinguish the taxonomic groups and to find species of interest. If necessary, figures showing skulls, teeth, other morphological characters or footprints are presented to aid species identification. Subspecies are only mentioned when they are different in their colour patterns or when they really should be considered full species. The species accounts comprise measurements, characters for identification, taxonomic notes, separation to similar species, ecology and habitat, distribution and the status of the species.





New books about Suiformes

Although considered to be extinct in the region, two rhino species, the Asian two-horned rhino (*Dicerorhinus sumatrensis*) and the Lesser one-horned rhino (*Rhinoceros sondaicus*), are described and regarding ungulates the extinct Schomburgk's deer (*Rucervus schomburgki*).

The author follows the taxonomic classification by Wilson and Reeder (2005). Therefore, the Eurasian wild boar (*Sus scrofa*) is mentioned as a single species but in a taxonomic note Francis writes that the subspecies *Sus scrofa vittatus* from the Malay Peninsula and Indonesia is "distinctly smaller with sparser hair" and is therefore considered a distinct species by some authors (like Melletti and Meijaard, 2018)). The two different wild boar forms are also shown on the colour plate. Following Melletti and Meijaard (2018) the wild boars in South-east Asia north of the Malay Peninsula belong to the species *Sus moupinensis*. Francis' book also has a species account of the Vietnamese warty pig (*Sus bucculentus*). This "species" is not illustrated on a colour plate and Francis summarise the most recent investigations and writes about the uncertainty, if this is a real species. Melletti and Meijaard (2018) consider *Sus bucculentus* to be an extreme specimen of *Sus moupinensis*. The third pigs account deals with the bearded pig (*Sus barbatus*). Francis's description is a well written summary about the biology of this species. Furthermore, he writes that the bearded pig of the Malay Peninsular "is at imminent risk of extinction" due to over-hunting and habitat loss. It has vanished from large protected areas because of the disruption to traditional migration routes and overhunting.

Overall, Francis has done a huge effort compiling all the mammal species living in mainland South-east Asia. He even writes about uncertain species like the Vietnamese warty pig and mentions different subspecies, whenever helpful to distinguish them in the field. This book is the most up-to-date source for mammals of this region. It is a good overview of all the different species and is helpful to distinguish species in the field by using the beautiful colour illustrations and the species accounts. It is also a very useful start to delve deeper into the different South-east Asian mammal species. A short glossary and a list of selected reference work underlines this. The book will hopefully help to raise interest in mammalian biodiversity in South-east Asia and the threatened species there. I am sure that it will be one of the main references for future research in mammalian diversity in this area.

Reviewed by Thiemo Braasch

Field Guide to the Mammals of South-East Asia

By Charles M. Francis

416 pages, 81 plates with colour illustrations, 74 b/w illustrations, colour distribution maps

Second edition, 2019

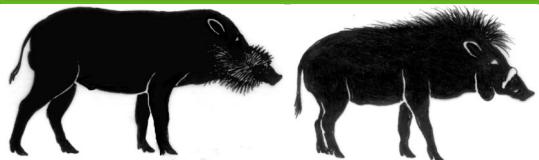
Bloomsbury Wildlife, London, UK

References

- Melletti, M. and E. Meijaard (eds.) 2018. Ecology, Conservation and Management of Wild Pigs and Peccaries. Cambridge University Press, Cambridge, UK.
- Wilson, D. E. and D. M. Reeder 2005. Mammal Species of the World: a Taxonomic and Reference. Third edition, John Hopkins University Press, Baltimore, USA.



Articles in the news



Town near Barcelona uses wolf urine to keep wild boar away

<https://www.theguardian.com/world/2019/aug/22/town-near-barcelona-uses-wolf-urine-to-keep-wild-boar-away>

Stephen Burgen, Thu 22 Aug 2019



A wild boar in an urban area near Barcelona, Spain. Photo: SEFaS/Ajuntament de Barcelona

Lack of rain may be forcing animals to seek food from rubbish bins in Aiguafreda

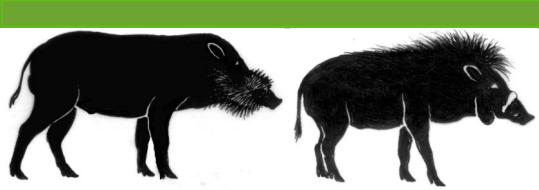
A small town outside Barcelona is using wolf urine to deter wild boar that have been coming in from the surrounding countryside.

After trying a variety of deterrents, the town council of Aiguafreda has agreed, in association with the local hunters' association, to see if the smell of the pheromones of the wild pigs' principal predator will keep them at bay.

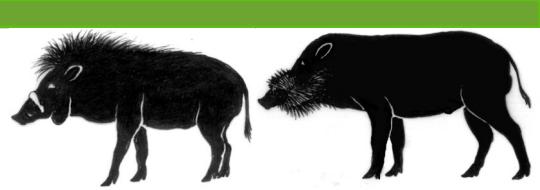
At least 10 boars have been sighted in the town recently. "There's not much food in the woods because it hasn't rained, so they come into town looking for food," Albert Alexandre Temprado, a local hunter, told *El País*. While boar numbers in the countryside can be controlled by hunters, this isn't a viable option in populated areas. Earlier this year the town tried using polyurethane to deter them, but the effect wore off within a few days. The council has created a perimeter of powdered wolf urine around the town, a method it insists is environmentally friendly and has no effect on domestic dogs. Temprado admitted that it remained to be seen whether it was effective.

Meanwhile, local authorities have warned people not to approach the boars, as they can become aggressive, or to leave food out for them. They also advise that they should keep rubbish containers closed to stop the animals from foraging. The boars are an invasive species and extremely adaptable. They have increasingly encroached on urban areas, much as foxes have in British cities. Research by the University of Barcelona suggests that some wild boars are even passing up on natural sources of food found in the woods in favour of foraging among rubbish. In recent years, groups of the animals have regularly been sighted in Barcelona, especially in neighbourhoods close to their natural habitat in the wooded Collserola hills to the west of the city. They have also been spotted close to the city centre. The boars carry disease and also cause numerous road accidents. Barcelona has employed a variety of methods to control numbers, among them targeting females of breeding age. In 2017 the city launched an experimental campaign of sterilisation using a vaccine. The technique has already been used in Britain and the United States. Early reports suggested that the vaccine had reduced the local Barcelona population by around 400.





Articles in the news



Mating behavior and movement patterns influence dynamics of animal diseases

<https://www.sciencedaily.com/releases/2019/08/190819112729.htm>

Date: August 19, 2019, Source: Forschungsverbund Berlin

Swine fever, rabies, bird flu - outbreaks of diseases in wildlife populations often also affect farm animals and humans. However, their causes and the dynamics of their spread are often complex and not well understood. A team of scientists led by the Leibniz Institute for Zoo and Wildlife Research (Leibniz-IZW) has now carried out an analysis of long-term data of an outbreak of classical swine fever in wild boars in the German federal state of Mecklenburg-Vorpommern that occurred between 1993 and 2000. The results suggest that non-infected regions have a higher risk of infection due to changes in movement patterns, particularly during the mast and rutting seasons (autumn and winter), and thus highlighting the importance for focusing intervention efforts on specific individuals, seasons and areas in the event of future outbreaks. The findings are published in the *Journal of Animal Ecology*.

The study was conducted by a team of scientists from the Helmholtz Centre for Environmental Research (UFZ), the Friedrich Loeffler Institute (FLI) and the University of Potsdam under the direction of Leibniz-IZW. "Studies such as these help us to uncover the temporal and spatial dynamics of diseases such as classical swine fever and to use these findings to derive possible causes for long-lasting epidemics as well as measures to prevent new infections and outbreaks," explains first author Cédric Scherer (Leibniz-IZW). The seasonal patterns of disease spread varied dramatically. "Interestingly, at the county level, infection was more likely to occur in autumn and winter, while individual wild boars, especially the young, are most likely to become infected in spring during birth season," reports Stephanie Kramer-Schadt, who heads the Leibniz-IZW project. "We assume that this is due to the increased movement activity in autumn and winter. In particular, the search for mating partners and the shortage of food lead to more frequent changes of location and thus likely enable the spread of the disease beyond district boundaries," Kramer-Schadt continues. Contrary to common interpretations, the density of wild boar in a municipality was not decisive. "This finding is understandable, as almost all districts have more wild boar than necessary for the spread of infectious diseases," explains epidemiologist Hans-Herrmann Thulke (UFZ), who co-initiated the study.

The detailed long-term data collected by the authorities in Mecklenburg-Vorpommern during the outbreak made it possible to investigate the temporal and spatial differences in the spread of the disease. The authors analysed the data for different phases of disease spread on the one hand and for individual animals and entire municipalities on the other.

Classical swine fever (or European swine fever) is a viral infection affecting wild and domestic pigs. Despite similar symptoms, the pathogens of classical swine fever and African swine fever are not related in the course of the disease. Long-lasting outbreaks of classical swine fever among wild boars often lead to the spread of the infection to agricultural pig farms. This can cause considerable economic damage if millions of domestic pigs are emergency slaughtered and export bans are imposed on pork products.

In order to limit the spread of classical swine fever in a wildlife population, vaccination baits could be used and/or the density of wild boar could be reduced by hunting. Although lowering the density to a theoretical minimum was often discussed as a measure, this study shows that in later times of an outbreak it was not the density but the contact rates, which likely increased due to changes in movement behaviour and made it possible for the disease to persist for several years.





Articles in the news

In order to prevent such persistence or future outbreaks, the focus should therefore be on reducing the contact rates between wild boar groups.

Journal Reference:

Cédric Scherer, Viktoria Radchuk, Christoph Staubach, Sophie Müller, Niels Blaum, Hans-Hermann Thulke, Stephanie Kramer Schadt. Seasonal host life-history processes fuel disease dynamics at different spatial scales. *Journal of Animal Ecology*, 2019; DOI: 10.1111/1365-2656.13070

Farmers jailed in Australia for smuggling Danish pig semen in shampoo bottles

<https://www.theguardian.com/australia-news/2019/aug/14/australian-farmers-jailed-for-smuggling-danish-pig-semen-in-shampoo-bottles>

Lisa Martin Wed 14 Aug 2019

Two men from GD Pork pleaded guilty in WA to breaching biosecurity laws to gain ‘unfair’ breeding advantage

Two pig farmers in Western Australia will be jailed after being convicted of illegally importing Danish pig semen concealed in shampoo bottles. Torben Soerensen has been sentenced to three years in prison, while Henning Laue faces a two-year sentence after pleading guilty to breaching quarantine and biosecurity laws. The Perth district court was told boar semen had been illegally imported from Denmark multiple times between May 2009 and March 2017. The semen was used in GD Pork’s artificial breeding program and several breeding sows were direct offspring of Danish boars. Federal agriculture minister Bridget McKenzie said breaches of biosecurity laws would not be tolerated.“This case shows a disturbing disregard for the laws that protect the livelihoods of Australia’s 2,700 pork producers, and the quality of the pork that millions of Australians enjoy each year,” McKenzie said. “GD Pork imported the semen illegally in an attempt to get an unfair advantage over its competitors, through new genetics.” Western Australian Farmers Federation spokeswoman Jessica Wallace said the offences was “a selfish act” that could cripple an entire industry. “How extremely disappointing,” she said. National Farmers federal chief executive Tony Mahar hopes the penalties act as deterrent to others contemplating biosecurity breaches. Industry body Australian Pork said pigs were highly susceptible to disease and major potential threats included African swine fever and foot and mouth disease. In Europe there have been cases of African swine fever on the Italian island of Sardinia for decades and the disease has spread to the European Union. The European Food Safety Authority said most outbreaks occurred in small farms and were contained relatively quickly. But the disease was still spreading locally among wild boar, where containment was more difficult. In Asia there have been outbreaks in China and Vietnam. Infected pigs show symptoms including fever, weakness and vomiting. Sudden death can also occur. The company, GD Pork, which is a subsidiary of a Danish company, received a fine of \$500,000 but is in liquidation. Administrators were appointed in October last year and sold off farms at Pinjarra and Kojonup as well as livestock in April this year. The federal agriculture department began investigating the business in February 2017. Authorities searched the Pinjarra farm and seized pig mating records in March 2017. In July the same year, in a separate raid, they seized samples of hair from individual pigs for genetic testing. An administrators’ report on the business said it borrowed an extra \$10.26m from lenders after the raids but at no time did GD Pork tell the banks of potential prosecution by government agencies.





Articles in the news



Ancient pigs endured a complete genomic turnover after they arrived in Europe

<https://www.sciencedaily.com/releases/2019/08/190812152200.htm>

Date: August 12, 2019, Source: University of Oxford

New research led by Oxford University and Queen Mary University of London has resolved a pig paradox. Archaeological evidence has shown that pigs were domesticated in the Near East and as such, modern pigs should resemble Near Eastern wild boar. They do not. Instead, the genetic signatures of modern European domestic pigs resemble European wild boar.

Published in *Proceedings of the National Academy of Sciences*, the study shows how this has happened. Working with more than 100 collaborators, researchers from Oxford's School of Archaeology sequenced DNA signatures from more than 2,000 ancient pigs including genomes from 63 archaeological pigs collected across the Near East and Europe over the last 10,000 years.

The findings revealed that the first pigs to arrive into Europe alongside farmers 8,000 years ago had clear Near Eastern genetic ancestry. Over the course of the next 3,000 years, however, ancient domestic pigs hybridised with European wild boar to such an extent that they lost almost all their Near Eastern ancestry. Some low level of Near Eastern ancestry, however potentially remained in the genome of modern European domestic pigs, and this likely explains their characteristic black, and black and white spotted coat colours. Higher level of Near Eastern ancestry were also maintained in pig populations on Mediterranean islands maintained probably because these populations experienced comparatively less gene flow with European wild boar relative to pigs on the continent.

Professor Greger Larson, Director of the Palaeogenomics & Bio-Archaeology Research Network (PalaeoBarn) at Oxford and senior author of the study, said: "Having access to ancient genomes over such a large space and time has allowed us to see the slow-motion replacement of the entire genome of domestic pigs. This suggests that pig management in Europe over millennia was extensive, and that though swineherders maintained selection for some coat colours, domestic pigs interacted with wild boar frequently enough that they lost the ancestral signature of the wild boar from which they were derived."

Dr. Laurent Frantz, lead author of the study at Queen Mary University of London, said: "We are all taught that the big change was the initial process of domestication, but our data suggests that almost none of the human-selection over the first 2,500 years of pig domestication has been important in the development of modern European commercial pigs."

Now that the team have pieced together a timeline of the genomic history of pigs in western Eurasia, the next steps in the research will be to precisely identify, in the genome of modern European domestic pigs, the few genes that retained their original Near Eastern ancestry. This will allow us to assess whether the artificial selection applied by early farmers in the Fertile Crescent, over 10,000 years ago, left any further legacy in modern pigs beyond coat colour.

Journal Reference:

Laurent A. F. Frantz, James Haile, Audrey T. Lin, Amelie Scheu, Christina Geörg, Norbert Benecke, Michelle Alexander, Anna Linderholm, Victoria E. Mullin, Kevin G. Daly, Vincent M. Battista, Max Price, Kurt J. Gron, Panorama Alexandri, Rose-Marie Arbogast, Benjamin Arbuckle, Adrian Bălăşescu, Ross Barnett, László Bartosiewicz, Gennady Baryshnikov, Clive Bonsall, Dušan Borić, Adina Boroneanț, Jelena Bulatović, Canan Çakırlar, José-Miguel Carretero, John





Articles in the news

Chapman, Mike Church, Richard Crooijmans, Bea De Cupere, Cleia Detry, Vesna Dimitrijevic, Valentin Dumitraşcu, Louis du Plessis, Ceiridwen J. Edwards, Cevdet Merih Erek, Aslı Erim-Özdoğan, Anton Ervynck, Domenico Fulgione, Mihai Gligor, Anders Götherström, Lionel Gourichon, Martien A.M. Groenen, Daniel Helmer, Hitomi Hongo, Liora K. Horwitz, Evan K. Irving-Pease, Ophélie Lebrasseur, Joséphine Lesur, Caroline Malone, Ninna Manaseryan, Arkadiusz Marciniak, Holley Martlew, Marjan Mashkour, Roger Matthews, Giedre Motuzaitė Matuzeviciute, Sepideh Maziar, Erik Meijaard, Tom McGovern, Hendrik-Jan Megens, Rebecca Miller, Azadeh Fatemeh Mohaseb, Jörg Orschiedt, David Orton, Anastasia Papathanasiou, Mike Parker Pearson, Ron Pinhasi, Darko Radmanović, François-Xavier Ricaut, Mike Richards, Richard Sabin, Lucia Sarti, Wolfram Schier, Shiva Sheikhi, Elisabeth Stephan, John R. Stewart, Simon Stoddart, Antonio Tagliacozzo, Nenad Tasić, Katerina Trantalidou, Anne Tresset, Cristina Valdiosera, Youri van den Hurk, Sophie Van Poucke, Jean-Denis Vigne, Alexander Yanevich, Andrea Zeeb-Lanz, Alexandros Triantafyllidis, M. Thomas P. Gilbert, Jörg Schibler, Peter Rowley-Conwy, Melinda Zeder, Joris Peters, Thomas Cucchi, Daniel G. Bradley, Keith Dobney, Joachim Burger, Allowen Evin, Linus Girdland-Flink, Greger Larson. Ancient pigs reveal a near-complete genomic turnover following their introduction to Europe. *Proceedings of the National Academy of Sciences*, 2019; 201901169 DOI: 10.1073/pnas.1901169116

A hog in wolf's clothing

<https://www.sciencedaily.com/releases/2019/08/190806142335.htm>

Date: August 6, 2019, Source: PLOS

Human and wildlife conflict has increased along with expanding human populations, particularly when wildlife endanger humans or their livelihoods. Most research on human-wildlife conflict has focused on the ways tigers, wolves, and other predators impact livestock even though noncarnivores also threaten livestock. New research by Dr. Shari Rodriguez and Dr. Christie Sampson, both from Clemson University, publishing on August 6 in the open-access journal PLOS Biology, examines the effects of these less-studied relationships, particularly for feral hogs and elephants, and the potential consequences of excluding these animals from research focused on mitigating wildlife impacts on livestock.

"Our study highlights the importance of including species not traditionally considered in the livestock protection conversation, and finding similarities in how the effects of non-Carnivora species can be addressed through the same methodologies as species such as wolves, tigers, or lions," says Dr. Rodriguez.

Results show that these species can have significant effects on livelihood by killing young and small livestock and damaging livestock farming infrastructure. They may also affect local communities' perception of the species, which in the case of species of conservation concern such as elephants could potentially reduce people's willingness to support conservation initiatives.

"Sharing experiences across taxa and adopting methodology found to be successful for other [predatory] species may help us to improve the tools we use to promote co-existence and conservation efforts for elephants," reported Dr. Sampson.

Journal Reference:

Shari L. Rodriguez, Christie Sampson. Expanding beyond carnivores to improve livestock





Articles in the news

protection and conservation. PLOS Biology, 2019; 17 (8): e3000386 DOI: 10.1371/journal.pbio.3000386

True identity of imposter 'pigs' on 17th century map overturns early colonial history of Barbados

<https://www.sciencedaily.com/releases/2019/05/190516131750.htm>

Date: May 16, 2019, Source: Simon Fraser University

Which came first, the pigs or the pioneers? In Barbados, that has been a historical mystery ever since the first English colonists arrived on the island in 1627 to encounter what they thought was a herd of wild European pigs. A recent discovery by an SFU archaeologist is shedding new light on the matter. Christina Giovas uncovered the jaw bone of a peccary, a South American mammal that resembles a wild pig, while researching a larger project on prehistoric animal introductions in the Caribbean. "I didn't give it much notice at the time, but simply collected it along with other bones," says Giovas, the lead author of a study just published in PLOS ONE. "It was completely unexpected and I honestly thought I must have made a mistake with the species identification." Giovas and collaborators George Kamenov and John Krigbaum of the University of Florida radiocarbon-dated the bone and conducted strontium isotope analysis to determine the age and whether the peccary was born on Barbados or had been imported from elsewhere. The results showed the peccary was local and dated to 1645-1670, when the English wrote their account of finding wild European pigs on the Caribbean island. The researchers were not only able to show there had been a previously undetected historic peccary introduction but that the region's earliest celebrated maps depicted peccaries that had been mistaken for pigs by the English.

Giovas says the findings upend Barbados' accepted colonial history and reflect how quickly Europeans began to alter New World environments by altering species distributions.

"Checking historical and archaeological records, we determined the most likely source of peccary introduction was from Spanish or Portuguese ships passing the island in the 16th century -- and most likely left as a source of meat for future visiting sailors," she says.

Journal Reference:

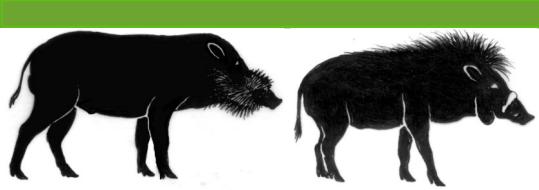
Christina M. Giovas, George D. Kamenov, John Krigbaum. 87Sr/86Sr and 14C evidence for peccary (Tayassuidae) introduction challenges accepted historical interpretation of the 1657 Ligon map of Barbados. PLOS ONE, 2019; 14 (5): e0216458 DOI: 10.1371/journal.pone.0216458

Wild boars make a home amid Hong Kong's high rises and highways

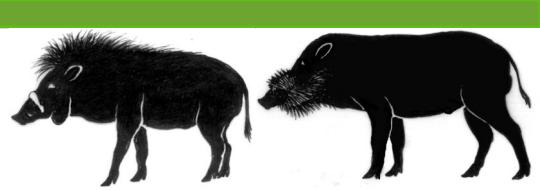
<https://www.nationalgeographic.com/animals/2019/04/hong-kong-urban-dwelling-wild-boars/>
Laurel Chor, PUBLISHED April 2, 2019

On a Wednesday morning in one of Hong Kong's high-end residential areas, a large wild boar napped peacefully on the side of a road. It was seemingly oblivious to the rush hour traffic whizzing past mere feet away, which caused great offense to local resident Mrs. Kuk. As she snapped pictures on her phone, she said she "always" sees this specific male around: "He's becoming more and more daring. Look at him sleeping here, as if us humans weren't even around!" The last time she encountered him, he was digging through trash. She called the police.





Articles in the news



The city of 7.3 million isn't exactly known as a bastion for wildlife; foreigners and locals alike typically see it as jungle of steel and asphalt. But its image belies rich fauna and flora: three-quarters of its land is undeveloped and almost 40 percent is protected, providing a lush habitat for a remarkably high level of biodiversity.

For most of the city's history, people and wild boars, Hong Kong's largest native terrestrial animal, coexisted in peace. The animals were either a minor nuisance to villagers, or they were a rare, lucky sighting for hikers who ventured out into country parks at dawn or dusk. But in the past five years, something's changed: they seem to be everywhere.

In 2018, Hong Kong received a record number of complaints about the wild boar: 929, more than triple the number just five years prior. Most are made by frightened citizens who don't know what to do during an encounter. Others require police intervention, for instance when the animals wander into urban areas and can't find their way back to the forest. In some rare cases, people have gotten minor injuries from bites and being charged.

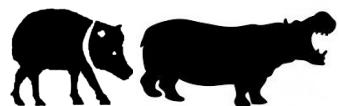
To deal with the problem, the department of agriculture has a six-person team dedicated to responding to complaints and figuring out solutions, which the government plans on tripling in size by the end of 2019. For this fiscal year alone, it's allocated almost \$450,000 to the problem.

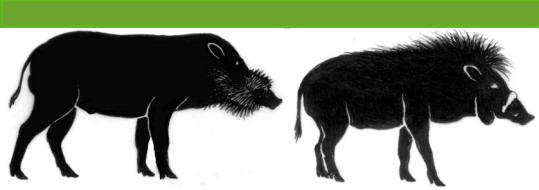
There aren't any estimates for how many wild boars there are in Hong Kong, but with no natural predators in the area and continuous sources of human food, it's clear the pigs' population has become an issue. The wild boar (*Sus scrofa*), also known as the Eurasian wild pig, is a highly adaptable omnivore that can weigh anywhere from 150 to 600 pounds. These mammals' range extends as far west as Marrakech and as far east as Brisbane, making it one of the most widely distributed mammals in the world. They've also been introduced to the Americas, where they're considered pests.

With such a wide range, it's no surprise that Hong Kong authorities aren't alone in having to manage urban boars. Barcelona and Brussels have their own ongoing pig struggles, for example. But Hong Kong is special in two regards. Firstly, with the city's towering skyscrapers built along the flanks of forest-covered mountains, the boars easily venture into hyper-urban environments, like in between apartment buildings or even inside malls. Secondly, people won't stop feeding the pigs.

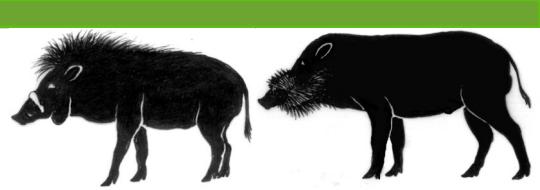
"This is the main reason that pigs have started coming to urban areas," explains Chan Po-Lam Chan, who's on the government wild boar team. "People love the pigs very much."

For 35 years, Hong Kong attempted to control the population the same way that many other places have: by hunting them. Two teams of civilian volunteers were given license to shoot and kill the animals, but the government halted the program in 2017. As pig encounters became increasingly common, so did their popularity, making lethal population control methods rather contentious. (A few citizens even formed an organization called the "Hong Kong Wild Boar Concern Group" to advocate against it.) It had become too dangerous anyway, considering the boar's increasingly urban range. Less than two years ago, the government began experimenting with birth control. Female are shot with tranquilizers, captured, then either given a contraceptive vaccine or sterilized through surgical means. As a final measure, they're released in more remote areas of Hong Kong. The wild boar population should eventually diminish in size, but in the meantime, the government has begun an aggressive public education campaign. Illustrated banners featuring anime-style characters have been put up around country parks, warning against feeding, chasing, or taking selfies with the animals. "[Education] is really challenging, because some people are really determined to feed them," Po-lam said, with more than a hint of





Articles in the news



exasperation in her voice. Their persistence is almost to be admired. Despite fines and court summons, some offenders continue to feed them; in one case, one was spotted again the very next morning after getting caught. Despite her frustrations, Po-lam doesn't necessarily hold it against the animal lovers. In one incident, her team responded to a call about a boar that had gotten its leg entangled in some wire. Too wary of people, the pig refused to let them approach. They only made progress when they enlisted the help of someone that the pig recognized—a regular feeder. Paul Zimmerman, a Dutch-born district politician, has had to create a special folder for his constituents' increasing number of wildlife-related complaints: "Dogs, cats, snakes, boar, and cockatoo". (Hong Kong has a small population of wild cockatoo, which sometimes get poached for the pet trade.) When he checked the folder's email count, he found 484. Wild boar now rival traffic and transportation as the number-one topic of the grievances he receives. But he doesn't really mind: "In a way, it's kind of fun to deal with that. There's an issue with the wild boar – but it's fantastic there are so many."

DISCLAIMER

- *with respect to content:*

IUCN encourages meetings, workshops and other fora for the consideration and analysis of issues related to conservation, and believes that reports of these meetings are most useful when broadly disseminated. The opinions and views expressed by the authors may not necessarily reflect the formal policies of IUCN, its Commissions, its Secretariat or its members.

- *with respect to geography:*

The designation of geographical entities in this book, and the presentation of the material, do not imply the expression of any opinion whatsoever on the part of IUCN concerning the legal status of any country, territory, or area, or of its authorities, or concerning the delimitation of its frontiers or boundaries.

The IUCN/SSC Wild Pigs, Peccaries and Hippos Specialist Groups (WPSG, PSG and HSG) are three of several Specialist Groups of the Species Survival Commission (SSC) developed by the IUCN to foster conservation, research and dissemination of information for species of conservation concern.

These groups consist of technical experts focusing on the conservation and management of wild pigs, peccaries and hippos.

The broad aim of the these groups is to promote the longterm conservation of wild pigs, peccaries and hippos and, where possible, the recovery of their populations to viable levels.

Pigs, peccaries and hippopotamuses are nonruminant ungulates belonging to the Suborder Suiformes of the Order Artiodactyla (the even-toed ungulates). Within the Suborder Suiformes, pigs belong to the Family Suidae, peccaries to the Family Dicotylidae and hippopotamuses to the Family Hippopotamidae.

