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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

Dear fellow reader,

it is a great pleasure to present you this issue of Suiform Soundings!

Unfortunately, I have to inform you that Matthew Linkie has left our editorial board. Matthew has done a great job writing reviews on articles and commenting manuscripts for several years. The editorial board wants to thank him for his hard work and all his input in every issue of Suiform Soundings! Thanks a lot, Matt! We miss you and wish you all the best for the future!

You may have noticed that Suiform Soundings has not been published in February or March this year. As you may know all the editorial work, the peer review and the layout for each issue of Suiform Soundings is done voluntarily by passionate people. In addition to that the amount of articles submitted to Suiform Soundings has decreased continuously during the last years. Therefore, the editorial board has decided to publish Suiform Soundings at least once a year. If more articles are submitted and accepted within six months we could also publish a second issue of Suiform Soundings depending on the time, the members of the editorial board can afford.
We do not have any deadline for submissions anymore!

It is up to you, the reader of Suiform Soundings, if we get a few or many submissions to Suiform Soundings.

Enjoy reading!

With warm regards,

Thiemo Braasch

Chief Editor Suiform Soundings

African Swine Fever

Adding a new dimension to African swine fever research: zoos provide African wild pigs for a collaborative research project

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Since its arrival in the Asia-Pacific region in August 2018, the African swine fever (ASF) virus has reached all countries and regions with threatened wild pig species (Luskin et al., 2021). As it was feared (Jori, 2014), ASF has caused mass die-offs in VULNERABLE bearded pigs (*Sus barbatus*) (Ewers et al., 2021; Meijaard et al., 2024) and VULNERABLE Philippine warty pigs (*Sus philippensis*) (Chavez et al., 2021). On the island of Negros, the virus reached Sulawesi warty pigs (*Sus celebensis*) in North Sulawesi in September 2023, killing several individuals (Azhar & Khairina, 2023) and led to the extinction of a whole captive population of CRITICALLY ENDANGERED Visayan warty pigs (*Sus cebifrons*) in June 2023 (Ward, pers. comm.). These outbreaks make unmistakably clear that the ASF virus (ASFV) is a threat to in-situ and ex-situ populations of endangered Asian wild pigs. The disease threatens all wild pig species endemic to Southeast Asia (Luskin et al., 2021), as well as backup ex-situ populations in European, American, and Asian zoos. Neither a treatment, nor a vaccine against the virus are currently available. In contrast to Asian pig species, Eurasian wild boar (*Sus scrofa*) and domestic pig (*Sus scrofa domesticus*), infection in African wild pigs, such as the common warthog (*Phacochoerus africanus*) or red river hog (*Potamochoerus porcus*), is apathogenic, despite virus replication within its pig host. Therefore, warthogs are recognised as reservoir hosts that sustainably the sylvatic cycle together with *Ornithodoros* soft ticks. In contrast, species of the genera *Sus* and *Babyrousa* are highly susceptible to the virus and die in over 95% of the cases.

It is important to understand ASF also under a One Health approach, where human, animal and environmental health is linked. The virus does not only threaten populations and even whole species of wild pigs, it also impairs the functionality of whole ecosystems. As ecosystem engineers, pigs are important for healthy ecosystems and are an important prey for predators. In addition, they are an important protein source for many local and indigenous people if hunting is done sustainable and a crash of their populations threatens food security in several regions (Meijaard et al., 2024), as well as the income of local communities. The latter affects access to health care, leading to a further deterioration of the situation. In order to make governments aware that not only the swine industry is affected, but also the wild pig communities, ecosystems and local people’s livelihoods in remote areas, the IUCN, the UN’s Food and Agriculture Organization (FAO) and the World Organisation for Animal Health (OIE) released an important Joint Statement in 2021 (FAO et al., 2021).

Global research activities on ASF, focusing on Eurasian wild boar and domestic pig as animal models, has not led to a full understanding of the virus-host system. Despite decades of research, safe and efficacious vaccines are still missing and progress in their development is slow. For in-situ conservation, an oral vaccine would be needed that could be spread with baits over large areas. Therefore, in September 2021 a joint research project on ASF in red river hogs and common warthogs was initiated at the request of the IUCN SSC Wild Pig Specialist Group to gain insight in the ASFV in its natural hosts. The study was designed and executed by the Friedrich-Loeffler-Institute (FLI), Germany`s Federal Research Institute for Animal Health who also runs the trials. Additional partners are the European Association of Zoo and Wildlife Veterinarians (EAZWV) and the Tapir and Suiform Taxon Advisory Group (Tapir and Suiform TAG) of the European Association of Zoos and Aquaria (EAZA). The EAZA agreed to transfer six red river hogs and six common warthogs born in European zoos to FLI for research on ASF. The aim is to understand why these African species do not get sick, understand the mechanisms that trigger the resistance and use this knowledge to advance the development of a vaccine or treatment. This collaborative project also serves as a good example for the One Plan Approach to Conservation Planning (OPA), as it brings together responsible parties working on the conservation of species in the wild and in human care.

Obviously, this research involved animal experiments, which are strictly regulated by the German Animal Welfare Law. In Germany, there is a thorough process in place to apply for respective permits, amongst others to assure the best possible animal welfare, e.g. the reduction of the number of individuals used to an absolute minimum, and the refinement of the experiment, following the 3R principle.

The animals have been carefully selected by the responsible EEP (EAZA Ex-situ Programmes) coordinators and where provided by Cologne Zoo and Opel-Zoo Kronberg (red river hogs), as well as by Allwetterzoo Münster, Osnabrueck Zoo and Magdeburg Zoo (common warthogs). Both species are managed as EEPs but the transfers of the individuals had no negative impact on the zoo populations as they are bred regularly in the zoos. The pigs are housed in a safe environment at FLI, according to all legal aspects. The red river hogs arrived at FLI in October 2023. After acclimatization, the animals were inoculated with the virus, blood and other samples were taken under general anaesthesia at regular intervals after the infection. At the end of the red river hog trials in February 2024, the animals were euthanized humanely and a full necropsy was performed to maximize the gain of knowledge, first results are promising. The trials with the common warthogs will run from March until June 2024. Samples are shared with five institutions in four other countries and integrated into a research network involving the Pirbright Institute, French Agricultural Research Centre for International Development and others. The research project is part of the EU-funded research project ASF-RASH (African Swine Fever pathogenesis and immune responses in Resistant And Susceptible Hosts). Being under close inspection of society, this exceptional decision of zoos to support and participate in this study points out the importance role zoos with their living collections can play in conservation and research. Even by keeping and breeding non-threatened species such as red river hogs and common warthogs.

Red river hogs in Opel Zoo Kronberg, Germany. Photo:J. Beckmann

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Social behaviour of Red River Hogs (*Potamochoerus porcus*) in zoos

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Abstract

Red river hogs (*Potamochoerus porcus*) show distinct social behaviour, which has not been studied thoroughly so far. The aim of the present study is to analyse and describe the social behaviour of the red river hogs in the social organisations of the Duisburg Zoo, Cologne Zoo and Aachen Animalpark. For this purpose, 160 hours of observation data were collected with focal-subgroup sampling, and photos and description of social contexts were taken. Social interactions appeared during 4.2 % of the time, while communication and physical contact played a constant role throughout all situations. The social behaviour was mainly characterised by affiliative touching. Agonistic behaviour was observed only to a small extent in connection with food resources or to establish a hierarchy. Play behaviour and agonistic behaviour included similar body signals, which could be differentiated by looking at the situational context of the signals. Submissive and aggressive behaviour differed in body language signals. Red river hogs are extremely social animals with a pronounced social behaviour. Follow-up studies could contribute to further knowledge about the social interaction and communication.

Keywords: Red river hog, Potamochoerus porcus, Social behaviour, Communication signals

Introduction

There are 18 pig species worldwide. Despite the broad taxonomy of Suiformes, not much is known about their social behaviour, either in common and widespread species, or in rare, endangered species. Mainly European wild boar (*Sus scrofa*) or domesticated pigs are the subject of scientific studies, but primarily for economic and ecological reasons. Pigs can roam their habitat as solitary animals or in various group organizations, such as bachelor groups or family groups, with or without males (Melletti et al. 2018). However, little is known about the social behaviour in these different groups.

Communication is essential for the interaction between individuals (Campbell et al. 2019). Intraspecific signals are used to exchange information (Kappeler 2020) and to organise and consolidate the social structure of a group (Frings 2021). The social coexistence of suids (family Suidae) is based on communication, which includes acoustic, visual, tactile and olfactory signals (Leslie & Huffman 2015). In the African species, the red river hogs (*Potamochoerus porcus*), acoustic communication is of central importance (Leus & Vercammen 2013). The sound repertoire includes different variations of grunts and squeaks (Leslie & Huffman 2015).

Dominance hierarchies play a decisive role in the descriptions of the social behaviour of *Sus scrofa* (Ortega-Salgado 2018). Risky confrontations and the associated high stress levels can be avoided by the predictability of social behaviour (Kappeler 2020; Sachser 2021). Agonistic

behaviour occurs especially in newly formed groups and in established groups with closely ranking neighbours, as the high level of energy involved can lead to a change in the hierarchy (Schnebel & Griswold 1983). The hierarchy is established with agonistic interactions through species-specific aggressive behaviour, such as threatening, biting and chasing, and through submissive behaviour, such as ducking and fleeing (Kappeler 2020). Animals that have a higher rank position show more aggressive behaviour (Ortega-Salgado 2018).

In addition to agonistic behaviour, animals show affiliative behaviour such as mutual licking, scratching or cuddling, which is associated with positive emotions and well-being. Like positive touching, playing is also part of affiliative behaviour (Sachser 2021).

Red river hogs (*Potamochoerus porcus*), which are found in West and Central Africa (Grubb 1993), are social animals that live in groups of highly variable sizes of up to 60 individuals (Leus & Vercammen 2013; Leslie & Huffman 2015). The permanent family units are smaller with 6-20 animals and usually consist of several adult females, subadults and piglets, which are accompanied by an adult male (Meijaard et al. 2011; Melletti et al. 2018).

This study examines the captive social behaviour of *Potamochoerus porcus* with a focus on behaviour and communication in the captive environments of Cologne Zoo, Duisburg Zoo and Aachen Animalpark, all in Germany. This study examines (1) the proportion of social behaviour of the overall behaviour and the frequency of affiliative and agonistic behaviours. It also investigates (2) whether body language expressions can be clearly assigned to affiliative touching, play behaviour and agonistic behaviour. (3) Finally, the study investigates in which situations red river hogs use acoustic communication signals.

Methods

Data collection

The observations were carried out on eight individuals over eight weeks in February and March 2023 at Cologne Zoo, Duisburg Zoo and Aachen Animalpark at different times of day. The animals were divided as follows: an 11-year-old red river hog mother together with her three male young born on 25th March 2022 were observed at Cologne Zoo. Additionally, two older female red river hogs at Duisburg Zoo and a 14-year-old sibling pair (male and female) at Aachen Animalpark were also observed.

The observation time of 160 hours was divided equally between the observation groups (two animals each). Focal subgroup sampling method was used (Altmann 1974). The behaviour of the animals was documented using an ethogram (Table 1). When the animal had physical contact with conspecifics during the "inactive" behaviour, it was noted down as well. The quantitative data collection was carried out using the ZooMonitor app (Lincoln Park Zoo 2022). For the qualitative data part, photo documents of interactions between the animals were created and situation descriptions were collected (ad libitum sampling). The photographs were taken with a Canon 700 D camera with Canon EF-S 18-55 mm and Canon EF-S 55-250 mm lenses. Notes on acoustic communication signals were also recorded ad libitum, showing different variations of sounds in different situations. The sound recordings were made using smartphones and assigned to a description of the situation. Due to time constraints, the sounds could not be analysed sonographically, but were described qualitatively.

Tab. 1: Ethogram for the behavioural observation of red rive hogs, adapted from Thalken (2022), Schmidt (2016), Saebel (2007) and Rademaker et al. (2015). Green = non-social behaviour, blue = affiliative social behaviour, red = agonistic social behaviour.

Behaviour	Definition
Food intake	Searching for and ingesting food, e.g. eating, sniffing, digging, drinking
Locomotion	Movement of the individual from one point to another
Alert	Looking up attentively at another animal or the surroundings, body posture with raised head, little to no movement, but no freezing; sniffing unrelated to foraging or social contact, there may be physical contact between the animals, which is unrelated to play behaviour or competition
Freezing	Abrupt stopping and freezing, often simultaneously in all group members, the condition lasts for a few seconds, head slightly raised, eyes no longer blinking but staring into the distance
Excitement	Excited pacing or running, frequent loud sniffing, eyes focussed on the cause of excitement, signs of stress such as squeaking, riding up, without aggression or play
Inactive	Sleeping or resting, standing, sitting or lying quietly with eyes open or closed, no visible tension; relief from faeces
Object manipulation	Playing, carrying an object around, nibbling on furnishings, the action is not directly related to food intake (e.g. no food enrichment)
Cleaning movement	Nibbling, licking or scratching their own body
Rolling / scrubbing	Rolling, rubbing parts of the body or the whole body against an object or the floor
Stretching	Stretching individual body parts or the whole body; yawning
Allogrooming	Social grooming, nibbling, licking or scratching another individual
Being touched	Touching by another individual in the form of allogrooming, nose-to-nose contact or nosing body, where the individual passively allows the touch or changes position in favour of the touch
Rubbing against each other	Rubbing parts of the body or the whole body against another individual
Nose-to-nose contact	At least two animals touch each other with their noses, no allogrooming
Nose-body contact	Touching another animal with the nose without displacing or pushing it away; nose-to-nose contact and allogrooming are excluded
Playful snout push	Frontal running towards each other and head-to-head ramming, pushing another individual away with the head in a playful context
Playful mounting	Lateral, frontal or dorsal jumping onto another animal; playful body contact
Playful tussling	Playful nibbling, snapping, nipping or running after them
Displacement	Maintaining the distance to another animal; if the distance falls below a certain level, the animal reacts with immediate rejection, e.g. in the event of food competition; this excludes an aggressive biting attempt with visibly open teeth
Pushing away	Pushing away a nearby or lying conspecific with the snout, the side of the body or the hindquarters
Aggressive snout push	Bumping the head head-on against the head of another animal without a playful context
Bite attempt	Aggressive attacking of an animal with the snout, the open teeth are visible, it does not have to come into contact with them
Mounting	Mounting another animal, which then moves away
Tussle	Aggressive altercation between at least two animals, regardless of who started it, squealing may occur
Chasing / Pursuing	Chasing and pursuing another animal that moves away, both animals involved move away from the starting position
Dodging	Increasing the distance between two individuals in response to actively chasing, displacing or pushing away the other individual
Other behaviours	Behaviours not listed in the ethogram
Not in sight	The individual is not visible

Data analysis

For the quantitative behavioural analysis, the frequencies of the behaviours were calculated per 30 minutes, so that 30 minutes correspond to one data unit. For selected tests and presentations, the social behaviours were pooled. For the group analyses, the data of the individuals were pooled without taking individual differences into account. The data collected on the behavioural patterns of the red river hogs were then analysed using IBM SPSS Statistics software (version: 29.0.0.0 (241)) (Field 2005). For the qualitative analysis, the photos were used to describe the body language signals typical of the behaviours listed in the ethogram. The situations noted ad libitum were used to describe the observed behavioural sequences. For the evaluation of acoustic communication, the combination of sounds and behaviour of different situations was summarised (Ahire & Prashanth 2020).

Results

The eight red river hogs displayed a social behaviour for 4.2 % of the time observed. The total social behaviour consisted of 7.3 % agonistic behaviour and 92.7 % affiliative behaviour (Fig. 1), which in turn was made up of 48.1 % touching and 44.6 % play. The largest proportion of play behaviour was "playful tussling". “nose-to-nose contact", "playful snout push", "being touched" and "nosing body" were also frequently observed.

Description of Behaviours

Affiliative touches were initiated gently with the top of the snout. This was characterised by relaxed to closed eyes and loosely backward-pointing ears (Fig. 2). In the case of "**Rubbing**

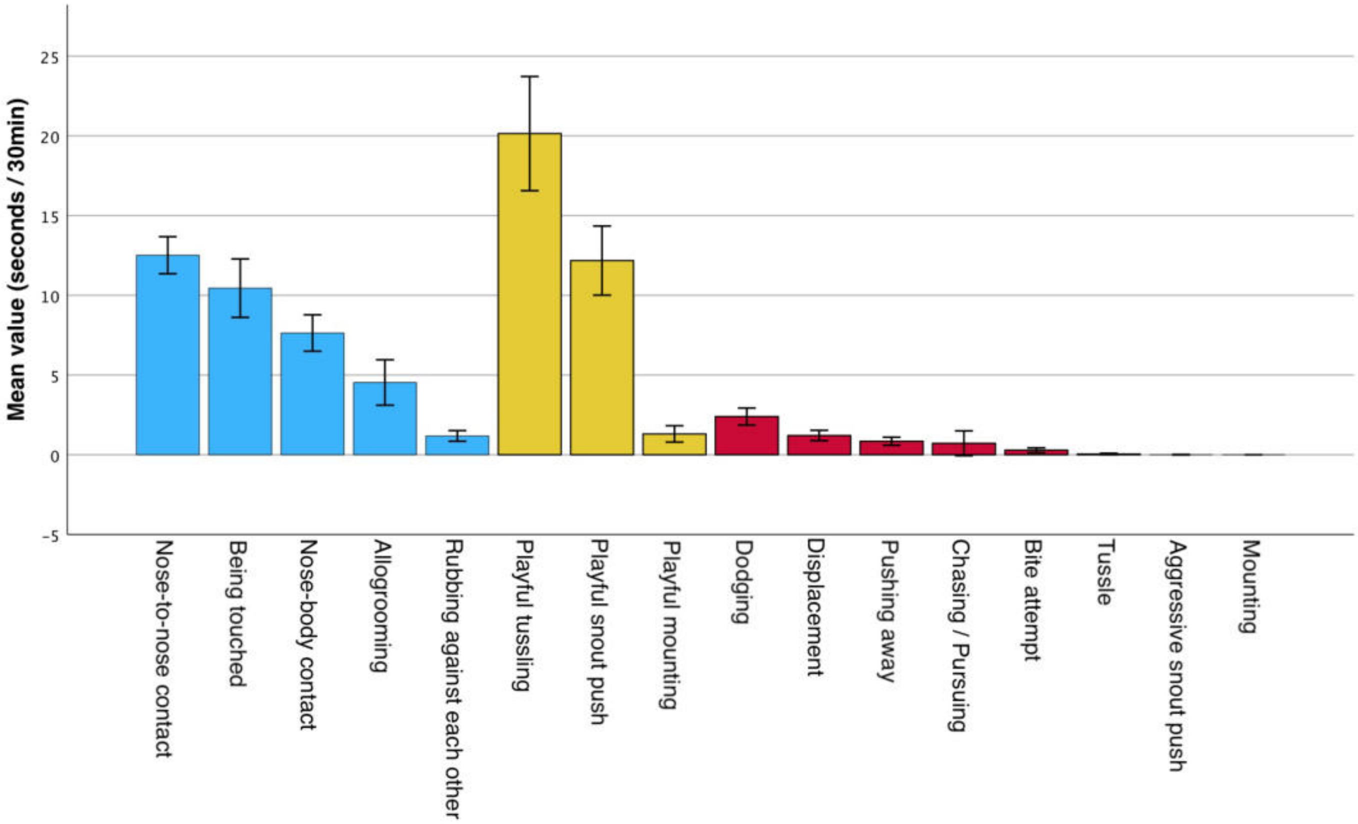

Fig. 1: Mean value of the time (seconds per 30 minutes) of the social behaviours summarised for the red river hogs living with conspecifics in Aachener Tierpark, Duisburg and Cologne Zoo. blue=affiliative touching, yellow=play behaviour, red=agonistic behaviour.

Fig. 2: Gentle touches with relaxed to closed eyes and ears turned loosely backwards.

against each other", the whole side of the body was rarely involved; here too, the movement usually originated from the snout. In “**Nose-to-nose contact**” between two pigs, the touching was associated with sniffing, slightly vibrating movements of the snout. The contact was usually initiated by both animals, with the animals stretching their heads towards each other (Fig. 3a). Nose-to-nose contact could also occur from one pig, whereby the activity (e.g. eating or inactive) of the touched pig remained unchanged (Fig. 3b). The body was not tense during gentle nose-to-nose contact, but this could change in a different context. For example, nose-to-nose contact can occur during play, when the body was tense (Fig. 3c). During “**Nose-body contact**”, the side of the body at the level of the kidneys or shoulder blade was usually sniffed and the animal leaned its snout under the belly of the other animal, forehead on the side of the other animal (Fig. 4). Nosing body also took place in the anogenital area. Here the snout pointed upwards. In this context, the red river hogs sometimes nibbled on the tail of the interaction partner or pushed it upwards or to the side with their snout. During “**Allogrooming**”, the snout disc was also used, and in some cases the entire frontal snout and teeth were used. Rubbing and nibbling touches were observed, especially to clean the interaction partners with the teeth and snout disc. During mutual allogrooming, both pigs groomed the snout-mouth area of the other (Fig. 5). If only one pig groomed, the touched pig usually lay on its body side at the beginning or was already lying down and behaved passively. In the mother-young group, it was repeatedly observed that a young animal threw itself with its belly to the side in front of the mother, after which the mother began to make repeated, upward movements of the snout front on the belly of the young animals.

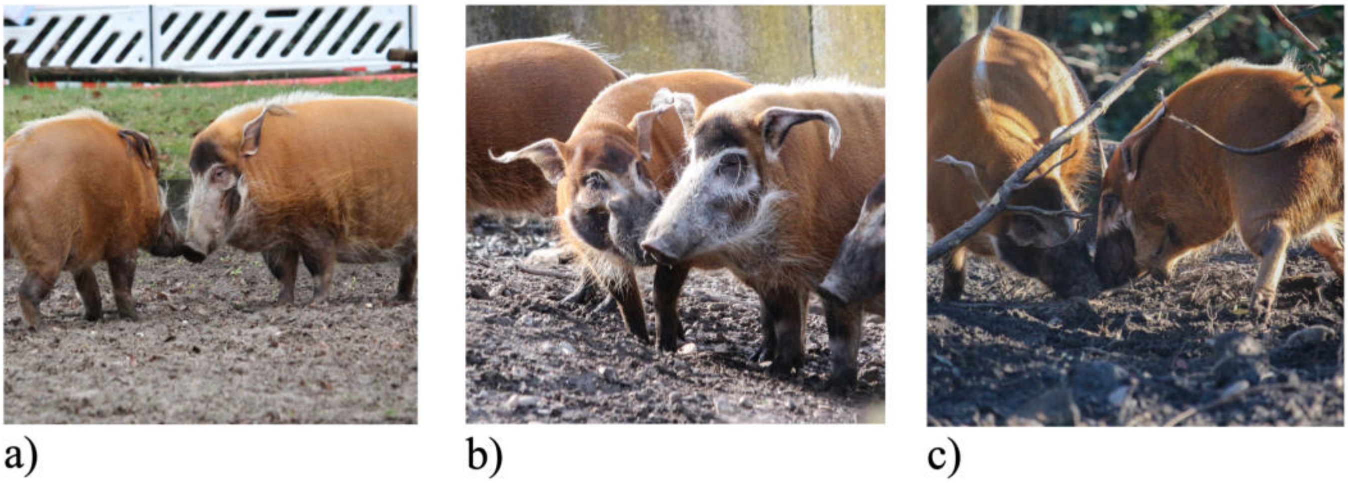

Fig. 3: Nose-to-nose contact. a) Starting from both, b) Starting from the young animal, mother remains attentive, c) While playing, with tense body.

Playful snout bumps were characterised by two animals pushing against each other head-on with their snouts. In doing so, they ran towards each other at speed, collided or pushed against each other with their heads (Fig. 6). Within a snout bump it could vary who pushed whom away. A nose-to-nose contact could also lead to a snout bump, but in this case without speed and the position was maintained. The more powerful variant of the snout bump was mainly observed in the young pigs, while the calmer variant without changing position was also shown by the adult animals. A playful "dancing" was observed in the young animals as an introduction to the playful snout bump. This involved the pig repeatedly tossing its head and making a bouncing humping movement with a wagging tail and tense ears. The pig moved slowly in a slightly curved line with high body tension towards the standing interaction partner (Fig. 7). **Playful mounting** was demonstrated by the young animals, whereby they jumped onto the back of their play partner with their front legs. In the context of a playful tussle, the young animal usually jumped head-on onto the partner, which reinforced the mounting with its snout by lifting or throwing it up (Fig. 8a). Playful mounting was also observed while the interaction partner focussed on other activities such as eating. In most cases, this did not result in a change in behaviour (Fig. 8b). In no case was submissive behaviour observed. Lateral mounting was observed in all animals, for example when something higher, such as leaves, could be reached.


Fig. 4: Leaning the snout under the belly.


Fig. 5: Mutual allogrooming while both stand.

In this study, the **playful tussle** includes the behaviour of nibbling, nipping, snapping, chasing and running around in a playful context. In contrast to nibbling, in which lips and teeth touched the body several times, nipping behaviour involved a quick, single, targeted touch with the teeth, which could also end in a light bite. Both behaviours usually took place when the animals stood in front of each other. The heads were pushed sideways towards each other, with the snouts of both animals touching the other between the head and shoulder (Fig. 9). The behaviour could also initially originate only from one animal while the interaction partner was, for example, resting. It was observed several times how the nibbling and nipping increased in intensity until the inactive pig showed a reaction. The young pigs reacted playfully to this, whereas in the mother, it also triggered displacement or aggressive biting attempts. When snapping, which was often observed in the course of playful hunting, the snout was open longer and the touch took place in the lateral area. The young animals chased each other. In most cases, all three males were involved and there was constant switching between hunter and hunted. Sudden tussles and snout bumps were also observed as a direct reaction to loud noises from the surroundings. No submissive behaviour was observed in these situations, but the play behaviour became more powerful and faster. In the course of a playful tussle, affiliative touching behaviour was often observed. Playful interactions were usually concluded with nose-to-nose contact, which did not occur during agonistic behaviour (Fig. 10). There were also rare transitions from play to agonistic behaviour (Fig. 11).

Fig. 6: Sequence of snout push a) nose-to-nose contact, b) lateral push, c) snout push.

Fig. 7: Introduction to the playful snout push with playful "dancing“

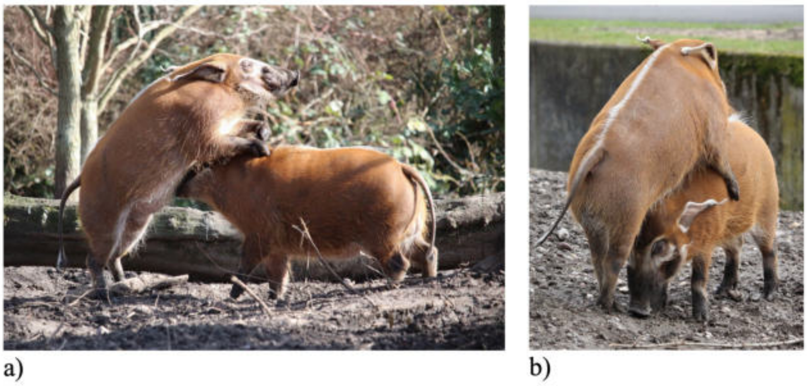

Fig. 8: frontal mounting. a) the lower pig reacts actively to the mounting, b) the lower pig remains passive.

Fig. 9: Playful tussle.

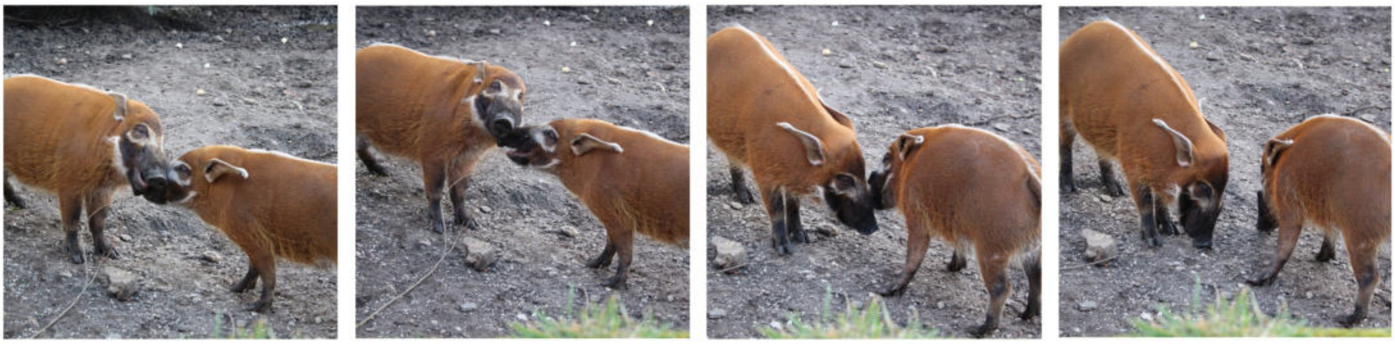

Fig. 10: Gentle tussle with final nose-to-nose contact.

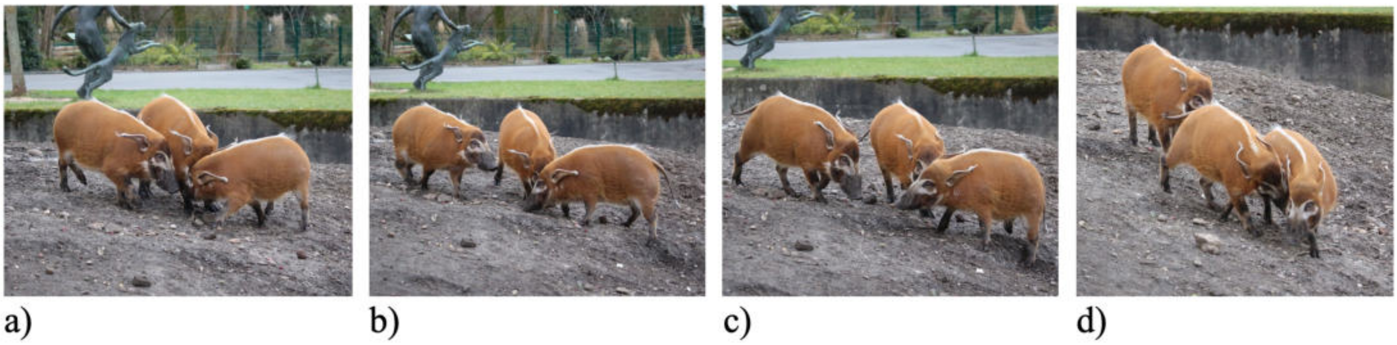

Fig. 11: Transition from "playful tussle" to agonistic behaviour. a) all young animals are involved in the game, b) young animal (right) head lowered and passive, young animal (left) head up and elongated body, c) young animal (right) body hollow towards other young animals, which are focused on it, d) young animal (right) clearly soft and continues to be attacked.

In agonistic behaviour, one pig showed dominant behaviour and triggered a submissive reaction in the interaction partner. Only within **aggressive behaviour** the behaviour led to a repeated attack despite submissive signals. Dominant behaviour was shown by focusing on the interaction partner with the eyes, the ears were first folded forward and then lay horizontally against the body, the head was raised and the body was stretched out (Fig. 12). In the case of submissive behaviour (**avoidance**), the pig lowered its head towards the ground, its gaze was on the attacker, the ears were positioned high up so that the tips of the ears were almost touching, the back arched upwards and one side of the body, usually the side facing the attacker, became hollow (Fig. 13).

The submissive pig remained in this posture until the aggressor turned his attention away from the interaction partner. In cases where the aggressor did not stop despite the submissive reaction, the submissive red river hog continued to evade (Fig. 14). If the warning body language turned into aggressive behaviour, the attack was reinforced despite submissive signals from the opponent. The sequence of the attacker's increased signalling was as follows: first the dominant body signals mentioned above were displayed, then the attacker moved towards the other pig until it came to **biting** into the air or into the side of the body with visibly open teeth. In the **aggressive tussle**, it was unclear who the aggressor was. In this study, the behaviour was only observed sporadically in the young animals and

Fig. 12: Dominant body signals. a) Young animal (right), ears folded forward, gaze focussed, b) young animal (right) body stretched, ears laid back.

resulted from a situation triggered by loud environmental noises.

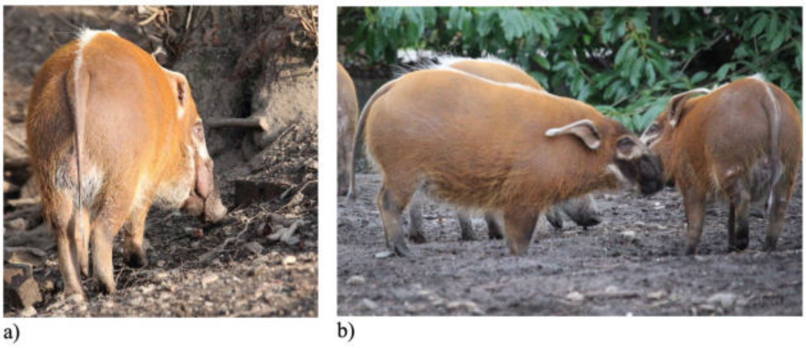
a) b)

Fig. 13: Submissive posture. Head towards the ground, ears high up on the neck, back arched upwards, the side of the body facing the attacker hollow, a) attacker was to the right of the pig shown, b) young animal (right) shows submissive posture.

In general, agonistic behaviour occurred primarily in feeding situations in which the pigs showed excitement through noises and physical tension even before feeding. The young animals often began to play wildly in response to loud ambient noises. If they did not keep their distance from the mother, the latter would first snap in the direction of the young animals while lying down. If the young pigs did not move away, she would jumped up and snap clearly in their direction (Fig. 15). The young pigs would interrupt the play behaviour and move away. The mother would then usually lay down again and continued to rest. When the red river hogs at Duisburg Zoo were fed without spatial separation, the female usually moved away without interrupting the actual activity (foraging or eating) and thus gave the male priority to the food source.


Fig. 14: Displacement during feeding, despite a submissive reaction, the young animal in front in the first photo attacks until the attacked pig clearly gives way.

Social interactions were also observed in relation to excitement, attention, inactive behaviour and locomotion. If a red river hog showed excited or attentive behaviour, this was adopted by all conspecifics. When excited, the young animals orientated themselves strongly towards the mother and sought physical contact with her (Fig. 16). Locomotion across the terrain also mainly took place simultaneously within the group. When inactive, the red river hogs had physical contact with conspecifics 42.5 % of the time.

The red river hogs communicated with sounds over long periods of time. The whole sound repertoire was covered from the whole range from high to low tones in different frequencies, volumes and sequence repetitions. It was observed that grunting sounds were constantly emitted, especially when foraging, which were reciprocated by conspecifics. The pigs also communicated alternately with sounds when they were kept apart and not visible to each other. Quiet and deep grunting was increasingly observed in situations that were relaxed, sociopositive encounters or

Fig. 15: Active agonistic reaction of the mother to the young running over her.

Fig. 16: Excitement in the mother-young group, young animals orientate themselves towards their mother.

wandering away. The young animals also made "mmh" sounds in these situations. In tense situations, before feeding or in noisy, unfamiliar surroundings, the red river hogs made loud squeaking or barking noises. A comparison of the social groups and individuals revealed clear differences in the vocalisations in certain situations. In the three groups, the exciting time before feeding was commented on differently: in Cologne with loud squeaking, in Aachen with loud barking and in Duisburg with grunting.

Discussion

The evaluation of the quantitative data shows that social behaviour accounts for 4.2 % of the total behaviour displayed. These results are comparable with studies in wild boar, which show that survival-securing behaviours occur significantly more often than social interactions (Erdtmann & Keuling 2020). Social behaviour is mainly affiliative behaviour, which is typical for social mammal communities and has also been described in wild boar (Schmidt 2016). At 44.6 % of social behaviour, playing behaviour accounted for a similarly large proportion as affiliative touching behaviour at 48.1 %. The remaining 7.3 % of agonistic behaviour allows conclusions to be drawn about the prevailing hierarchies in the groups (Saebel 2007). To answer question 1, it is important to address the role of social behaviours in the species behavioural repertoire. Communication was not in the foreground during the feeding and resting phases and was not included in the ethogram. Data labelled with "inactive" with physical contact and the qualitative analysis show that communication nevertheless makes up a relevant part of social behaviour in these essentially "non-social" behaviours. Even when inactive, the red river hogs sought physical contact. The individuals also orientated themselves towards the group during locomotion, so that they often moved synchronously between feeding and resting places, as also described by Leslie & Huffman (2015). Group members often showed alert, excited behaviour and freezing at the same time. For example, alarming sniffing can make the group alert and ready to flee (Leslie & Huffman 2015) and the subsequent relaxation of an animal can signal safety to other group members. Such situations have been observed in the mother-young group. Schmidt (2016) also describes this behaviour in females and their young. The young animals orientated themselves towards their mother and this was usually followed by nose-to-nose contact.

A qualitative analysis was used to assign the body language expressions to the behavioural categories of affiliative touching, play behaviour and agonistic behaviour. The results show that the individual signals cannot be clearly assigned to one type of behaviour. The signals shown and the social behaviours often occurred in combinations in the groups observed. Just by observing the typical signs of dominant behaviour, such as raised head and horizontally erected ears, which are also described by Leus & Vercammen (2013), an aggressive biting attempt could not be clearly distinguished from playful nipping. Play behaviour could only be ruled out on the basis of the submissive reaction of the interaction partner. Submissive red river hogs, as also described in wild boar, showed submissive behaviour towards the dominant individual by arching their back, downward orientation of the head with the snout to the ground (Schnebel & Griswold 1983) and ears laid sideways on top (Leus & Vercammen 2013). The observation of the red river hogs also showed that the attentive gaze remained focussed on the aggressor. Furthermore, Schnebel & Griswold (1983) describe that wild boars avoided looking into the eyes of the dominant animal. Conflicts between animals in the group, which can lead to aggressive behaviour, are avoided by clear hierarchies (Kappeler 2020; Sachser 2021). Even when two different groups of red river hogs meet in the wild, ritualised threatening gestures occur, but serious fights are rare (Melletti et al. 2018). The energetically high use of aggressive behaviour is only justified if it results in advantages such as a higher ranking position (Schnebel & Griswold 1983). In the long-term relationships observed for these red river hogs, the dominant behaviour ended due to the submissive reaction of the interaction partner. Aggressive behaviour resulted from an increase in the dominant body signals. The aggressor moved towards the other pig until it came to biting the air or the side of the body with visibly open teeth. As Ortega-Salgado (2018) also describes in wild boar, individuals tend to exhibit agonistic behaviour due to external influences, such as insufficient resources. The increase in signals as feedback from the adult animals to the behaviour of the young animals enables them to learn in the transition to adolescence when the signals are serious and therefore no longer play (Bekoff & Pierce 2017). Body language signals cannot be clearly assigned to individual behaviours. Smooth communication is only possible in a stable hierarchy once the communication signals have been established between the animals (Bekoff & Pierce 2017). As social animals, similar to wild boar, it can be assumed that the structuring of the group with rank positions and a well-established hierarchy is essential for the cohesion and survival of the group (Ortega-Salgado 2018).

The perceived acoustic signals of the red river hogs included sounds in different frequencies, volumes and sequence repetitions, as is typical for Suidae (Frädrich 1971). Acoustic communication signals were emitted continuously, especially during the feeding phases. Melletti et al. (2018) emphasised the importance of soft grunts during feeding and locomotion to maintain contact and group cohesion. Grunts play an important role in the transmission of different types of information (Leslie & Huffman 2015). Along with physical tension, the red river hogs squeaked or barked loudly before feeding or in noisy, unfamiliar surroundings. The loud noises may have represented a potential threat to the red river hogs, which they commented on by squeaking

(Leslie & Huffman 2015). Acoustic signals play an important role in intra-species communication in Suidae (Frädrich 1971). This is confirmed by the observations. Further studies could use sonograms to analyse how the acoustic communication signals of the red river hogs can be further differentiated, which sounds the red river hogs use to pass on specific information and how the sounds of the individual individuals differ. The examination of the sounds in the present study shows the importance of acoustic communication in red river hogs, but should only be understood as an impulse for further studies in which comparative sonograms could be used.

Conclusion

Even though the red river hogs observed in this study spent only a relatively small proportion of their time on social interactions, they showed pronounced social behaviour characterised by affiliative touching. In principle, "non-social" behaviours such as inactivity or locomotion nevertheless have a social component, e.g. when sleeping in physical contact or coordinating movements in the group. The red river hogs showed agonistic behaviour mainly when competing for food and establishing the hierarchy. The body language communication signals of the red river hogs are finely tuned and only clear in combination and in the context of the behavioural sequences. Acoustic communication also plays an important role. This study is intended to be a basis for further behavioural studies in zoos and in the wild.

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Aroma profiles of young coconut mesocarp foraged by babirusa (*Babyrousa celebensis*)

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Abstract

The Sulawesi babirusa (*Babyrousa celebensis*) has a strong preference for the kernel (endosperm) that forms inside the hard shell (endocarp) of the coconut (*Cocos nucifera*). However, they are unable to crack the shell. Recent observations have shown that babirusa in zoological collections can only crack open young coconuts. They forage on the basal part of the young coconut husk (mesocarp). The aim of this study was to identify differences in the volatile profiles of the coconut mesocarp. Dynamic headspace GC-MS analysis using the multi-volatile method detected 23 major compounds in the young coconut mesocarp, including highly volatile compounds that contribute to food aroma. The detected amounts of 16 aroma compounds showed a maximum at the base of the coconut and a decreasing trend towards the apex. This trend was consistent with the preference of animals for the young coconut mesocarp. The findings strongly supported the view that the babirusa's selection of the basal part of the young coconut mesocarp was initiated by olfactory cues involving highly volatile compounds.

Key words: Babyrousa celebensis, food preference, GC-MS analysis, volatile compound, young coconut husk.

Introduction

The babirusa (genus *Babyrousa*) is a wild pig endemic to Sulawesi and a limited number of neighbouring islands in Indonesia (Macdonald et al., 2008; Macdonald et al., 2016; Leus et al., 2016). Babirusa are omnivorous (Macdonald, 1993) and are known to consume a variety of leaves, roots, fruits and animal material (Macdonald, 1993; Leus, 1996). Coconut kernels, i.e. botanically solid endosperm of the coconut palm (*Cocos nucifera*), are a preferred food item of Togian babirusa (*B. togeanensis*) and Sulawesi babirusa (*B. celebensis*), although the animals are unable to crack the hard shell of mature coconuts (Selmier, 1983; Leus, 1996; Ito et al., 2020).

Sulawesi babirusa in zoological collections were able to crack open and forage young coconuts (Ito et al., 2020) which had not yet developed a hard shell and solid endosperm (Fig. 1). Feeding experiments with young coconuts split in half showed that these babirusa tended to forage on the basal side of the young fleshy husk (mesocarp), immediately after approaching the test food (Ito et al., 2021; Fig. 2). Why did the animals choose the basal side of the mesocarp when the mesocarp encases the entire coconut shell? One possibility was that they were attracted to the volatile compounds associated with the base of the coconut mesocarp. Many studies of the aroma components of coconut palms have analysed the solid endosperm (Lin & Wilkens, 1970;

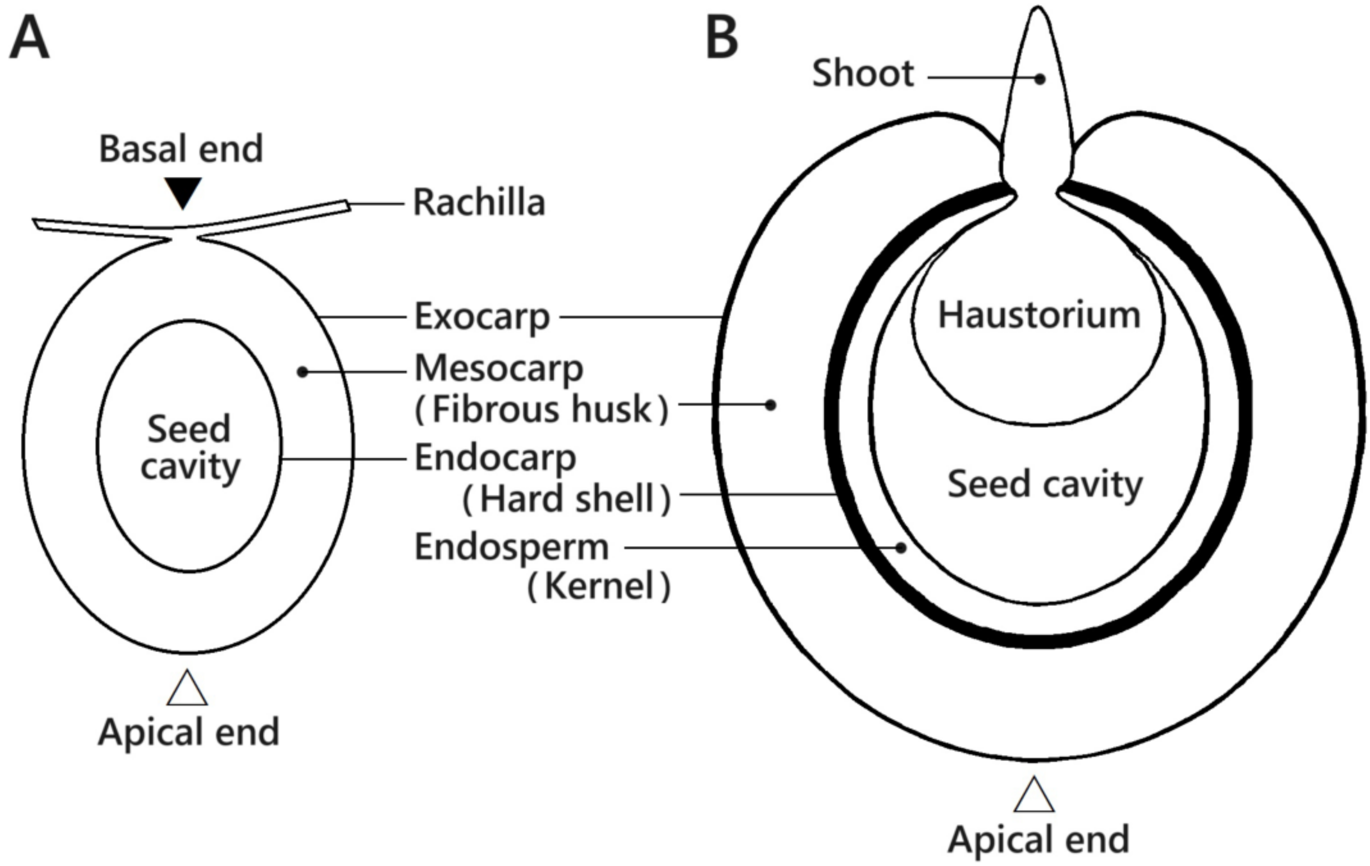

Fig. 1: Diagrams of growth changes in the internal structure of coconuts. A: Young coconut. B: Mature germinating coconut.

Saittagaroon et al., 1984), the liquid endosperm or coconut water (Prades et al., 2012), coconut sap (Purnomo, 2007) and even processed products such as coconut milk (Wang et al., 2020) and coconut oil (Santos et al., 2011; Dimzon et al., 2021). However, there appears to be no literature focusing on the aromatic components of the young coconut mesocarp. An attempt was therefore made to compare the volatile profiles of the base and the apex of the young coconut mesocarp by dynamic headspace (DHS) gas chromatography-mass spectrometry (GC-MS) analysis. Preliminary data had shown that samples of basal mesocarp emitted more methylbutanal than apical samples (Ito et al., 2021). However, improvements in analytical methodology were later identified; optimisation of the procedure, time and temperature of the process from coconut harvesting to mesocarp tissue sampling, and selection of a better adsorbent material for the simultaneous extraction of a wider range of volatile compounds from the mesocarp samples. The latter was because the properties of the Tenax TA adsorbent (Rabaud et al., 2002; Dettmer & Engewald, 2002) used in the preliminary analyses may have made the DHS-GC-MS method technically unable to detect highly volatile compounds with lower boiling points than methylbutanal.

For exhaustive detection of volatile compounds over a wider range of boiling points, we prepared controlled, highly fresh, mesocarp samples and employed sequential DHS sampling with the multi-volatile method (DHS-MVM; Ochiai et al., 2014), which uses multiple trapping conditions with different adsorption properties. Specifically, two types of adsorbent tubes were used: a carbon-based adsorbent tube with a high specific surface area for low-boiling point compounds and a Tenax TA tube for medium- to high-boiling point compounds.

Here, we present chromatographic evidence for 1) highly volatile compounds newly detected from the young coconut mesocarp by this method and 2) a tendency for these volatile compounds to be biased towards the basal side of the young coconut mesocarp. This was consistent with the tendency for food preference, exhibited by babirusa, to be directed towards the basal side of the young coconut mesocarp.

Materials and methods

Feeding mark area value as an indicator of food preference

The surface area of the feeding marks made by Sulawesi babirusa on longitudinal sections of young coconuts has already been measured (Ito et al., 2021; Fig. 2). Briefly, in a feeding experiment using 111 halved coconuts (whole coconut weight: M = 839 g, SD = 172.3), the leftover coconuts with feeding marks were collected. Of these, 106 were moulded with plaster for long-term storage as 3D evidence, while the remaining five were preserved in ethanol. To assess the position and surface area (mm^2) of the feeding marks, radial compartments were assigned to the photographs of the 106 gypsum impressions by superimposing polar grids at 30° intervals, with the poles positioned at the centre of the seed cavity and the polar axis (0°) through the basal end of the coconut (Fig. 3A). This approach was based on their observed feeding behaviour pattern. They used their mandibular incisors to scoop out the coconut mesocarp from the centre, i.e. the bottom, of the seed cavity towards the periphery of the fruit (Fig. 2B). The total surface area of the feeding mark within each radial compartment was measured using ImageJ software (National Institutes of Health, USA).

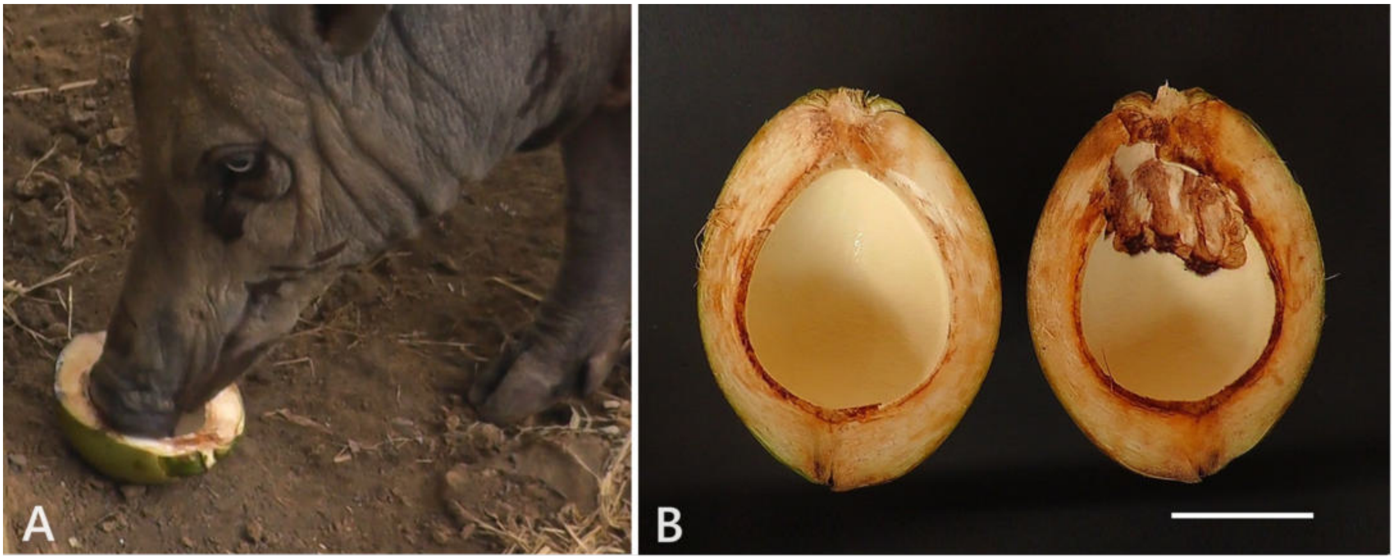

Fig. 2: A female Sulawesi babirusa feeding on a longitudinal halved young coconut and feeding marks on the cut surface.

A: Sniffing the cut surface of the halved coconut. Even after the halved coconuts begin to spin or wobble as the animals manipulate the halves with their snouts, the animals selected and scooped the basal part of the coconut with their mandibular incisor teeth.

B: An example of the reference half of the coconut (left) and the leftover half with feeding marks (right). The basal end of the halves is directed upward. Whole coconut weight: 740 g. The scale bar: 5 cm.

Data processing on feeding mark area values

Coconuts were somewhat longer in the basal–apical direction, resulting in a relatively small area of equatorial compartments (Fig. 3A). To compare the food preferences for each compartment, the total feeding-mark area within each of the 12 radial compartments was adjusted by matching the compartment area of each of the 12 radial compartments to the area of the compartment covering 0° to 30°, and the adjusted feeding-mark areas were then used for the evaluation. Furthermore, the adjusted dataset of the 12 radial compartments (Fig. 3A) was reconstructed into a new dataset of six radial compartments by changing the angle of the polar grid from 30° to 60° (Fig. 3B) to correspond to the three mesocarp sampling points for GC-MS analysis (Fig. 3C). The six radial compartments were numbered clockwise, with the first compartment covering 0° to 60°. Finally, as final data for an analysis of increasing or decreasing trends between the three radial compartments aligned from the basal end to the apical end of the fruit, we calculated the mean of the adjusted feeding-mark area (mm^2) for each symmetrical compartment pair, i.e. basal pair of nos. 1 and 6, equatorial pair of nos. 2 and 5, and apical pair of nos. 3 and 4.

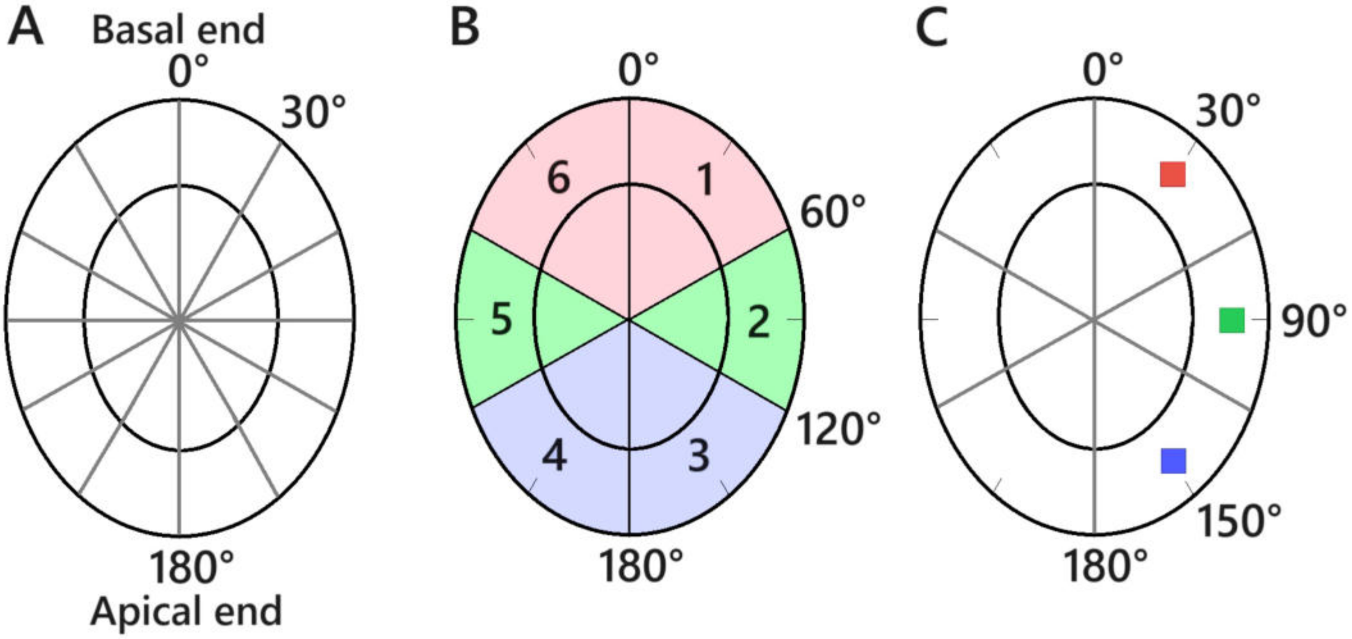

Fig. 3: Diagrams of the assessment sites on the longitudinal section of young coconuts.

A: 12 radial compartments to determine the location and total surface area of feeding marks (Ito et al., 2021).

B: Six radial compartments reconstructed to correspond to the mesocarp sampling points for GC-MS analysis (Fig. 3C). Light red: basal pair. Light green: equatorial pair. Light blue: apical pair.

C: Mesocarp tissue sampling points for GC-MS analysis. Red: angle 30°. Green: angle 90°. Blue: angle 150°.

Plant material for GC-MS analysis

A total of 20 coconuts weighing less than 1 kg each were harvested in Bali, Indonesia. The coconuts were immature, with the mesocarp still fresh, the thin endocarp not yet hardened into a shell and the solid endosperm not yet formed inside the endocarp (Fig. 1). Seven were used to investigate the analytical methods and optimal conditions for the detection of highly volatile compounds, while the remaining 13 were used to collect actual data on volatile compounds. To exclude variations in the detection of volatile compounds due to coconut growth in this comparative study, we have presented GC-MS data for five coconuts with a narrow range of whole coconut weights between 605 and 675 g (M = 637 g, SD = 24.9).

Mesocarp sample preparation

Mesocarp tissue was collected from three geometrically defined points on the cut surface of each coconut, as follows: First, the whole coconut was split longitudinally from the base to the apex using a stainless-steel knife. Second, using the method for the measurement of the feeding mark area, a polar grid was superimposed on the cut surface to determine the sampling points. Third, tissue samples were taken from the centre of the mesocarp layer at angles of 30°, 90° and 150° on the polar grid (Fig. 3C), corresponding to the measurement of feeding-mark area values (Fig. 3B). Finally, the sampled tissue was cut into approximately 5 mm cubes, weighed to 2.0 g, immediately placed in individual 20 ml headspace vials (Agilent Technology Japan, Tokyo, Japan) and kept frozen at –20°C until GC-MS measurement.

Instruments

The volatile compounds were analysed using an Agilent 8890 GC coupled to a 5977B quadrupole MSD (Agilent Technologies, Palo Alto, CA, USA) equipped with a MPS Robotic Pro autosampler, a thermal desorption unit (TDU) and a cooled injection system-programmed temperature vaporizer (CIS-PTV) (GERSTEL, Mulheim an der Ruhr, Germany).

Sequential dynamic headspace sampling using multi-volatile method (DHS-MVM)

The frozen tissue samples were thawed at room temperature for 30 min. Based on the ambient temperature of 25°C recorded in coconut feeding experiments (Ito et al., 2021), the DHS sampling temperature was also set at the same 25°C. To extract a wider range of volatile compounds from the mesocarp sample, two different adsorbent traps were used for DHS-MVM sampling (Ochiai et al., 2014). As shown in Table 1, the highly volatile compounds in the vial kept at 25°C were first purged with nitrogen gas and trapped at 30°C on the first trap of a TDU tube packed with Carbopack B/Carbopack X (GERSTEL K.K., Tokyo, Japan). Then, the remaining volatile compounds in the vial were purged with nitrogen gas and trapped at 30°C on the second trap tube packed with Tenax TA (GERSTEL, K.K., Tokyo, Japan).

Tab. 1: DHS-MVM sampling conditions.

First DHS sampling			Second DHS sampling		
DHS	Vial incubation	: 25 °C (5 min)	DHS	Vial incubation	: 25 °C (5 min)
	TDU tube adsorbent, temp.	: Carbopack B/X, 30 °C		TDU tube adsorbent, temp.	: Tenax TA, 30 °C
	Purge gas	: Nitrogen		Purge gas	: Nitrogen
	Purge volume, flow rate	: 650 ml, 100 ml/min		Purge volume, flow rate	: 60 ml, 10 ml/min
	Transfer line temp.	: 150 °C		Transfer line temp.	: 150 °C
	Dry purge volume, flow rate	: 300 ml, 50 ml/min		Dry purge volume, flow rate	: 600 ml, 50 ml/min
TDU	: 30 °C → 720 °C/min → 300 °C (3 min)		TDU	: 30 °C → 720 °C/min → 240 °C (3 min)	
	Transfer Line Temp.	: 300 °C		Transfer Line Temp.	: 300 °C
CIS	: –40 °C (1 min) → 720 °C/min → 240 °C (20 min)		CIS	: 10 °C (1 min) → 720 °C/min → 240 °C (20 min)	
	Liner adsorbent	: Tenax TA		Liner adsorbent	: Tenax TA

Thermal desorption GC-MS analysis

The two adsorbent tubes as the first trap and second trap were sequentially desorbed with the TDU in the reverse order of the DHS sampling (Table 1). The TDU was heated using a temperature programme from 30°C to 240°C for the second trap and to 300°C for the first trap. Compounds desorbed from the second trap were focused at 10°C on the CIS-PTV inlet, while compounds desorbed from the first trap were then focused at –40°C on the same PTV inlet. After desorption from the two traps, the PTV inlet was heated from –40°C to 240°C to inject the compounds into the GC column for a single GC-MS run. GC-MS analysis was performed according to the established method under the conditions listed in Table 2.

Tab. 2: Analytical conditions of GC-MS.

GC		MS	
Carrier gas	: Helium	Interface temp.	: 250°C
Injection	: Split (1 : 2.5)	Ionization	: EI, 70 eV
Column	: DB-WAX	Ion source temp.	: 230°C
	(60 m, 0.25 mm i.d., 0.25µm film thickness)	Scan range	: m/z 29–350
Column flow rate	: 1.2 ml/min		
Oven temp.	: 40°C (10 min) → 4°C/min → 200°C (10 min)		

GC-MS data processing

The GC-MS data were processed for deconvolution using the Unknowns Analysis tool in the MassHunter Quantitative Analysis software package (Agilent Technologies). The compound identification of each peak was made by comparison of the mass spectrum with the NIST17 Mass Spectral Library (National Institute of Standards and Technology, USA) and by comparison of the Kovats retention index (RI) calculated using the C8–C20 alkane standard with the RI database of Aroma Office software (Nishikawa Keisoku, Tokyo, Japan). Peak area values were calculated based on the target ion (TI, i.e. a generated ion that most characterises the target compound). The average of the three replicate measurements was evaluated.

Statistical analysis

All analyses were performed in R version 4.2.2 (R Core Team, 2022), with $p < 0.05$ indicating statistical significance. A decreasing trend in the feeding-mark area in the order of three compartment pairs from the basal pair to the apical pair was assessed using the Jonckheere-Terpstra test in the R package 'PMCMRplus' (Pohlert, 2022). The same test was used to determine an increasing or decreasing trend in the TI peak area values for volatile compounds in the order of three sampling points from 30° to 150°.

Results

Feeding mark area on the coconut longitudinal section

Fig. 4 shows a comparison of the adjusted values of the feeding mark areas for three pairs of radial compartments. The feeding-mark areas had a maximum in the basal pair and a decreasing trend in the direction from the basal pair to the apical pair (Jonckheere-Terpstra test, $p < 0.001$).

Volatile compounds

Fig. 5 shows an overlay of typical total ion chromatograms of the three mesocarp samples taken at angles of 30°, 90° and 150°. Based on their mass spectra and RIs, 23 major peaks were identified, comprising 12 aldehydes, 3 ketones, 4 alcohols, 2 esters, 1 furan and 1 sulphur compound (Table 3). Of these, 14 compounds (60.9%) with peak numbers 1 to 14 were highly volatile compounds with boiling points below 100°C.

Comparison of the peak area values among the three tissue sampling points

The overall view of the total ion chromatogram (Fig. 5A) showed that a group of peaks of low-

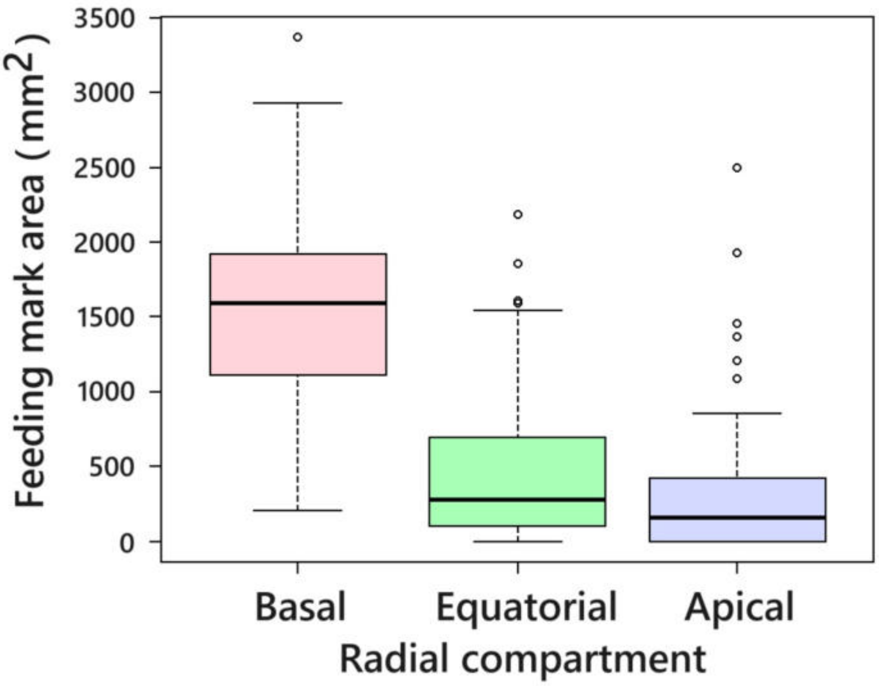

Fig. 4: A box plot comparing the feeding mark areas of the three radial compartments on the longitudinal halved coconut.

The whiskers are extended to 1.5 times the interquartile range from the box limit. Open circles represent outliers. n = 106. The feeding mark area decreases from the fruit base towards the apex (Jonckheere-Terpstra test, $p < 0.001$).

boiling compounds seen in the early stage of elution were prominent in the sample at an angle of 30° (red line). Based on the increasing or decreasing trends of the TI peak area values observed in the sequential order of the tissue sampling points (Table 3), the 23 compounds were classified into the following three categories:

1. Volatile compounds with maximum peak area values at the basal sampling point (angle 30°) and a decreasing trend towards the apical sampling point (angle 150°), i.e. fruit base ≥ equator ≥ apex: dimethyl sulphide, 2-methylpropanal, methyl acetate, 2-propenal, 2-methyl-

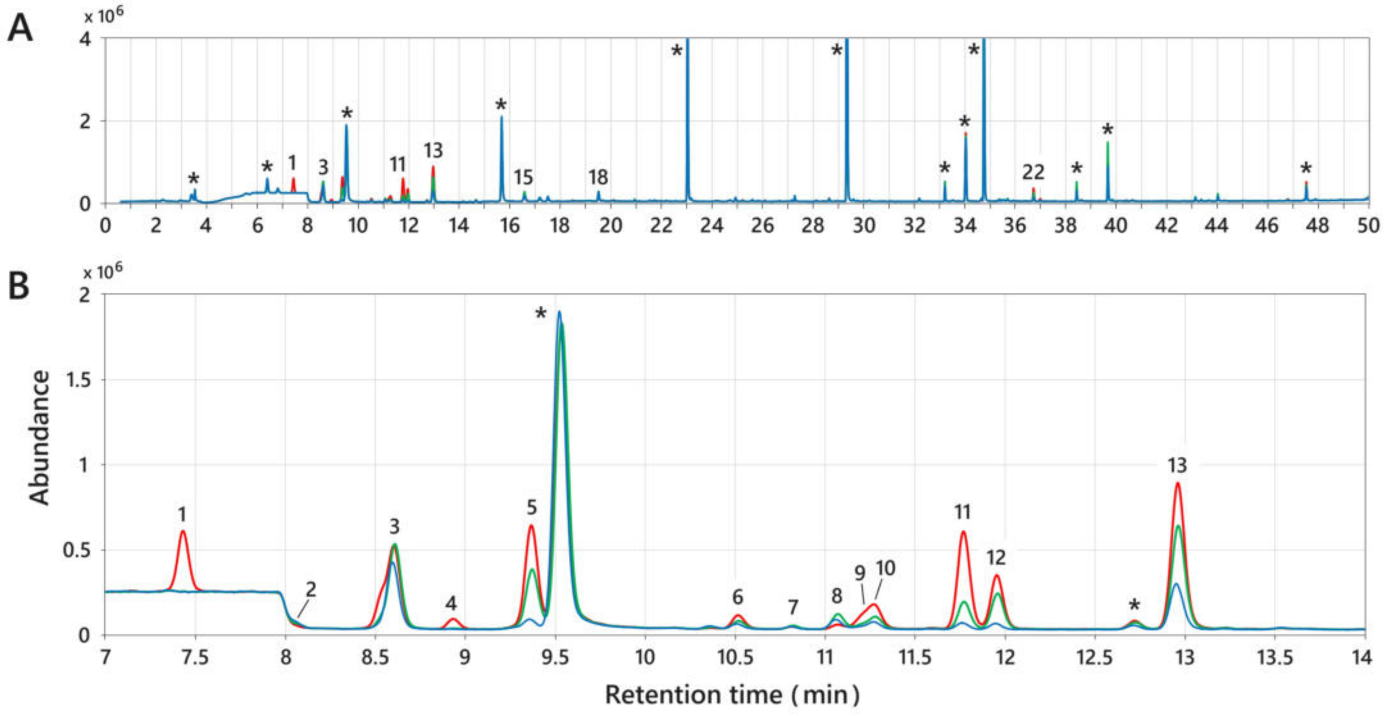

Fig. 5: Overlays of typical total ion chromatograms of volatile compounds emitted from the young coconut mesocarp.

Whole coconut weight: 675 g. Numbered peaks are identified in Table 3. Peaks marked with an asterisk are background peaks found in the blank runs. Red line: mesocarp sample at an angle of 30°. Green line: 90°. Blue line: 150°.

A: Overall view. B: Magnified view for the RT range 7–14 min in Fig. 5A.

Tab. 3: Volatile compounds of the young coconut mesocarp identified by DHS-MVM GC-MS analysis.

Peak No. *1	RT *1	RI	Compound	CAS No.	TI m/z	Peak area value *2			Jonckheere-Terpstra test *3
						Angle 30°	Angle 90°	Angle 150°	
1	7.46	776	Dimethyl sulphide	75-18-3	62	401 (254.2)	2 (2.1)	1 (0.2)	Decreasing, p=0.0004372
2	8.09	797	Propanal	123-38-6	58	25 (2.9)	143 (61.1)	109 (34.0)	Increasing, p=0.01516
3	8.57	813	2-Methylpropanal	78-84-2	72	182 (78.0)	46 (15.7)	38 (17.9)	Decreasing, p=0.0009141
4	8.96	827	Methyl acetate	79-20-9	74	36 (19.0)	3 (1.0)	2 (0.6)	Decreasing, p=0.0001337
5	9.40	841	2-Propenal	107-02-8	56	1,238 (353.7)	275 (257.2)	148 (22.9)	Decreasing, p=0.002556
6	10.55	880	2-Methyl-2-propenal	78-85-3	70	137 (25.9)	87 (15.7)	80 (19.4)	Decreasing, p=0.0006355
7	10.85	890	Ethyl acetate	141-78-6	61	19 (6.6)	21 (8.4)	13 (4.4)	Decreasing, p=0.1122
8	11.10	899	3-Methylfuran	930-27-8	82	75 (63.2)	254 (232.4)	109 (68.9)	Increasing, p=0.3172
9	11.26	903	Methanol	67-56-1	31	177 (58.9)	55 (21.8)	43 (10.4)	Decreasing, p=0.0009141
10	11.32	904	2-Butanone	78-93-3	72	127 (18.1)	74 (13.9)	70 (19.4)	Decreasing, p=0.003528
11	11.80	915	2-Methylbutanal	96-17-3	57	606 (201.3)	124 (56.6)	88 (31.6)	Decreasing, p=0.0009141
12	11.99	919	3-Methylbutanal	590-86-3	58	245 (96.2)	87 (50.9)	46 (22.7)	Decreasing, p=0.0004372
13	13.00	941	Ethanol	64-17-5	46	393 (125.4)	315 (60.6)	232 (92.7)	Decreasing, p=0.01516
14	14.68	979	2,3-Butanedione	431-03-8	86	54 (6.6)	50 (7.5)	32 (6.8)	Decreasing, p=0.001833
15	16.60	1021	2-Methyl-2-butanol	75-85-4	59	367 (107.7)	293 (42.0)	186 (28.9)	Decreasing, p=0.0006355
16	17.61	1042	2-Butenal	4170-30-3	70	8 (1.1)	15 (3.2)	15 (2.8)	Increasing, p=0.01516
17	18.52	1061	2,3-Pentanedione	600-14-6	100	14 (4.7)	7 (1.2)	6 (1.3)	Decreasing, p=0.001833
18	19.52	1082	Hexanal	66-25-1	56	89 (18.8)	264 (72.7)	198 (45.1)	Increasing, p=0.02532
19	20.13	1095	2-Methyl-2-butenal	1115-11-3	84	54 (8.7)	16 (5.1)	12 (3.1)	Decreasing, p=0.0006355
20	21.03	1115	3-Pentanol	584-02-1	59	85 (49.0)	134 (30.5)	56 (21.8)	Decreasing, p=0.1578
21	25.61	1222	(E)-2-Hexenal	6728-26-3	69	8 (2.0)	22 (7.7)	38 (15.1)	Increasing, p=0.0002005
22	36.74	1538	Benzaldehyde	100-52-7	106	212 (31.9)	162 (27.7)	99 (28.3)	Decreasing, p=0.0004372
23	40.41	1660	Benzeneacetaldehyde	122-78-1	91	83 (31.1)	17 (13.8)	6 (3.1)	Decreasing, p=0.0002976

*1: Peak number and retention time in minutes correspond to the label in Fig. 5.

*2: Mean (SD) of peak area values by mesocarp sampling point, n = 5, (x 1000).

*3: Alternative hypothesis and p-value in the Jonckheere-Terpstra test in the order of the three mesocarp sampling points from angle 30° to angle 150°.

2-propenal, methanol, 2-butanone, 2-methylbutanal, 3-methylbutanal, ethanol, 2,3-butanedione, 2-methyl-2-butanol, 2,3-pentanedione, 2-methyl-2-butenal, benzaldehyde and benzeneacetaldehyde.

2. Volatile compounds with minimum peak area values at the basal sampling point (30°) and an increasing trend towards the apical sampling point (150°), i.e. fruit base ≤ equator ≤ apex: propanal, 2-butenal, hexanal and (E)-2-hexenal.

3. Other volatile compounds with no increasing or decreasing trend in peak area values: ethyl acetate, 3-methylfuran and 3-pentanol.

Discussion

DHS-MVM GC-MS analysis

A previous study, using classical DHS sampling, reported that the basal side of the young coconut mesocarp was characterised by the high emission of methylbutanal with the early eluting peak on the chromatographs (Ito et al., 2021). In contrast, the present study, using DHS-MVM sampling, detected 10 additional highly volatile compounds with eluting peaks earlier than methylbutanal. Clearly, this analytical method was effective for the exhaustive detection of highly volatile compounds that might be perceived by animals with a keen sense of smell at 25°C.

Undetected coconut aromas

Lactones are responsible for the characteristic aroma of coconuts (Lin & Wilkens, 1970), but they were not detected at any of the tissue sampling points in the present study. This was due to the spatially and temporally different tissue types inside the coconuts. The volatile compounds profiled here originated from the young coconut mesocarp, whereas the coconut aromas, represented by the lactones, originated from the kernels of older growing coconuts (Fig. 1).

Characteristic volatile compounds

Almost half (52.2%) of the volatiles detected were aldehydes. The largest peak area from the basal sample (angle 30°) was 2-propenal (synonyms: acrolein, acrylaldehyde), with its aromatic property described as almond and cherry at 0.10% in dipropylene glycol (The Good Scents Company Information System). Three aldehydes, 2-methylpropanal, 2-methylbutanal and 3-methylbutanal, with relatively large peaks in the basal sample are also key aroma-active, short-chain aldehydes found in many foods. These aldehydes volatilise not only from fresh foodstuffs, but also from fermentation and cooking processes, i.e. Strecker degradation of amino acids associated with the Maillard reaction that occurs during the heating of sugar-amino acid mixtures (Smit et al., 2009). For example, these are formed as the water-flour mixture, i.e. the dough, is fermented and baked, contributing significantly to the rich flavour and aroma of bread (Cho & Peterson, 2010; Pico et al., 2015). Recent studies of human perceptual interactions have revealed aroma synergies between these aldehydes (Chen et al., 2020; Zhu et al., 2017). Other aldehydes with smaller peak areas detected in the present study also contribute to fruity, floral or leafy aromas.

Other notable findings include the new detection of highly volatile dimethyl sulphide at an angle of 30°. In human olfaction, dimethyl sulphide is often perceived as an unpleasant odour. However, at certain concentrations it contributes to the unique flavours and aromas of various foods and beverages. For example, dimethyl sulphide in beer with a flavour threshold of about 0.03–0.05 mg/l contributes to the taste of lager-type beers in the range of 0.05–0.1 mg/l, but above 0.1 mg/l it can impart an undesirable cabbage-like odour to the beer (Stafisso et al., 2011; Bamforth, 2014; Parker, 2015). It is also interesting to note that dimethyl sulphide and methylbutanal have been reported as important flavour components in truffles, which are known to be sought out by pigs and trained dogs (Splivallo et al., 2011; Epping et al., 2022).

Uneven distribution of detected volatile compounds in the basal-apical direction of the coconut

Of the 23 major compounds detected, 16 (69.6%) showed their maximum peak area value at the base of the young coconut and a decreasing trend towards the coconut apex (Table 3). Interestingly, this is consistent with the decreasing trend in the babirusa's food preference based on the feeding mark area data (Fig. 4). Given that the greater presence of as many as 16 aroma-active compounds at the base of the young coconut mesocarp attracts animals, their coconut-base feeding-preference behaviour seems rationally explainable. In particular, seven compounds, dimethyl sulphide, 2-propenal, 2-methylbutanal, 3-methylbutanal, 2-methylpropanal, ethanol and 2-methyl-2-butanol would appear to be promising attractant candidates for the animal; they showed large differences in peak area values between the three sampling points, specifically a large concentration gradient between the fruit base and the apex.

Conversely, the four compounds showing a gradient in the opposite direction should also be noted. These four compounds, with their maximum at the coconut apex may to some degree be unpleasant-smelling to the babirusa and affect them adversely. If so, then such compounds will also direct the animals' feeding behaviour to the preferred coconut-base.

This demonstration of a skewed distribution of multiple aroma-active compounds to one end of the coconut strongly supports the view that the babirusa's selection of the coconut base is not opportunistic. It appears to be due to olfactory cues involving highly volatile compounds probably produced on the basal side of the young coconut mesocarp.

Limitations

We have presented chromatographic evidence for several aroma-active volatiles being emitted from the base of the young coconut. These suggest candidate compounds that could serve as olfactory cues for the babirusa's selection of the base of the mesocarp. Unfortunately, the olfactory thresholds of each of these compounds are still unknown in babirusa. Perceptual interactions among aroma compounds with similar structures have also been reported (e.g. Saison et al., 2009). In such circumstances, the quantification of each compound or the comparison of the detected amounts of each compound in the present study are not sufficient to identify the actual cue compounds. The olfactory preference of babirusa for each candidate compound identified here needs to be measured from a behavioural perspective in future studies.

Acknowledgements

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Articles in the news

Norway considers ‘boar-proof fence’ along border with Sweden

Miranda Bryant, 19 Feb 2024
https://www.theguardian.com/world/2024/feb/19/norway-considers-boar-proof-fence-along-border-with-sweden

Measures to eradicate wild boar population designed to stem risk of African swine fever outbreak.
Norway could build a fence along its border with Sweden as part of a package of measures designed to eradicate its wild boar population after an outbreak of African swine fever in Sweden last year. Up to 2,000 wild boars face slaughter in Norway under the plan submitted by the country’s food safety authority and its environment agency, on the grounds of the “great danger” boars pose to commercial pig farming.
As well as monitoring the population and its impact, the bodies also recommend improving the efficiency of wild boar hunting, allowing meat from shot wild boars to be sold, and introducing requirements for producers to implement a “boar-proof fence” to protect pigs reared outdoors.
Other measures could include building a fence on the Norwegian side of the border to prevent boars from crossing into the country from Sweden, where the population is estimated to be up to 300,000. Denmark successfully cut its wild boar population after installing a fence on its border with Germany.
African swine fever, a serious viral disease affecting wild boars and pigs but not humans, was found in dead wild boars near Fagersta, 90 miles (145km) north-west of Stockholm, in August and September.However, Karl Ståhl, Sweden’s state epizootiologist, said there was currently “zero” risk of swine fever in Sweden after the last wild boar to test positive died in September, adding that the country has no active circulation of the disease.
The disease has been present in Europe since 2007 and the EU area since 2014.
Norway’s agriculture and food minister, Geir Pollestad, said earlier this month that authorities were working on “new and strengthened measures” to bring wild boar numbers as low as possible.“If we get swine fever in Norway, it will have major consequences for those involved in pig production, but will also place major restrictions on the ability to hunt, [perform] forest operations and engage in outdoor activities in the areas affected by the infection,” he said.
Norway’s largest wild boar population is in Østfold, a county in the south-east that borders Sweden, but they have also been spotted in Innlandet, an agricultural county near Østfold, and farther north. Ole-Herman Tronerud, Norway’s chief veterinary officer, said a fence on the border with Sweden could have an impact on wild boar population numbers, but that “a lot of investigating and information gathering” needed to be done first.
He added: “We have stated that the infection risk for ASF to Norway hasn’t increased as a result of the outbreak in Sweden in the short term, nor in the long term, as long as the outbreak can be contained in Sweden.”

‘The pigs have disappeared’: swine fever threatens food source for millions as disease hits wild herds

Phoebe Weston, 19 Jan 2024
https://www.theguardian.com/environment/2024/jan/19/african-swine-fever-asian-wild-pigs-borneo-aoe

Articles in the news

Bornean bearded pigs foraging on Teluk Assam beach in Malaysian Borneo. Many people there depend on them for their protein needs. Photograph: Nature Picture Library/Alamy

Scientists call for urgent intervention, as bearded pig populations are devastated by the deadly virus on islands such as Borneo.

Populations of wild pigs are crashing due to the spread of African swine fever (ASF), threatening the livelihoods of millions who depend on them for food, researchers warn.

With a fatality rate of almost 100%, ASF has swept across Asia, Europe and Africa, devastating domestic and wild pig populations over the past 10 to 20 years. The impacts are especially significant in Borneo, in south-east Asia, where bearded pig numbers have declined by between 90% and 100% since it arrived on the island in 2021, researchers said.

These pigs were once the most common large mammal species on the island, playing an important role as ecosystem engineers, dispersing seeds over large distances, according to a letter published in the journal Science. “These pigs have disappeared,” said Prof Erik Meijaard, the letter’s lead author and former chair of the IUCN Wild Pigs Specialist Group.

“I’ve gone around to everyone doing camera trapping in Borneo, and consistently we’re seeing pigs disappearing. They haven’t seen pigs on camera traps for years,” said Meijaard. He has also monitored seven camera tracking programmes in Malaysia, Indonesia and Brunei, which were not on the island of Borneo, and found their pig populations plummeted in 2019 and 2020. “As soon as [ASF] jumps into a population it eradicates everything,” he said.

Meijaard believes the bearded pig may need to be relisted from vulnerable to critically endangered as a result of ASF. There was no evidence that wild pig populations would fully recover in Borneo or other south-east Asian islands such as Java and Sumatra in Indonesia, Timor-Leste and the Philippines, the scientists said.

In Borneo, the loss of bearded pigs is already having an enormous impact on cultures and communities that depend on them for food. Local studies suggest bearded pigs once accounted for 81% of hunted wildlife by weight in some villages. Now, that number is closer to zero. “It’s a food security issue and a poverty issue. People are just fully dependent on access to wild and feral pigs for their protein needs,” said Meijaard.

The disappearance of this key protein source puts pressure on other species: in the absence of pigs, millions of local people were likely to shift their focus to hunting endangered species such as pig-tailed macaques, the scientists warned.

The loss of wild pigs can also affect the ecosystem as a whole. Bearded pigs disperse the seeds of trees as they eat fruits and migrate large distances, defecating them out throughout the forest. They also turn over soil with their snouts, which cleans undergrowth and gives tree roots access to more soil nutrients. The forests of Borneo are among the world’s most diverse ecosystems, but only 50% remain as a result of decades of logging and expansion of farmland, particularly palm oil plantations.

The scientists called for urgent research and interventions, while acknowledging the impacts on communities. The focus should be urgently to prevent the spread of ASF to other regions, the letter recommended.

“Although African swine fever has garnered substantial attention in countries with major pork industries, its effects in Borneo have been largely overlooked,” researchers wrote. “The loss of pigs disrupts food security and ecosystems and threatens other endangered wildlife.”

Trials for creating an effective vaccine have showed positive results, but this would be more effective for domestic pigs. Vaccinating wild pigs would be “logistically hugely complex and expensive to implement”, said Prof Benoit Goossens from Cardiff University, another author of the letter.

James Wood, an epidemiologist from the University of Cambridge, who was not involved in the letter, said it raised important questions about the global narrative of wild pigs being vectors of disease, and therefore a threat to the domestic pig industry. He said: “The authors describe, in contrast, how wild pig species, which in Borneo and other south-east Asian islands are central to both the culture and nutrition of many different peoples, are being devastated by ASF virus, which has been spread around the world by human-mediated movement of pigs and pig products.

“All efforts should be made to prevent the further spread of ASF between south-east Asian islands, in particular through trade in pigs and pig products, as the effects there can be far worse than just in the swine industry.”

Dr Harriet Bartlett from University of Oxford, who was not involved in the paper, agreed that the effects of the disease had been focused on the pig industry. “Expanding our focus beyond the immediate economic concerns to include the broader ecological and societal implications will be important to effectively address ASF,” she said.

Is America ready for 'Super Pigs'? Wild Canadian swine threaten to invade the US

Sara Chernikoff, USA TODAY, November 24, 2023
https://www.aol.com/america-ready-super-pigs-wild-110611391.html?guccounter=1

A difficult to eradicate population of wild hogs are roaming Canada and officials worry they'll soon spill over to the United States. This population of "super pigs" often consists of crossbreeds that combine the survival skills of wild Eurasian boar with the size and high fertility of domestic swine, according to the Associated Press.

Minnesota, North Dakota and Montana are already taking measures to prevent an invasion of the "super pig."

These wild pigs are spreading out of control in Alberta, Saskatchewan and Manitoba, posing a new threat to native species.

Wild hogs are one of the most invasive animals

Since their introduction to the U.S. in the 1500s, the feral swine population expanded across more than three-quarters of the country. According to the Department of Agriculture, their population has grown to more than 9 million. The wild animal has expanded westward and northward, with states like California, Hawaii, and Michigan reporting a fairly large feral hog population. Ryan Brook, a professor at the University of Saskatchewan and one of Canada’s leading authorities on the problem, told the Associated Press that feral swine are, “the most invasive animal on the planet” and “an ecological train wreck.” According to the U.S. Department of Agriculture, feral hogs cause approximately $2.5 billion in agricultural damages each year.

'Super pigs' are difficult to eradicate

The wild pigs are smart and adaptable, making them very good at surviving brutal winters in Canada. Officials say they will eat anything, including wildlife and crops for survival. They spread diseases to hog farms like African swine fever. They tear up land easily and they reproduce quickly. Brook told the Associated Press that even when 65% or more of a wild pig population is killed every year, the population will still increase. The success rate for hunters is only about 2% to 3%. “The only path forward is you have to be really aggressive and you have to use all the tools in the toolbox," said Brook.

Managing the feral hog problem

In some states, total elimination of feral hogs is the end goal for conservationists.

The Missouri Feral Hog Elimination Partnership killed 9,857 feral hogs in 2021, bringing the total number of hogs killed since 2016 to more than 54,000. Public hunting is one of the most popular mitigation tactics of wild hogs and has become a common recreational activity. But hogs often relocate in response to the pressures of hunting. Fencing and trapping can be more effective in mitigating wild hog populations, but require more upkeep and investment, according to Captain Experiences.

Which states are most impacted by wild hogs? Florida, Georgia and Texas have the most feral hog reports in the U.S., according to data from the University of Georgia Center for Invasive Species and Ecosystem Health. In 2023 alone, Texas had 2,425 feral hog spottings, followed by 1,377 in Georgia.

Italy culls tens of thousands of pigs to contain African swine fever

Sophie Kevany, 25 Sep 2023

https://www.theguardian.com/world/2023/sep/25/italy-african-swine-fever-asf-outbreak-lombardy-culls

Outbreaks in the Lombardy ‘pork belt’ were extinguished, say experts, but wild boar could act as a reservoir.

Huge pig culls took place last week in Italy in an attempt to contain the country’s largest outbreak of African swine fever (ASF) virus since the 1960s, which threatened the entire pig-farming sector. ASF is deadly to pigs and poses a serious threat to the global pig industry but is not a danger to humans, according to the World Organisation for Animal Health (WOAH).

The virus, the organisation said, “is highly resistant in the environment … [and can] survive on clothes, boots, wheels, and other materials”. It added: “It can also survive in various pork products, such as ham, sausages or bacon,” meaning that “human behaviours can play an important role in spreading this pig disease across borders if adequate measures are not taken”.

As of May this year, 24 different variants, or genotypes, of the virus had been identified. WOAH said that mortality rates for pigs that contract the virus can be up to 100%.

Almost 34,000 pigs were culled in Italy last week after a cluster of outbreaks in Lombardy, a region known as Italy’s pork belt and one of Europe’s main pig-producing areas.

“The cluster of outbreaks [in Lombardy] was the largest in Italy caused by the ASF virus genotype II,” said Francesco Feliziani, who leads Italy’s national reference lab for swine fever.

He said the Lombardy outbreak had been “quickly extinguished” but “posed a major threat to the entire sector as the region is the largest producer of pigs in our country".

Because there is no vaccine for ASF, Feliziani said culls to contain the disease were compulsory. The underlying problem, he said, "remains the presence of the virus in the wild boar populations", which provide a reservoir for the virus. "In Europe, the threat [of ASF] is very strong; the pressure of the virus is high and it seems inevitable that the disease will involve other domestic herds," he said.

ASF was disrupting pig breeding around the world, Feliziani said, but he warned that non-intensive, traditional livestock farming models, which might not have sufficient levels of biosecurity, were particularly at risk and could disappear altogether. "This would have strong economic repercussions on many social strata and would also affect the biodiversity of rural areas where intensive livestock farming is not possible, and which survive thanks to the typicality of products reared according to traditional methods," he said.

To control ASF outbreaks in China, producers are building multistorey pig farms that are deemed to have higher standards of disease control compared with backyard herds.

Video footage of the Lombardy culls, filmed by the NGO We Animals Media in collaboration with NGO Essere Animali, showed "an overview of the procedure, including an infected farm that had been adapted to work as a mobile slaughterhouse, operating nonstop for over a week", a spokesperson said in an email.

"Workers received pigs from other infected farms and herded them into temporary gas chambers set up inside containers, where the animals were killed," they said.

While ASF posed a "significant risk to wild boar diversity" in Asia, this was not the case in Italy, where there were large numbers of native animals, the spokesperson added.

The Italian culls, although large, were not the biggest so far in Europe, said Vincent ter Beek, the editor of Pig Progress, who has been tracking the ASF outbreak around the world.

"ASF also occurred in Romania a few years back," he said. "In comparison … [the Italian culls] are relatively small numbers. And let's not talk about numbers in Russia or China. I'm not trying to downplay anything, the amount is terrible for both producers and pigs, but it's not the biggest in the EU." Humans and wild boar were the biggest risks for spreading the disease, he said. "Humans can make the virus appear 500km down the road in a wild boar population, as happened in Sweden a few weeks back, and wild boar then spread it among themselves."

Given that wild boar are not tracked and traced, Ter Beek said the disease could spread in any direction but, he added, the spreading of the disease by boar "doesn't usually happen fast, it goes bit by bit". Ter Beek said that Germany appeared to be doing well at controlling ASF and its efforts could provide a blueprint for dealing with the virus in wild boar, "even though terrains and boar population densities are different everywhere".

The result of the virus spreading among boar would probably be "a wild boar population that is vastly lower, temporarily," said Ter Beek. However, he added, an abundance of food and relatively mild winters meant numbers would rebound fairly quickly, with the ASF virus coming back in waves from time to time, making it hard to eradicate from a country.

Experts from the Federation of Veterinarians of Europe said: "Since 2017, more than 2.3 million pigs were lost due to ASF in Europe. Although it is harmless to humans, it can be deadly for pigs and has serious socioeconomic consequences for affected countries. As no vaccine exists yet in Europe, early detection, prevention and reporting are key to curbing this deadly disease. We all should take this seriously."

Wild pig populations in U.S. can be managed

University of Georgia, October 10, 2023
https://www.sciencedaily.com/releases/2023/10/231010133543.htm

Summary: Recent conservation efforts have proven effective at controlling wild pig populations in the Southeastern United States, according to new research. Within 24 months of the start of control efforts in the study area located around the Savannah River Site in Aiken, South Carolina, researchers found a reduction of about 70% in relative abundance of pigs and a corresponding decline in environmental rooting damage of about 99%.

Recent conservation efforts have proven effective at controlling wild pig populations in the Southeastern United States, according to new research from the University of Georgia's Savannah River Ecology Laboratory and Warnell School of Forestry and Natural Resources.

Within 24 months of the start of control efforts in the study area located around the Savannah River Site in Aiken, South Carolina, researchers found a reduction of about 70% in relative abundance of pigs and a corresponding decline in environmental rooting damage of about 99%.

The study will help conservation groups understand and plan for managing a problem with both environmental and economic costs, as wild pigs were responsible for over $1.5 billion in property and crop damage in 2007, according to the study.

"Through their destructive foraging habits, wild pigs cause extensive damages to crops across the country" said Jim Beasley, a professor and researcher in Warnell and SREL. "Wild pigs also carry several diseases that can be transferred to livestock, adding to their substantial agricultural impact."

Pigs were introduced to the United States centuries ago as a food source and quickly established wild populations. Feral domestic pigs bred with purebred Eurasian boar that were introduced for hunting, and hybridized wild pigs spread across the landscape due to prolific reproductive rates and a willingness to eat just about anything. Populations exploded in the late 1980s and early 1990s, causing a substantial increase in damages to agricultural producers. In response, many large-scale control programs were put in place to reduce populations across the landscape, usually through lethal methods. In this study, Beasley and his team investigated whether such programs succeeded and, if so, whether environmental damages were reduced as well.

The team worked with 19 mixed-forest agricultural properties in South Carolina, surveying the pig populations, as well as the agricultural and environmental damages, following the implementation of a professional control program over a three-year period. "Before the trappers went in and began management efforts, we placed remote cameras around the properties to assess the initial population of wild pigs. Every six months, we would go back out and reassess the populations to see how effective the management methods were," Beasley said.

"Most studies estimate that you need to remove 40% to 60% of a wild pig population each year to maintain or significantly reduce a population, and they exceeded that threshold," Beasley said. "With sustained management the population should continue to shrink over the next several years. However, what is unknown is how quickly the population will recover if management efforts cease." When pigs forage, they upturn roots and soil with their snouts, damaging natural habitats and other animals. As natural omnivores, pigs also eat amphibians and other small creatures, potentially impacting their populations over time. Beasley attributes the population explosion to a few explanations, including humans illegally moving wild pigs to the areas where hunting them is

legal year-round, as well as to warmer climates in recent decades.
"It's really a combination of both human-driven factors and natural expansions of populations," Beasley said.
Journal Reference:
Joseph W. Treichler, Kurt C. VerCauteren, Charles R. Taylor, James C. Beasley. Changes in wild pig (*Sus scrofa*) relative abundance, crop damage, and environmental impacts in response to control efforts. Pest Management Science, 2023; DOI: 10.1002/ps.7671

How did the bushpig cross the strait? A great puzzle in African mammal biogeography solved by genomics

University of Copenhagen - Faculty of Science, January 8, 2024
https://www.sciencedaily.com/releases/2024/01/240108153154.htm

Summary:
Africa has a huge diversity of large mammals, but their evolutionary relationships and movement across the continent over time often remain a mystery. A new scientific study sheds light on longstanding questions about the interplay between evolution and geography in one of these mammals, namely the iconic African bushpig, and helps settle a major question regarding prehistoric human activities shaping biodiversity patterns in Africa.

Africa has a huge diversity of large mammals, but their evolutionary relationships and movement across the continent over time often remain a mystery. A new scientific study sheds light on longstanding questions about the interplay between evolution and geography in one of these mammals, namely the iconic African bushpig, and helps settle a major question regarding prehistoric human activities shaping biodiversity patterns in Africa.
In the ongoing biodiversity crisis, large terrestrial animals are more threatened by extinction than any other group of organisms. The African continent holds an impressively intact large-mammal community, but there is still a lot we do not know about how these species evolved, became diverse and adapted to the changing climate and habitats. Many of these questions can be addressed by investigating the genomes and genetic variation across species.
New research, published in Nature Communications, uses genomics to answer these evolutionary questions that have been debated amongst scientists for decades: 1) how and when did bushpigs cross the Mozambique Channel and arrive at the island of Madagascar, 2) is there one or two species of bushpigs?
"This study is a result of a large international collaboration with researchers from Africa and Europe. We sequenced 67 complete bushpig genomes and by using a range of different genetic analyses, we were able to address these long-standing puzzles in African evolution and biogeography," explains one of the senior authors of the study, Associate Professor at the Department of Biology, Rasmus Heller.
Were pigs ferried across the channel during the Medieval era?
The island of Madagascar separated from the African mainland around 160 million years ago, resulting in a largely unique flora and fauna. Remarkably, the bushpig is the only large, wild terrestrial mammal species that has somehow historically crossed the 400-kilometer-wide Mozambique Channel and made it from mainland Africa to the island of Madagascar.

"Our study establishes that the bushpig was introduced to Madagascar ?1,000-5,000 years ago from South/South-East Africa," Rasmus states. Their arrival therefore coincides with the arrival of humans to Madagascar from a region around southern Africa. Rasmus continues: "The likely explanation for this is that people transported these bushpigs across the channel. These results contradict previously published studies which dated the arrival of bushpigs ?480,000 years ago, well before humans were present on the island." It has been suggested that some endemic Madagascar species might have arrived by rafting as passengers on floats of vegetation.

"Intriguingly, our results raise a host of new questions: was the bushpig actually brought to Madagascar as a somewhat domesticated species? There is no archaeological or other evidence of bushpig domestication ever occurring, despite them being an important source of protein for many rural communities. And who was it that transported these animals to Madagascar? Was it Bantu-speakers, Austronesian-speakers or both? These questions and others still remain to be explored," explains Renzo F. Balboa, postdoc at the Department of Biology and one of the leading authors of the study.

Does two actually equal one?

African bushpigs, which primarily are found in East/Southern Africa, and red river hogs, which are found in West/Central Africa, were considered the same species in the past, but were subsequently redefined as two species around the 1990s, largely due to their quite distinctive looks.

The red river hogs are, as the name implies red, and have long, tufted ears reminiscent of a comical Star Wars character, while eastern and southern African bushpigs are greyish and look more like our own wild boar, although with a beautiful white mane thrown in for good measure.

Biologists have been arguing for decades about whether these two forms are actually one or two different species -- a debate that is characteristic of similar scientific uncertainty surrounding many other African mammals.

"In this study, we were able to conclude that red river hogs and bushpigs have had lots of gene flow, which means they are not only able to potentially interbreed, but they have in fact done so extensively when they have met in central Africa. Furthermore, the branching of the two types in the Tree of Life is not all that old, only a few hundred thousand years, which is not long in the evolutionary scheme of things. Hence, we now know that although there are two quite different-looking lineages of bushpigs, their biological separation is incomplete, depending on how you define species," explains Laura D. Bertola, postdoc at the Department of Biology and the other leading author of the study.

Laura continues: "Genomic data can give us insights into patterns of biodiversity on a much higher resolution than previously possible. For example, we can infer detailed population structure, but also underlying processes like gene flow and selection. Gaining improved insights into patterns of biodiversity and the underlying processes that drive them, will be crucial for effective conservation measures."

Africa is a unique continent regarding the diversity of the megafauna which is still around. Studying the evolutionary history of these species can give us important insights into African biodiversity, which is highly relevant at a time where biodiversity is being lost at an alarming pace. The new findings contribute to our understanding of prehistoric relations between Africa's humans and wildlife, but also the very fundamentals about how much biodiversity there is on this amazing continent.

"This study is a great example of how involving local researchers and wildlife management

authorities can lead to more robust and inclusive scientific research," co-author Vincent Muwanika, Associate Professor of Conservation Biology, at Makerere University, Uganda, concludes.

Journal Reference:

Renzo F. Balboa, Laura D. Bertola, Anna Brüniche-Olsen, Malthe Sebro Rasmussen, Xiaodong Liu, Guillaume Besnard, Jordi Salmona, Cindy G. Santander, Shixu He, Dietmar Zinner, Miguel Pedrono, Vincent Muwanika, Charles Masembe, Mikkel Schubert, Josiah Kuja, Liam Quinn, Genís Garcia-Erill, Frederik Filip Stæger, Rianja Rakotoarivony, Margarida Henrique, Long Lin, Xi Wang, Michael P. Heaton, Timothy P. L. Smith, Kristian Hanghøj, Mikkel-Holger S. Sinding, Anagaw Atickem, Lounès Chikhi, Christian Roos, Philippe Gaubert, Hans R. Siegismund, Ida Moltke, Anders Albrechtsen, Rasmus Heller. African bushpigs exhibit porous species boundaries and appeared in Madagascar concurrently with human arrival. Nature Communications, 2024; 15 (1) DOI: 10.1038/s41467-023-44105-1

‘How do I know these words?’: philosophical cocaine hippo is star of Berlin film festival

Philip Oltermann, 20 Feb 2024
https://www.theguardian.com/film/2024/feb/20/pepe-cocaine-hippo-berlin-film-festival-nelson-carlo-de-los-santos-arias-pablo-escobar

Nelson Carlo de los Santos Arias’s docudrama Pepe, about Colombian drug lord Pablo Escobar’s megaherbivore, gives the ill-fated creature its own voice.

Some facts about Pepe are certain. He was heavy even for his thick-set genus, reported to have weighed between four and five tonnes. With a land speed of up to 22 mph and ivory stakes protruding from those pink gums at random angles, he was a forceful reminder that his species is one of the deadliest on the planet, causing an estimated 500 human deaths per year.

Native to sub-Saharan Africa but born in Colombian cocaine king Pablo Escobar’s private menagerie and shot in its vicinity after escaping from captivity in 2009, Pepe the unhappy hippo was also undisputedly and tragically out of place.

The question on everyone’s lips at this week’s Berlin film festival, however, is what Pepe means. Dominican director Nelson Carlo de los Santos Arias’ buzzy arthouse film of the same name, which is one of 20 films competing for the Golden Bear in the festival’s coveted main competition, tells the story of Escobar’s famed pets from the beast’s point of view. In growling voiceovers, interspersed with grunts and wheezing groans, Pepe soliloquises about his fate.

But the creature’s symbolic significance is elusive. Is the hippo a bad omen, whose attacks on humans are harbingers of personal betrayals, as a Namibian guide explains the animal’s mythical meaning to a group of European safari tourists? Is Pepe the reincarnation of “the boss”, evading his hunters in the undergrowth of the Magdalena Valley like his former owner? Escobar, the most wanted drug lord of the 1980s, died in a shoot-out in 1993. But his animals, like his legacy of terror, outlived him.

Are Colombia’s cocaine hippos ciphers for migratory movements in an ever more globalised world? Escobar originally brought three hippos to his Hacienda Nápoles estate from Africa in 1981, but the animals adapted to their new habitat and by November last year the South American state’s hippo population had grown to approximately 170. Speaking at a press conference after the film’s premiere on Tuesday morning, De Los Santos Arias likened Pepe to


Escobar’s inheritance … a hippo swims in the Magdalena river in Puerto Triunfo, Colombia in 2022. Photograph: Fernando Vergara/AP

the cimarrons – African slaves who abandoned their Spanish masters in mid-16th century and hid in the mountains of Panama.

Is Pepe’s story also the story of colonialism? The film, which its director developed while participating in a German-state-funded Berlin residency, identifies Pepe’s country of origin as Namibia, a former German colony, and the hunter who was hired by the Colombian state to track down and shoot the animal had the same nationality.

“In the film, there is a philosophical image, which is the circularity of coloniality,” De Los Santos Arias said. “How do we escape from there? Perhaps only in death.”

Or is Pepe a philosophical meditation on physicality and language, an attempt to think about the world hippopotamically? The animal’s voiceover dramatises his family’s feuds and battles in epic terms, in Spanish, Afrikaans and Mbukushu, a language native to modern-day Namibia. How he has acquired these human tongues, he does not know: “How do I know these words? How do I know what a word is?”

At a festival where organisers and directors have felt the pressure to state their stances on geopolitical events in unequivocal terms, Pepe makes the case that films are sometimes allowed to be several things at once. Even though De los Santos Arias said he had never read Moby-Dick, he proposed that his cocaine hippo had a white whale-ish quality, seizing the imagination of Magdalena River fishers and cinemagoers alike, without ever revealing its true meaning. “Hippos and whales have the same ancestors,” he said. Both mammals have oil-producing skin glands on their hairless skin, and both communicate via underwater vocalisations. “When you spend time with hippos, you start seeing the whale-ishness of them.”

Earliest known European common hippopotamus fossil reveals their Middle Pleistocene dispersal

PLOS, November 22, 2023
https://www.sciencedaily.com/releases/2023/11/231122192328.htm

Summary:
Modern hippos first dispersed in Europe during the Middle Pleistocene, according to a new study.

Modern hippos first dispersed in Europe during the Middle Pleistocene, according to a study published November 22, 2023 in the open-access journal PLOS ONE by Beniamino Mecozzi of the Sapienza University of Rome and colleagues.
Modern hippos, *Hippopotamus amphibius*, arose from African ancestors during the Quaternary, a time when hippos were widespread in Europe.
However, the details of the modern species' origin and dispersal into Europe are unclear and highly debated.
In this study, Mecozzi and colleagues provide new insights via analysis of a fossil hippo skull from the study area of Tor di Quinto in Rome.
The skull of Tor di Quinto, currently housed at the Earth Science University Museum of Sapienza University of Rome, is among the most complete hippo specimens known from Pleistocene Europe, but its significance has been unclear due to uncertainties about its age and where exactly it was originally excavated.
Following restoration of the skull in 2021, researchers were able to analyze the composition of sediments found within the skull cavities, revealing a match to the local Valle Guilia Formation, indicating a geologic age for this skull between 560,000-460,000 years old.
Cranial and dental morphologies also confirmed the identity of this skull as the modern species *Hippopotamus amphibius*.
This research reveals this skull to be the oldest known fossil of this modern hippo species in Europe.
These results shed light on the history of hippos in Europe, reinforcing the hypothesis of an early dispersal during the Middle Pleistocene and bolstering broader understanding of the deep history of these large mammals.
Hippos are highly influential species within modern and ancient ecosystems, and they are valuable indicators of past climate and environmental conditions.
The authors add: "Restoring the mammal skeletons exposed at the University Museum of Earth Science, Terra, Sapienza University of Rome offers new data for old fossils. The multidisciplinary study of the skull from Cava Montanari (Roma) redefines the first dispersal of *Hippopotamus amphibius* in Europe."
Journal Reference:
Beniamino Mecozzi, Alessio Iannucci, Marco Mancini, Daniel Tentori, Chiara Cavasinni, Jacopo Conti, Mattia Yuri Messina, Alex Sarra, Raffaele Sardella. Reinforcing the idea of an early dispersal of *Hippopotamus amphibius* in Europe: Restoration and multidisciplinary study of the skull from the Middle Pleistocene of Cava Montanari (Rome, central Italy). PLOS ONE, 2023; 18 (11): e0293405 DOI: 10.1371/journal.pone.0293405

Hippos' prominent tusks and wide gaping mouths prevent efficient, grinding chewing

PLOS, October 4, 2023
https://www.sciencedaily.com/releases/2023/10/231004150543.htm

Summary:
Hippos' huge tusks and wide gape restrict grinding jaw movements, making their chewing inefficient, according to a new study.

Hippos' huge tusks and wide gape restrict grinding jaw movements, making their chewing inefficient, according to a study by Annika Avedik and Marcus Clauss at the University of Zurich, Switzerland publishing October 4 in the open-access journal PLOS ONE.

Hippos have the widest gape of any mammal but are very inefficient at chewing, which limits how much they can eat.

A possible explanation is that the size and arrangement of their teeth prevents them grinding their jaws side-to-side.

To investigate, researchers observed chewing in common hippos (*Hippopotamus amphibius*) and pygmy hippos (*Choeropsis liberiensis*) using video footage of zoo animals.

They also measured the size and arrangement of teeth in the skulls of museum specimens from 86 common and 21 pygmy hippos, and looked for signs of wear that indicate how the animals chewed their food.

There was little difference for either species in the width of their upper and lower jaw or cheek teeth, suggesting a mainly vertical chewing motion.

The size and positioning of their canine teeth don't prevent side-to-side chewing, but long lower canine teeth limit the extent of this grinding action.

Most importantly, common hippos have interlocking upper and lower front teeth which almost completely prevent side-to-side motion.

Video footage and wear analysis confirmed that pygmy hippos use a slight side-to-side grinding motion when chewing, whereas common hippos rely almost exclusively on vertical jaw movements.

The slight side-to-side chewing movements used by living hippos suggest that the ancestors of both modern species relied more extensively on grinding jaw movements.

Why modern hippos lost this ability remains unclear, but chewing efficiency may have been compromised in favor of evolving a rigid jaw and a wide gape, which is an asset during fights with other hippos.

Inefficient chewing might have restricted common hippos to a semi-aquatic lifestyle, the authors say.

The authors add: "Most herbivores grind their food by moving the jaw sideways. Hippos have given up on this because they need a rigid jaw for fighting."

Journal Reference:
Annika Avedik, Marcus Clauss. Chewing, dentition and tooth wear in Hippopotamidae (*Hippopotamus amphibius* and *Choeropsis liberiensis*). PLOS ONE, 2023; 18 (10): e0291825
DOI: 10.1371/journal.pone.0291825

New scientific articles

General articles about Suiformes

Thermoregulation in the wild boar (*Sus scrofa*)
Ruf, T., Vetter, S.G., Painer-Gigler, J., Stalder, G. and C. Bieber 2023
Journal of Comparative Physiology B, 193(1):689-697
The wild boar (*Sus scrofa*) originates from warm islands but now inhabits large areas of the world, with Antarctica as the only continent not inhabited by this species. One might be tempted to think that its wide distribution results from increasing environmental temperatures. However, any effect of temperature is only indirect: Abundant availability of critical food resources can fully compensate the negative effects of cold winters on population growth. Here, we asked if temperature as a habitat factor is unimportant compared with other habitat indices, simply because wild boars are excellent thermoregulators. We found that the thermoneutral zone in summer was approximately 6–24°C. In winter, the thermoneutral zone was lowered to 0–7°C. The estimated increase in the heart rate and energy expenditure in the cold was less than 30% per 10°C temperature decline. This relatively small increase of energy expenditure during cold exposure places the wild boar in the realm of arctic animals, such as the polar bear, whereas tropical mammals raise their energy expenditure several fold. The response of wild boars to high Ta was weak across all seasons. In the heat, wild boars avoid close contact to conspecifics and particularly use wallowing in mud or other wet substrates to cool and prevent hyperthermia. Wild boars also rely on daily cycles, especially of rhythms in subcutaneous temperature that enables them to cheaply build large core–shell gradients, which serve to lower heat loss. We argue it is predominantly this ability which allowed wild boars to inhabit most climatically diverse areas in the world.

Probabilistic Genetic Identification of Wild Boar Hybridization to Support Control of Invasive Wild Pigs (*Sus scrofa*)
Smyser, T. J., Pfaffelhuber, P., Giglio, R. M., DeSaix, M. G., Davis, A. J., Bowden, C. F., Tabak, M. A., Manunza, A., Bâlteanu, V. A., Amills, M., Iacolina, L., Walker, P., Lessard, C. and A. J. Piaggio 2024
Ecosphere, 15(2):1-17
The rapid expansion of wild pigs (*Sus scrofa*) throughout the United States has been fueled by unlawful introductions, with invasive populations causing extensive crop losses, damaging native ecosystems, and serving as a reservoir for disease. Multiple states have passed laws prohibiting the possession or transport of wild pigs. However, genetic and phenotypic similarities between domestic pigs and invasive wild pigs—which overwhelmingly represent domestic pig and wild boar hybrids—pose a challenge for the enforcement of such regulations. We sought to exploit wild boar ancestry as a common attribute among the vast majority of invasive wild pigs as a means of genetically differentiating wild pigs from breeds of domestic pig found within the United States. We organized reference high-density single nucleotide polymorphism genotypes (1039 samples from 33 domestic breeds and 382 samples from 16 wild boar populations) into five genetically cohesive reference groups: mixed-commercial breeds, Durocs, heritage breeds, primitive breeds, and wild boar. Building upon well-established genetic clustering approaches, we structured the test statistic to describe the difference in the likelihood of a given genotype's ancestry vectors (sensu genetic clustering analysis) if derived strictly from the four described domestic pig reference groups versus allowing for admixture from the wild boar group. By fitting

statistical distributions to test statistics of reference domestic pigs, we characterized the distribution of the null hypothesis that a given genotype descends strictly from domestic pig reference groups. We tested the approach with simulated genotypes and empirical data from an additional 29 breeds of domestic pig represented by 435 unique genotypes; all associated test statistics for simulated and empirical domestic pig challenge sets fell within the distribution of reference domestic pigs. We then evaluated 6566 invasive wild pigs sampled across the contiguous United States, of which 63% exceeded the maximum threshold for domestic pigs and could be statistically classified as possessing wild boar ancestry. This approach provides a scientific foundation to enforce regulations prohibiting the possession of this destructive invasive species. Further, this computationally efficient and generalizable approach could be readily adapted to quantify gene flow among ecological systems of conservation or management concern.

Potential use of porcine zoogenetic resources (*Sus scrofa domestica*) in silvopastoral, for family livestock production systems

Alfonso Pardo, S., Mahecha-Ledesma, L., Gallego Castro, L. A., and J. Angulo Arizala 2023
Agronomía Mesoamericana, 34(3):1-22

Introduction. In Colombia, there has been an observed increase of over 100 % in pork consumption over the last decade, positioning it as the animal-origin protein that has grown the most in the country. This surge has driven the pork industry to evolve into a sustainable and competitive sector both nationally and internationally. This productive advancement has been made possible through high-tech processes and improvements that meet the current supply demands. However, access to such technological processes and improvement practices by family livestock production systems remains limited. Objective. To analyze the use of porcine zoogenetic resources under silvopastoral models for potential implementation in family livestock production systems focused on piglet raising and fattening. Development. Through the use of key terms and search formulas, eighty documents addressing central topics such as porcine zoogenetic characteristics, with an emphasis on the Colombian creole pig breed "San Pedreño", forage, and shrub alternatives for nutritional supplementation of pigs within silvopastoral systems, animal welfare criteria, and development opportunities in creole pigs' production, were collected and analyzed. Conclusion. This review emphasizes the social importance of contextualizing family livestock systems with alternatives that lead to greater productive, environmental, and economic sustainability. It also aims for increased competitiveness and recognition of their products through optimal management of natural, food, and zoogenitic resources in each region. Consequently, value-added products are generated from sustainable production systems, ensuring food security for families implementing these alternatives. Further research is needed to evaluate potential zoogenetic and nutrition alternatives.

Home ranges and movement patterns of wild boars (*Sus scrofa*) at the northern edge of the species' distribution range

Miettinen, E., Melin, M., Holmala, K., Meller, A., Väänänen, V. M., Huitu, O. and M. Kunnasranta 2023
Mammal research, 68(1):611-623

In Finland, the wild boar (*Sus scrofa* L.) lives on the northernmost edge of the species' distribution range, and the population mainly originates from individuals immigrating from Russia. Most of the

current population lives in the southeastern part of the country, and the wild boar is steadily expanding further. To develop effective risk and population management in novel northern wild boar regions, detailed information about the species' local ecology is required. To estimate wild boar movement patterns, 17 adult wild boars were monitored using GPS collars from May 2020 to September 2022 in the core region of the current distribution. The average total home ranges of wild boars (87.1 ± 17 km^2 MCP, 33 ± 5.5 SE km^2 95% KDE) were larger compared with studies from southern latitudes. The length of nocturnal activity times varied seasonally. All studied individuals at the border zone (N = 15) showed continuous transboundary movements, with home range core areas located mainly on the Russian side. Wild boar locations were predominantly in the Russia border zone, especially resting sites during the daytime. Most locations in Finland were from night-time feeding excursions. Our study shows that, although home ranges are large, adult wild boars are relatively sedentary also in northern latitudes. However, the movement capacity of the species enables the transboundary spread of diseases such as African swine fever. Our results provide information for risk management and emphasize the importance of transboundary collaboration in the monitoring and management of common wild boar populations.

The natural flavonoid compound deguelin suppresses sperm (*Sus scrofa*) functions through abnormal activation of the PI3K/AKT pathway

Woo Jin, L., Jae Hwan J., Seung Ik J., Eun Ju J., Ju Mi H., Jeong-Won B., Jae Jung H., Dae-Hyun K. and K. Woo-Sung 2023

Reproductive Toxicology, 120(1):1-7

Deguelin is a natural flavonoid extracted from plants belonging to the *Lonchocarpus*, *Derris*, or *Tephrosia* genera. It inhibits AKT activity in tumors and has the potential to be used as a treatment for malignant tumors. However, the risks associated with the use of deguelin on male fertility have not yet been explained in detail. Therefore, this study was conducted to investigate the effects of deguelin on sperm functions during capacitation. First, boar spermatozoa were exposed to different concentrations of deguelin (0.1, 1, 10, 50, and 100 μM). Next, sperm functional assessments, such as sperm motility, capacitation status, intracellular ATP level, and cell viability, were performed. The expression levels of PI3K/AKT-related proteins and the phosphorylation of their tyrosine residues were also evaluated by western blotting. No significant difference was observed in cell viability; however, deguelin considerably decreased sperm motility and motion kinematics in a dose-dependent manner. Although no significant difference was observed in the capacitation status, acrosome reaction decreased at high concentrations of deguelin (50 and 100 μM). Furthermore, intracellular ATP levels were significantly decreased in all deguelin treatment groups compared with those in the control group. Results of western blotting revealed that deguelin substantially diminished tyrosine phosphorylation. Interestingly, in contrast to previous studies showing that deguelin inhibits AKT activity, our results showed that it increased the expression of PI3K/AKT pathway-related proteins. Collectively, these findings indicate that deguelin exerts negative effects on sperm functions due to abnormal PI3K/AKT signaling activation. We believe that this is the first study to provide evidence that deguelin can regulate sperm functions independent of PI3K/AKT pathway inhibition. Furthermore, its detrimental effects on male fertility should be considered while developing or using deguelin as a therapeutic agent.

New scientific articles

Biomarcadores de estrés oxidativo en jabalí (*Sus scrofa*) del Noroeste de la Península Ibérica

García Muñoz, J., Portillo Moreno, A., Solomando González, J. C., Fernández Casado, D., Martínez Morcillo, S., Míguez Santiyán, M. P., Soler Rodríguez, F., López Beceiro, A., Fidalgo Álvarez, L. E. and M. Pérez López 2023

Ecosistemas, 32(3):1-12

The existence of polluting chemical compounds in the environment is a threat both to living beings and to the ecosystem as a who-le. Ecotoxicology is therefore developing new tools, such as the use of biomarkers, with the aim of evaluating the effect of these pollutants. Many studies have discussed the role of oxidative stress indicators as potentially useful parameters in the field of environmental pollution. However, studies focused on wildlife, and more specifically on wild boar (*Sus scrofa*), are scarce, despite the wide geographical distribution of this ungulate, which would allow its use as a bioindicator in environmental biomonitoring programmes. In the present study, the levels of two oxidative stress biomarkers, malondialdehyde (MDA) and glutathione reductase (GR), were determined in the kidney tissue of wild boar from NW Spain. In addition, the influence of sex on the values obtained was evaluated. The overall mean values were 1.811 ± 0.426 nmoles/mg protein for MDA, and 0.079 ± 0.019 picomol/min/mg protein for GR activity. With regard to the influence of the sex factor, statistically significant differences were found in the levels of MDA, with higher levels of oxidative stress in males than in females. These results constitute a baseline of oxidative stress biomarker levels in game species for use in future biomonitoring studies.

Agricultural damage following the recent expansion of wild boar (*Sus scrofa*)—farmer perceptions and preconditions

Miettinen, E., Pellikka, J., Kunnasranta, M. and O. Huitu 2024

International Journal of Pest Management, 1-13

The wild boar (*Sus scrofa*) population has recently increased in Fennoscandia, leading to increasing interactions with humans, e.g. in the form of hunting opportunities or property damages. These experiences may shape the attitudes towards wild boars and affect their population management. We studied attitudes among 165 farmers towards wild boar by means of survey data. We also made preliminary estimates of wild boar damage costs in Finland. Our analysis revealed three attitude groups among farmers, emphasizing various perspectives: “hunting resource”, “pest-of-concern”, and “ambivalent”. The benefits, costs, feelings, and perceived wild boar population development partly explained the division. The direct annual damage costs in southeast Finland were broadly estimated to be circa 990,000€ and mitigation costs circa 350,000€. Reconciling differing opinions and goals into a widely accepted management strategy is a key precondition for sustainable coexistence. While the level of economic loss is so far not substantial, monitoring of crop damages is vital. Our results provide a valuable baseline for future evaluations, as the wild boar population is expected to grow.

Assessing population structure and migration patterns of wild boar (*Sus scrofa*) in Japan

Sawai, K., Arakawa, A., Taniguchi, M., Xiao, B., Sawai, M., Osaki, M., Yamaguchi, E., Hayama, Y., Murato, Y., Shimizu, Y., Kondo. S. and T. Yamamoto 2023

Scientific reports, 13(1):1-9

Geographical wildlife patterns reflect historical range expansion and connectivity and provide

insights into wildlife population management. In our large-scale phylogeographic population analysis of wild boars (*Sus scrofa leucomystax*) in Japan, we identified 15 clusters using 29 microsatellite markers, each structured within a range of approximately 200 km. This suggests that evolution was essentially driven by isolation by distance, and that the range of gene flow was limited. One cluster contained subpopulations located approximately 900 km apart, indicating the occurrence of past anthropogenic introductions. Moreover, we estimated effective migration to visualize the geographic genetic population diversity. This analysis identified six potential barriers, one of which involved large plains and mountainous areas in the Kanto region of eastern Japan. This barrier likely persisted in the two eastern clusters for an extended period, restricting migration to the neighboring areas. Overall, our study sheds light on the demographic history of wild boar in Japan, provides evidence of past anthropogenic introductions from distant areas, and highlights the importance of geographic barriers in shaping genetic diversity and population dynamics. This knowledge will be beneficial for forming informed wildlife management strategies toward the conservation of genetic integrity and ecological balance of wild boar populations in Japan.

Understanding the interface between European wild boar (*Sus scrofa*) and domestic pigs (*Sus scrofa domesticus*) in Sweden through a questionnaire study

Ernholm, L., Ståhl, K., Neimanis, A., Widgren S. and S. SternbergLewerin 2023
Acta Veterinaria Scandinavica, 65(1):1-9

Background In recent years, the wildlife/livestock interface has attracted increased attention due to disease transmission between wild and domestic animal populations. The ongoing spread of African swine fever (ASF) in European wild boar (*Sus scrofa*) emphasize the need for further understanding of the wildlife/livestock interface to prevent disease spill-over between the wild and domestic populations. Although wild boar may also act as a potential source for other infectious disease agents, ASF is currently the most severe threat from wild boar to domestic pigs. To gather information on the wild boar situation at commercial pig producing farms in Sweden, a digital questionnaire survey was distributed through the animal health services. Results Most pigs produced for commercial purposes in Sweden are raised without outdoor access. Of the 211 responding pig producers, 80% saw wild boar or signs of wild boar activity in the vicinity of their farm at least once during the year. Observations were significantly correlated with geographical region, but there was no correlation between farm characteristics (farm size, main type of production, outdoor access) and observed wild boar presence or proximity. However, a reported higher frequency of wild boar observations was positively correlated with the observations being made in closer proximity to the farm. Hunting and strategic baiting were the most common mitigation strategies used to keep wild boar at bay. Of the 14 farms raising pigs with outdoor access, 12 responded that these pigs could be raised solely indoors if needed. Pigs with outdoor access are required to be fenced in, but double fencing in these outdoor pig enclosures was not practiced by all. A perimeter fence surrounding any type of pig farm was very rare. More than half of the producers that grew crops with intended use for pigs reported crop damage by wild boar. Conclusion This study shows that although pigs raised for commercial purposes in Sweden are, to a large extent, kept indoors the potential for indirect contact with wild boar exists and must be considered. Variable local situations regarding wild boar abundance may require an adaptive approach regarding biosecurity efforts. Keywords African swine fever, Disease transmission, Wildlife-livestock interface

New scientific articles

DNA metabarcoding reveals consumption of diverse community of amphibians by invasive wild pigs (*Sus scrofa*) in the southeastern United States

Canright, V.R., Piaggio, A.J., Chinn, S.M., Giglio, R. M., Craine, J. M. and J. C. Beasley 2024
Scientific reports, 13(1):1-12

Invasive wild pigs (*Sus scrofa*) are one of the most widespread, destructive vertebrate species globally. Their success can largely be attributed to their generalist diets, which are dominated by plant material but also include diverse animal taxa. Wild pigs are demonstrated nest predators of ground-nesting birds and reptiles, and likely pose a threat to amphibians given their extensive overlap in wetland use. DNA metabarcoding of fecal samples from 222 adult wild pigs culled monthly from 2017 to 2018 revealed a diverse diet dominated by plant material, with 166 plant genera from 56 families and 18 vertebrate species identified. Diet composition varied seasonally with availability for plants and was consistent between sexes. Amphibians were the most frequent vertebrate group consumed and represented the majority of vertebrate species detected, suggesting amphibians are potentially vulnerable to predation by wild pigs in our study region. Mammal, reptile, and bird species were also detected in pig diets, but infrequently. Our results highlight the need for research on the impacts of wild pigs on amphibians to better inform management and conservation of imperiled species.

Exploring the potential links between gut microbiota composition and natural populations management in wild boar (*Sus scrofa*)

Vedel, G., Triadó Margarit, X., Linares, O., Moreno Rojas, J. M., de la Peña, E., García Bocanegra, I., Jiménez Martín, D., Carranza, J. and E. O. Casamayor 2023
Microbiological Research, 274(1):1-10

We surveyed wild boar (*Sus scrofa*) populations using 16S rRNA gene analysis of the gut microbiota in fresh faeces taken from 88 animals hunted in 16 hunting estates. The wild boar is a very convenient model system to explore how environmental factors including game management, food availability, disease prevalence, and behaviour may affect different biological components of wild individuals with potential implications in management and conservation. We tested the hypotheses that diet (according to stable carbon isotopes analyses), gender (i.e., animal behaviour studying males and females), and both health (analyses of serum samples to detect exposure to several diseases) and form statutes (i.e., thoracic circumference in adults) are reflected in changes in the intestinal microbiota. We focused on a gut functional biomarker index combining Oscillospiraceae and Ruminococcaceae vs. Enterobacteriaceae. We found that gender and the estate (population) were explanatory variables (c.a. 28% of the variance), albeit a high degree of overlapping among individuals was observed. The individuals with higher abundance of Enterobacteriaceae showed a gut microbiota with low diversity, mostly in males. Significant statistical differences for thoracic circumference were not found between males and females. Interestingly, the thoracic circumference was significantly and inversely related to the relative abundance of Enterobacteriaceae in males. Overall, we found that diet, gender, and form status were major factors that could be related to the composition and diversity of the gut microbiota. A high variability was observed in the biomarker index for populations with natural diet (rich in C3 plants). Although, we noticed a marginally significant negative trend between the index (higher abundance of Enterobacteriaceae) and the continuous feeding of C4 plants (i.e., supplementary maize) in the diet of males. This result suggests that continuous artificial feeding

in hunting estates could be one of the factors negatively influencing the gut microbiota and the form status of wild boars that deserves further investigations.

Identifying the Risk Regions of Wild Boar (*Sus scrofa*) Incidents in China

Zheng, B., Lin, X. and X. Qi 2023
Animals, 13(20):1-14

The objectives of this study were to identify the risk regions of wild boar incidents in China and to draw a risk map. Risk maps can be used to plan the prioritization of preventive measures, increasing management effectiveness from both a short- and a long-term perspective. We used a web crawler (web information access technology) to obtain reports of wild boar incidents from China’s largest search engine (Baidu) and obtained 196 valid geographic locations of wild boar incidents from the reports. Subsequently, a system of environmental variables—with climate, topography, landscape, and human disturbance as the main variable types—was constructed, based on human–land-system thinking. Finally, the Maxent model was applied to predict the risk space of wild boar incidents in China by integrating the geographic location information for wild boar incidents with the environmental variables. We observed that the types of environmental variables that contributed to wild boar incidents were in the descending order of climate (40.5%) > human disturbance (25.2%) > landscape (24.4%) > topography (9.8%). Among the 14 environmental variables, annual precipitation, the GDP index, and the mean annual temperature were the main environmental variables. The distance from woodland, distance from cultivated land, and elevation were the secondary environmental variables. The response curves of the environmental variables demonstrated that the highest probability of wild boar incidents occurred when the annual average temperature was 16 °C, the annual precipitation was 800 mm, and the altitudes were 150 m and 1800 m. The probability of wild boar incidents decreased with an increase in the distance from cultivated and forested land, and increased sharply and then levelled off with an increase in the GDP index. Approximately 12.18% of China was identified as being at a high risk of wild boar incidents, mainly on the eastern side of the Huhuanyong Line.

Understanding local pig hunter values and practices as a means toward co-management of feral pigs (*Sus scrofa*; pua’a) in the Hawaiian Islands

Luat-Hūʻeu, K. K., Blaich Vaughan, M. and M. R. Price 2023
Ecology and Society, 28(2):1-13

Differing values between communities and government resource managers may lead to conflict, particularly when community members are not involved in decision making. Increasingly, co-management arrangements have become an important tool to increase local capacity for resource management, increase trust between diverse community groups, and foster effective stewardship. However, co-management depends upon collaboration between users and managers and the ability to understand relationships between a given resource and those who use it, even when these communities are often viewed as contravening conservation efforts. Invasive species, such as feral pigs (*Sus scrofa*), present particular management challenges because they damage island ecosystems but are also integral to community life ways and food systems. Based on interviews with local pig hunters in the Hawaiian Islands, we explored the social-cultural values and practices of local pig hunters, their reasons for hunting, and possibilities for greater collaboration in feral pig management. Results highlight the importance of hunting for both food and other forms of well-being and cultural perpetuation, along with opportunities for (1) expanding mechanisms of access to improve hunting opportunities for invasive species; (2) integrating rights and responsibilities to meet management objectives; and (3) improving communication to enhance collaborative arrangements. Considering the context of managing community use of an ecologically detrimental invasive species, this study offers insights to guide co-management partnerships with community groups that are sometimes perceived as opposed to invasive species control efforts.

Third-party intervention and post-conflict behaviour in agonistic encounters of pigs (*Sus scrofa*)
Maffezzini, N., Turner, S. P., Bolhuis, J. E., Arnott, G. and I. Camerlink 2023
Frontiers in zoology, 20(1):1-15
Third-party interference in agonistic contests entails a deliberate intervention in an ongoing fight by a bystanding individual (third party) and may be followed by post-conflict social behaviour to provide support to a specific individual. The mechanisms behind third-party intervention are, however, still largely understudied. The aim of this study was to investigate third-party interference, with the predictions that (1) the interferer derives benefits from its action by winning a fight, (2) that patterns of intervention depend on familiarity, (3) that dyadic fights last longer than triadic fights, and (4) that interferers engage in non-agonistic social behaviours afterwards. Pre-pubertal pigs (Sus scrofa) (n = 384) were grouped with one familiar and four unfamiliar conspecifics (all non-kin) to elicit contests for dominance rank. Third-party interference was analysed for the first 30 min after grouping, along with the behaviour (nosing or aggression), contest duration, contest outcome, and interferer behaviour after the fight (post-conflict social behaviour).

An inbreeding perspective on the effectiveness of wildlife population defragmentation measures – a case study on wild boar (*Sus scrofa*) of Veluwe, The Netherlands
De Jong, J. F., De Jong, M. J., Megens, H., Van Hooft, P., Crooijmans, R. P., De Groot, G. A. and H. H. Prins 2024
Frontiers in Ecology and Evolution, 11(1):1-14
Pervasive inbreeding is a major genetic threat of population fragmentation and can undermine the efficacy of population connectivity measures. Nevertheless, few studies have evaluated whether wildlife crossings can alleviate the frequency and length of genomic autozygous segments. Here, we provided a genomic inbreeding perspective on the potential effectiveness of mammal population defragmentation measures. We applied a SNP-genotyping case study on the ~2500 wild boar *Sus scrofa* population of Veluwe, The Netherlands, a 1000-km2 Natura 2000 protected area with many fences and roads but also, increasingly, fence openings and wildlife crossings. We combined a 20K genotyping assessment of genetic status and migration rate with a simulation that examined the potential for alleviation of isolation and inbreeding. We found that Veluwe wild boar subpopulations are significantly differentiated (FST-values of 0.02-0.13) and have low levels of gene flow. One noteworthy exception was the Central and Southeastern subpopulation, which were nearly panmictic and appeared to be effectively connected through a highway wildlife overpass. Estimated effective population sizes were at least 85 for the meta-population and ranged from 31 to 52 for the subpopulations. All subpopulations, including the two connected subpopulations, experienced substantial inbreeding, as evidenced through the occurrence of many long homozygous segments. Simulation output indicated that whereas one or

few migrants per generation could undo genetic differentiation and boost effective population sizes rapidly, genomic inbreeding was only marginally reduced. The implication is that ostensibly successful connectivity restoration projects may fail to alleviate genomic inbreeding of fragmented mammal populations. We put forward that defragmentation projects should allow for (i) monitoring of levels of differentiation, migration and genomic inbreeding, (ii) anticipation of the inbreeding status of the meta-population, and, if inbreeding levels are high and/or haplotypes have become fixed, (iii) consideration of enhancing migration and gene flow among meta-populations, possibly through translocation.

Patterns of Nocturnal Activity of the Large Bornean Even-Toed Ungulates Visiting the Mineral Licks Across Different Moon Phases

Shein, L.W., Mojiol, A.R., Wahab R. and A. Arinafril
The Malaysian Forester, 86(2): 275-287
The most common visitors to the natural mineral licks in Sabah, Borneo, are the large even-toed ungulates, but their nocturnal activity patterns are influenced by the moon phase and interspecific competition. A camera trapping survey was conducted to examine the nocturnal activity patterns adopted by the large even-toed ungulate species in visiting four selected mineral licks in Segaliud-Lokan Forest Reserve across different moon phases. A total of 436 independent sightings of three large even-toed ungulate species were recorded within 345 nights of camera trapping in this research. The herbivorous-frugivorous Sambar Deer (*Rusa unicolor*) was found competing with the omnivorous Bearded Pig (*Sus barbatus*) for the usages of mineral licks under the same temporal niche. The activity level of the herbivorousfrugivorous Banteng (*Bos javanicus*) at night was dependent only on the existing lunar illumination. The present findings suggest that the change in lunar illumination can define the predation risk and visual acuity of terrestrial mammals. However, these influences are likely to have less of an impact on species with high lick dependency, such as the Sambar Deer and Bearded Pig at this forest reserve, especially when predator abundance is low, although further research is required to confirm the given matters in the future.

Conserving large mammals on small islands: A case study on one of the world's most understudied pigs, the Togean islands babirusa

Jati, A.S., Broto, B.W., Latifiana, K., Fraver, S., Dri, G.F., Rejeki, I.R., Bustang, and· A. Mortelliti
2024
Original Research, 33: 1207–1223
Conserving large mammals on small islands poses a great challenge, given their high resource demand within the limited space available. The endangered Togean Islands babi rusa (*Babyrousa togeanensis*) is one of these species, with a distribution range limited to four small islands in the Togean Archipelago, Indonesia. Despite being listed as endan gered, very little information is available on the distribution and ecology of this species. To address this critical knowledge gap, we here report the first field-based ecological study of the Togean Islands babirusa across its entire distribution range. Following a stratified random sampling procedure, we distributed camera traps at 103 stations across four is lands to collect data on the species distribution from July-October 2022. We performed an occupancy modeling analysis to assess the species' habitat use, with various habitat features estimated through remote sensing and field measurements as covariates. We found that forest and mangrove availability over a large area positively influenced

babirusa habi tat selection. Babirusas only made use of agricultural areas when large forest areas were available nearby. Our results highlight the benefits of redesigning the national park area to accommodate babirusa habitat requirements, specifically by reassigning the non-forested park areas (about 30% of the park area) to non-protected forests currently outside the park boundary (about 50% of total forested area). Our case study exemplifies key challenges associated with conserving large mammals on small islands and highlights the importance of following an adaptive management approach, which in this case implies shifting 30% of the current protected area.

Swine global genomic resources: insights into wild and domesticated populations
Benjamin, N.R., Crooijmans, R.P.M.A., Jordan, L.R., Bolt, C.R., Schook, L. B., Schachtschneider, K.M., Groenen, M.A.M . and A.L. Roca 2023
Mammalian Genome, 34: 520-530
Suids, both domesticated and wild, are found on all continents except for Antarctica and provide valuable food resources for humans in addition to serving as important models for biomedical research. Continuing advances in genome sequencing have allowed researchers to compare the genomes from diverse populations of suids helping to clarify their evolution and dispersal. Further analysis of these samples may provide clues to improve disease resistance/resilience and productivity in domestic suids as well as better ways of classifying and conserving genetic diversity within wild and captive suids. Collecting samples from diverse populations of suids is resource intensive and may negatively impact endangered populations. Here we catalog extensive tissue and DNA samples from suids in collections in both Europe and North America. We include samples that have previously been used for whole genome sequencing, targeted DNA sequencing, RNA sequencing, and reduced representation bisulfite sequencing (RRBS). This work provides an important centralized resource for researchers who wish to access published databases.

Premier inventaire post-crise des ongulés du Parc National du Mont Sangbé (PNMS) à l'Ouest de la Côte d'Ivoire
N'Guessan Dawy Assui, W.K., Bamba, ., Monket, A.E.H., Kouakou, Y.C., N'Guessan, K.A., Koffi, D.A., Tondossama, A. and J.-C. K. Bene 2023
Journal of Animal & Plant Sciences, 55(2): 10153-10170
The conservation of biodiversity in tropical forests, including protected areas, is a major challenge for managers in the face of the various pressures that these areas face. The lack ofknowledge on the biodiversity of protected areas makes sustainable management decisions difficult. In order to meet this challenge, regular monitoring of biodiversity and evaluation of management activities, through ecological monitoring and monitoring programs, are needed. . In Côte d'Ivoire, the successive socio-politico-military crises since 2002 have led to severe degradation of classified forests and national parks in the west, including the Mont Sangbé National Park (MSNP). After these crises, knowledge of wildlife diversity becomes imperative for effective conservation measures. In order to update the knowledge on ungulates, this study was carried out in the Mont Sangbé National Park (MSNP) and aims to identify ungulates, their spatial distribution, their conservation status and threats to these mammals. The methodology adopted consisted first of conducting surveys on the knowledge of ungulates in the area, among the managers of the MSNP and the riparian populations. Then, pedestrian surveys were carried out using linear

transects, systematically distributed throughout the study site. The evidence of the presence of fauna collected made it possible to certify the presence of twenty (20) species of ungulates in the MSNP. Several species are distributed throughout the park, while others are found only in savannahs or mountain forests. Among these species, five (5) are classified as Near Threatened (NT) and one is classified as Vulnerable (VU) according to IUCN categories. It should be noted that poaching is the major threat to ungulate species in this park.

Biogeography and conservation of desert warthog *Phacochoerus aethiopicus* and common warthog *Phacochoerus africanus* (Artiodactyla: Suidae) in the Horn of Africa
de Jong, Y.A., d'Huart, J.P. and T.M. Butynski 2022
Mammalia, 87(1)
Two species of warthog are currently widely recognised, the poorly known desert warthog *Phacochoerus aethiopicus* and the widely distributed common warthog *Phacochoerus africanus*. Spatial data for both species were collected during field surveys and from the literature, museums, colleagues, naturalists, local experts, and online resources to assess their biogeography in the Horn of Africa (HoA). Their distributions were overlaid with ArcGIS datasets for altitude, rainfall, temperature, and ecoregions. *Phacochoerus aethiopicus* appears to be restricted to Ethiopia, Kenya, and Somalia, with no records west of the Eastern Rift Valley (ERV). The estimated current geographic distribution of *P. aethiopicus* is 1,109,000 km^2. *Phacochoerus africanus* occurs in all five countries of the HoA and has an estimated current geographic distribution in the HoA of 1,213,000 km2. *Phacochoerus africanus* appears to be the more adaptable species although *P. aethiopicus* is able to live where mean annual rainfall is more variable. Although both species are allopatric over vast regions, they are sympatric in central east Ethiopia, north Somalia, central Kenya, north coast of Kenya, and southeast Kenya. Both suids remain locally common, their populations are, however, in decline due to the negative impacts on the environment by the rapidly growing human populations in all five countries.

The role of bushpigs (*Potamochoerus larvatus*) as seed dispersers in indigenous forests in the Soutpansberg Mountain range, South Africa
Hikel, K. B., Peters, M.K. and J Linden 2023
Animal Biology, 74(1)
Seed dispersal influences the survival and distribution of plant species and is an important mechanism for maintaining floristic diversity. Bushpigs (*Potamochoerus larvatus*) are large mammals of indigenous forests and well-wooded areas of eastern and southern Africa and may play an important role as seed dispersers. However, the diversity of fruits consumed and the effect of digestion on seeds remains poorly understood. This study was conducted from October 2018 to January 2019 and gives first insights into seed dispersal by bushpigs in the Soutpansberg Mountain range, South Africa. Here, we collected bushpig faeces and assessed the number of seeds and seed species found. Furthermore, germination experiments with digested and nondigested seeds and fruits were conducted. Our results show that bushpigs are omnivorous, consuming fruits and seeds of 126 different plant species. The proportion of seeds per plant species found in faeces was unhomogeneously distributed with a few hyperabundant species, in particular *Searsia chirindensis* (55%). The germination experiments showed that gut passage did, overall, not influence germination or seedling growth rates. However, seeds remaining within fruits showed reduced growth, pointing to a high importance of fruit consumption for seed fate. Our

results suggest that bushpigs are major seed dispersers of a large variety of fruiting plant species in wooded areas of Africa.

Intra-tooth stable isotope analysis reveals seasonal dietary variability and niche partitioning among bushpigs/red river hogs and warthogs

Yang, D., Uno, K.T., Cerling, T.E., Mwebi, O., Leakey, L.N., Grine, F. E. and A. Souron 2024
Current Zoology

How animals respond to seasonal resource availability has profound implications for their dietary flexibility and realized ecological niches. We sought to understand seasonal dietary niche partitioning in extant African suids using intra-tooth stable isotope analysis of enamel. We collected enamel samples from canines of red river hogs/bushpigs (*Potamochoerus* spp.) and third molars of warthogs (*Phacochoerus* spp.) in three different regions of central and eastern Africa. We analyzed multiple samples from each tooth and used variations in stable carbon and oxygen isotope ratios (δ13C and δ18O) and covariances between them to infer seasonal dietary changes. We found that most *Phacochoerus* display C4-dominated diets, while most *Potamochoerus* display C3-dominated diets. *Phacochoerus* and *Potamochoerus* that co-occur in the same region display no overlap in intra-tooth δ13C, which suggests dietary niche partitioning. They also show diverging δ13C values as the dry seasons progress and converging δ13C values during the peak of the rainy seasons, which suggests a greater dietary niche separation during the dry seasons when resources are scarce than during the rainy season. We found statistically significant cross-correlations between intra-tooth δ13C and δ18O in most specimens. We also observed a temporal lag between δ13C and δ18O in some specimens. This study demonstrates that intra-tooth stable isotope analysis is a promising approach to investigate seasonal dietary niche variation. However, large inter-individual variations in δ18O at certain localities can be challenging to interpret. Future studies that expand the intra-tooth stable isotope surveys or include controlled feeding experiments will improve its application in ecological studies.

African bush pigs exhibit porous species boundaries and appeared in Madagascar concurrently with human arrival

Heller, R., Balboa, R., Bertola, L and A Brüniche-Olse, and 29 more 2023
Research Square

Several African mammals exhibit a phylogeographic pattern where closely related taxa are split between West/Central and East/Southern Africa, but their evolutionary relationships and histories remain controversial. Bushpigs (*Potamochoerus larvatus*) and red river hogs (*P. porcus*) are recognised as separate species due to morphological distinctions, a perceived lack of interbreeding at contact, and putatively old divergence times, but historically, they were considered conspecific. Moreover, the presence of Malagasy bushpigs as the sole large terrestrial mammal shared with the African mainland raises intriguing questions about its origin and arrival in Madagascar. Analyses of 67 whole genomes revealed a genetic continuum between the two species, with putative signatures of historical gene flow, variable FST values, and a recent divergence time (<500,000 years). Thus, our study challenges key arguments for splitting *Potamochoerus* into two species and suggests their speciation might be incomplete. Our findings also indicate that Malagasy bushpigs diverged from southern African populations and underwent a limited bottleneck 1,000-5,000 years ago, concurrent with human arrival in Madagascar. These results shed new light on the evolutionary history of an iconic and

widespread African genus and provide insight into the longstanding biogeographic puzzle surrounding the bushpig's presence in Madagascar.

Global overview of conservation strategies applied to collary peccaries (*Pecari tajacu*). A Review

Azevedo Borges, A., Pereira Amorim, K. Y., Lima Olindo, S., and A. Fernandes Pereira
Revista Brasileira de Higiene e Sanidade Animal, 17(3):1-18

The high environmental degradation, especially of the Caatinga biome, together with the reduction of wild mammals that make up this environment, such as collared peccaries, is urgent to develop conservation strategies that can be applied to this species. Therefore, the knowledge of ecological aspects, population quantitative and strategies that have already been developed for the species may guide the next steps that will be taken. Thus, compiled information will enable the most effective direction to avoid the population decline of peccaries.

Uso de espacios naturales y antropizados por el pecarí de collar (*Dicotyles tajacu*) en la estación biológica La Selva, Costa Rica

Osorto Nuñez, M. H. and L. D. Alfaro Alvarado 2023
Revista Mexicana De Mastozoología (Nueva Época), 13(1):24–32

El objetivo de esta investigación fue analizar el uso de espacios naturales y antropizados por el pecarí de collar (*Dicotyles tajacu*) en la Estación Biológica La Selva (EBLS), Costa Rica. Se registraron grupos e individuos de pecaríes mediante observaciones directas e indirectas, contando un total 170 individuos adultos y 30 crías (media = 3.62, DS = 4.04). El uso del espacio a nivel de sitio difirió del uso esperado (p < 0.000, X2 observado = 134.14, X2 acumulado = 22.36). La prueba de bondad de ajuste de chi-cuadrado mostró una fuerte evidencia de que no existe un uso proporcional con el área de las categorías (X2 = 832.30, df = 10, n = 76, P > 0.0001). Los intervalos de confianza de Bonferroni (IC 95%) evidenciaron mayor proporción de uso observado con respecto al esperado para las categorías agroforestería abandonada y área con infraestructura. Estas áreas son manejadas por la administración de la EBLS y existen árboles frutales, huertos, construcciones y mayor intensidad de uso público, por lo que para los pecaríes representan zonas de alimentación, refugio y descanso.

Impact of Collared Peccaries *Dycotiles tajacu* (Artiodactyla: Tayassuidae) on understory vegetation in the tropical rainforest of the Nogal-La Selva Biological Corridor, Costa Rica

Osorto Nuñez, M. H., Alfaro Alvarado, L. D., Chinchilla Romero, F. and F. Guimarães Rodrigues 2024
Revista de Biología Tropical, 72(1):1-15

Introduction: Evidence suggests that herbivores, such as peccaries, shape vegetation structure and diversity through predation, trampling, dispersal, and rooting behavior. Objective: To evaluate the impact of peccaries (*Dicotyles tajacu*) on the understory vegetation of the tropical rainforest in the Nogal-La Selva Local Biological Corridor, Costa Rica, comparing a site with the absence of peccaries to another with the presence of these animals. Methodology: From June to November 2021, 20 experimental exclusions and 20 free access plots, each measuring 2 m^2 were used to quantify herbivory, the number of leaf blades, damaged leaves, healthy leaves, sapling height, and fallen biomass at both sites. Results: A higher sapling density was found in the Nogal Reserve, but a lower sapling diversity, while in La Selva there was a higher sapling diversity, but a

lower density of seedlings. Herbivory and sapling height in La Selva exceeded those in Nogal. The exclusion of peccaries reduced seedling damage but did not affect the dynamics of fallen biomass. Conclusion: For the design, implementation, and evaluation of the effectiveness of biological corridors, it is crucial to consider plant-animal interactions to enhance the flow of ecological processes through functional and structural connectivity, analyzed from interactions such as those presented in this paper.

The influence of climate and the presence of predators on the daily activity pattern of collared peccaries (*Dicotyles tajacu*, Cetartiodactyla)

Bohrer dos Santos, D., Barbosa Viana Junior, A., Teixeira Duarte, G., Silvério Pires, M. R. and C. Schetini de Azevedo 2024
Austral Ecology, 49(1):1-20

Collared peccaries (*Dicotyles tajacu*, Cetartiodactyla) adjust their daily activity patterns in response to different factors, such as the presence of predators or cli-matic factors (temperature and rainfall), as a way of ensuring survival. The knowledge of these patterns allows us to understand the interspecific interactions of the community. This study measured daily activity of the collared peccary, and evaluated how different climatic conditions, and the presence of predators influenced their activity patterns. Data were obtained from eight camera traps over 13 months in the Municipality of Ouro Preto, Brazil. The daily activity periods of collared peccaries and their predators were evaluated and the animals classified as diurnal, nocturnal, crepuscular, or cathemeral. Camera-trap records were used to assess whether temperature and rainfall affected daily activity patterns in peccaries. We found that neither rainfall nor temperature influence the activity pattern. Peccary activity overlapped with the activity of local predators. A low level of overlap was recorded with the activity of *Puma concolor* and high level of overlap with the activity of *Leopardus pardalis*, *Canis lupus familiaris*, and human activity. The low activity overlap of collared peccaries with *P. concolor* may be related to an attempt to decrease predation risk, while the high activity overlaps with domestic dogs and humans may be related to the low hunting pressure exerted in the region and also to the foraging opportunities for peccaries in areas closer to human settlements, where orchards are present. The high activity overlap with *L. pardalis* can be related to the smaller size of this predator and the aggressive group anti-predator behaviour of the collared peccary. Our results show that collared peccaries can adjust their daily activity when an apex predator is present, but this adjustment is not generalized to all predators.

Contribution to the knowledge on the diet of the collared peccary (*Dicotyles tajacu*) at the La Selva Biological Station, Costa Rica

Osorto Nuñez, M. H., Alfaro Alvarado, L. D., Chinchilla Romero, F. A. and F.H. Guimarães Rodrigues 2023
Therya Notes, 4(2):120-126

The diet of the collared peccary (*Dicotyles tajacu*) in the Neotropics is poorly known, although palm fruits are frequently reported. This study aimed to evaluate the diet of collared peccary groups at La Selva Biological Station (LSBS), Costa Rica. Between July and December 2021, 30 km of LSBS trails were traveled each month. A list of plant species consumed by peccaries was elaborated from direct visual observations. Samples of plant or fruit species collected in the field were identified at the family, genus, or species level. The diet of the collared

peccary inhabiting the LSBS consisted of 38 species belonging to 18 families. The most consumed species belong to the family Arecaceae. Socratea exorrhiza, Ficus colubrinae, Dussia macroprophyllata, Sacoglottis trichogyna, Iriartea deltoidea, and Dipteryx panamensis were the predominant species in the peccary diet. The most important plant component was fruits. The dispersal mode of most species consumed was Endo-stricto. For 53 % of plant species consumed by peccaries have no information on their IUCN conservation status. Given the diverse diet of the collared peccary, conservation actions should consider the protection of primary forests as food sources, in addition to restoration projects of tropical ecosystems to promote tree species that provide fruits attractive to peccaries.

Ranging ecology and resource selection of white-lipped peccaries (*Tayassu pecari*) in the world's largest tropical agricultural frontier

Costa, H. C. M., Storck-Tonon, D., dos Santos-Filho, M., da Silva, D. J., Campos-Silva, J. V. and C. A. Peres 2023
Ecology and Evolution, 13(1):1-13

Agricultural commodity production is one the main drivers of deforestation in Legal Brazilian Amazonia resulting in a deforested and/or fragmented landscape formed by forest remnants of different sizes and shape embedded within the agricultural matrix. As an ecosystem engineer and a crucial seed predator, white-lipped peccaries (*Tayassu pecari*) play a pivotal role in forest structure, biodiversity, and nutrient cycling. However, they are highly sensitive to habitat fragmentation and hunting pressure. White-lipped peccaries are, therefore, a wide-ranging “landscape species,” the spatial and ecological requirements of which can be used to guide conservation planning in human-modified landscapes. Using data from GPS-tracked individuals in large-scale mechanized agriculture landscapes in the state of Mato Grosso, Brazil's largest soybean and maize producer, we investigated the home range size and resource selection during both the crop and non-crop season. We observed a seasonal variation in home range size and an increased selection for croplands during the crop season. White-lipped peccaries favored native vegetation patches and also exhibited avoidance of locations distant from perennial water bodies and distant cropland locations far from forest remnants. This study can contribute to inform effective conservation strategies and land management practices aimed at preserving suitable habitats and promoting wildlife coexistence with working agricultural landscapes.

Cacería de tayassuidae en la cuenca de río Indio, Reserva Biológica Indio Maíz, Nicaragua

Mc.crea Daniels, P. D. and L. D. Wallace Morales 2024
Wani, 80(1):1-15

Wildlife hunting is an important activity for self-consumption and local commerce in certain communities; however, when it becomes selective, it has a negative impact on its continuity. The objective of the study was to characterize tayasuid hunting in the areas of the Río Indio basin, through a survey format applied to hunters (nine) with more than 10 years of experience and a semi-structured interview format directed at local authorities. (four). 100% of hunters have only found and captured the species *T. pecari* (Link, 1795), 89% of hunters claim to have captured specimens in forested areas, 78% near rivers,and 11% claim to have captured of agricultural activity, however, 50% of the rangers consulted and 100% of MARENA territorial indicated that *T. tajacu* can also be found (Linnaeus, 1758). The results indicate that there is no coincidence among those consulted regarding the most used hunting instrument; The hunters affirm that they prefer and use the spear, bow and arrow more (ancestral hunting), contrary to the local authorities: the most used are firearms (shotgun and 22 caliber weapon). Due to the selection and exclusive hunting pressure of *T. pecari* and poor environmental education on tayasuids, its hunting in the areas of the Indio River, Indio Maíz biological reserve, could have a high and negative impact, which is why preservation programs should be developed and alternatives for the use of this species is pressing.

Agroindustrial landscapes and white-lipped peccary habitat use in the Cerrado of Brazil

Painkow Neto, E., Barquero, G., Cullen Jr, L. and J. M. Vieira Fragoso 2024
Journal for Nature Conservation, 77(1): 1-10
The conversion of natural areas into agricultural land has increased human-wildlife interactions, often resulting in crop damage. This study focuses on the white-lipped peccary (*Tayassu pecari*), which thrives in landscapes where well-preserved, naturally-vegetated public and private lands are juxtaposed with agricultural fields. We investigated the habitat use and selection of four herds of white-lipped peccaries in a landscape mosaic along the southern border of Emas National Park in the Cerrado biome of Brazil. Our findings reveal that white-lipped peccaries prefer both corn plantations and gallery forests as habitats. Through high-frequency GPS telemetry, we observed a strong tendency to turn when herds were in agricultural areas and gallery forests, indicating feeding behavior. On the other hand, they typically move in straight lines for long distances when traversing bare soil fields and native Cerrado vegetation, suggesting they are merely passing through these habitats. The extensive feeding on corn crops in agricultural fields has resulted in significant financial losses for producers, leading to a conflict between white-lipped peccaries and landowners. Understanding the movement dynamics of the species and their intensive use of both private and public lands can aid in the development of management strategies that minimize or eliminate crop losses while ensuring the survival of this vulnerable species in landscapes comprising agricultural fields and native habitats.

New records of White-lipped Peccaries in altered landscapes of the Brazilian Midwest

Freitas Oliveira, R., Guimarães Silva, M.A., Andreani, T.L., Hannibal, W., Bastos, R. P., Moreira, J. C. and A. Ribeiro Morais 2023
Mammal Research, 69(1):177-182
The White-lipped Peccary (WLP) is a large-sized mammal that lives in groups and needs large, preserved areas to survive. Over the last decades, the distribution area of the WLP has been reduced, being absent from areas where its occurrence is expected, such as the central region of southwestern Goiás, Brazilian Midwest. Therefore, here we presented eight new records of WLP in southwestern of Goiás state, with information on group size and landscape context. WLPs were recorded by camera trap, and we extracted the percentage of native cover (NC%), mean of Euclidean nearest-neighbor distance (MENND), and largest native patch area (LP (hectares)) in the landscape occupied by them. The WLP group size ranged from 1 to 52 individuals in anthropized landscapes (4.6 to 30.7 of NC%), with a MENND range of 89.4 to 165 m and LP ranged from 48.8 to 297.9. These findings could be an indication that the species is returning to use the region. However, we stress that this area may not support viable WLP populations in the long-term due to the level of anthropization of the studied landscape.

New scientific articles

Are hippos Africa's most influential megaherbivore? A review of ecosystem engineering by the semi-aquatic common hippopotamus

Voysey, M.D., de Bruyn, P.J.N. and A. B. Davies 2023
Biol Rev Camb Philos Soc, 98(5):1509-1529

Megaherbivores perform vital ecosystem engineering roles, and have their last remaining stronghold in Africa. Of Africa's remaining megaherbivores, the common hippopotamus (*Hippopotamus amphibius*) has received the least scientific and conservation attention, despite how influential their ecosystem engineering activities appear to be. Given the potentially crucial ecosystem engineering influence of hippos, as well as mounting conservation concerns threatening their long-term persistence, a review of the evidence for hippos being ecosystem engineers, and the effects of their engineering, is both timely and necessary. In this review, we assess, (i) aspects of hippo biology that underlie their unique ecosystem engineering potential; (ii) evaluate hippo ecological impacts in terrestrial and aquatic environments; (iii) compare the ecosystem engineering influence of hippos to other extant African megaherbivores; (iv) evaluate factors most critical to hippo conservation and ecosystem engineering; and (v) highlight future research directions and challenges that may yield new insights into the ecological role of hippos, and of megaherbivores more broadly. We find that a variety of key life-history traits determine the hippo's unique influence, including their semi-aquatic lifestyle, large body size, specialised gut anatomy, muzzle structure, small and partially webbed feet, and highly gregarious nature. On land, hippos create grazing lawns that contain distinct plant communities and alter fire spatial extent, which shapes woody plant demographics and might assist in maintaining fire-sensitive riverine vegetation. In water, hippos deposit nutrient-rich dung, stimulating aquatic food chains and altering water chemistry and quality, impacting a host of different organisms. Hippo trampling and wallowing alters geomorphological processes, widening riverbanks, creating new river channels, and forming gullies along well-utilised hippo paths. Taken together, we propose that these myriad impacts combine to make hippos Africa's most influential megaherbivore, specifically because of the high diversity and intensity of their ecological impacts compared with other megaherbivores, and because of their unique capacity to transfer nutrients across ecosystem boundaries, enriching both terrestrial and aquatic ecosystems. Nonetheless, water pollution and extraction for agriculture and industry, erratic rainfall patterns and human–hippo conflict, threaten hippo ecosystem engineering and persistence. Therefore, we encourage greater consideration of the unique role of hippos as ecosystem engineers when considering the functional importance of megafauna in African ecosystems, and increased attention to declining hippo habitat and populations, which if unchecked could change the way in which many African ecosystems function.

Reproductive Characteristics of a Hippopotamus Population along the Runde River, Gonarezhou National Park, Zimbabwe

Peek, R. and T O'Connor
African Journal of Wildlife Research, 53(1)

The hippopotamus population along the Runde River in Gonarezhou National Park, Zimbabwe, attained a density in the late 1970s which threatened vegetation resources of this semi-arid park. A sample of 105 hippopotami taken in 1978 was used to determine the population's age and sex structure, and reproductive characteristics. An average school consisted of 11.4 individuals, comprising 2.2 adult bulls, 4.6 adult cows, 2.2 and 1.4 immature males and females, respectively,

and 0.8 calves. Females constituted 54% of the population, and 58% of foetuses; neither differed from parity. Testes mass and seminiferous tubule diameter increased with age according to a logistic function. Puberty commenced at about 4 years, and sexual maturity at 8–8.3 years, respectively at 47% (655 kg) and 65% (1070 kg) of mean adult male mass. Males were physically mature by 17.5 years. Based on the development of ovary mass, uterus mass, and uterine horn length of non-pregnant or pregnant females, the pubertal interval was 24 months commencing at 7 years when body mass reached 71% of mean adult female mass (964 kg), and sexual maturity commenced when body mass reached 78% of mean adult female mass (1050 kg). Females attained physical maturity at 13 years. Conceptions occurred in seven of eight sampled months, with most occurring in June and peak parturition estimated to occur in February. The pregnancy rate of sexually mature females was 36.8%, the incidence of pregnancy was 0.56 calves/female/year, anoestrus was 13.7 months, post-partum oestrus was 5.7 months, and the calving interval was 21.7 months. Calf mortality (<2 years) was 42%. Female births per female of reproductive age was 0.092. Reproductive characteristics of hippopotamus across Africa illustrate their plasticity in relation to climatic variation and population density, suggesting populations may be regulated without any need for management intervention.

Chewing, dentition and tooth wear in Hippopotamidae (*Hippopotamus amphibius* and *Choeropsis liberiensis*)

Avedik, A. and M. Clauss 2023
PLOS One, 18(10)

Among mammals, hippopotamids (‘hippos’) have been described as the species with the lowest chewing efficacy despite elaborate enamel folds on the occlusal surface or their cheek teeth, which was hypothesized to result from the lack of a grinding chewing motion. We investigated the chewing and dentition of the two extant hippo species, the common hippo (*Hippopotamus amphibius*) and the pygmy hippo (*Choeropsis liberiensis*), making (video) observations of live animals and gathering data on museum specimens (n = 86 H. amphibius and 26 *C. liberiensis* skulls). Hippos have a low degree of anisodonty (differences in width between maxillary and mandibular cheek teeth) and anisognathy (difference in width between the upper and the lower jaw), corresponding to a mainly orthal (up-and-down) chewing motion. The two hippo species differ slightly, but distinctively, in their anterior dental morphology and chewing mode. In both species, the canines do not completely prevent a lateral jaw movement but would, in theory, permit this movement until the mandibular canines get into contact with the maxillary protruding snout. This movement is only realized, to a small extent, in pygmy hippos, leaving distinct wear traces on their incisors and creating relatively wider wear facets on the maxillary canines. In common hippos, the interlocking upper and lower incisors prevent lateral jaw movement. Corresponding contact wear facets are evident on the medial aspect of the upper, and on the lateral aspect of the lower incisors–unless museal reconstructions mispositioned these teeth. If these facets are interpreted as an indication for a relic of a lateral jaw movement that was probably more prominent in hippo ancestors, i.e. if we assume that hippos evolved orthal chewing secondarily, several other characteristics of hippos can be explained, such as a low degree of hypsodonty (in the absence of distinct attrition due to a grinding chewing movement), a secondary loss of complexity in their enamel schmelzmuster, a secondary evolution of a wide mouth gape, a reduction in anisodonty compared to their ancestors, and the evolution of a bilaterally symmetrical (‘trifoliate’) enamel folding pattern on the molar occlusal surface from an ancestral

bunoselenodont condition. As an underlying driving force, selection for intraspecific combat with canines and incisors, necessitating a wide gape and a rigid jaw, has been suggested.

Forest loss during 2000–2019 in pygmy hippopotamus (*Choeropsis liberiensis*) habitats was driven by shifting agriculture

Erazo-Mera, E., Younes, N., Horwood, P.F., Paris, D., Paris, M. and N. Murray 2024

Environmental Conservation, 51(1): 55 - 63

The Upper Guinea Forest (UGF; West Africa), a global biodiversity hotspot, has lost more than 90% of its original area since 1900, threatening endemic species such as the endangered pygmy hippopotamus (*Choeropsis liberiensis*). However, little is known about the proximate causes of this deforestation. We classified Sentinel-2 data using the random forest algorithm to differentiate between three main human processes (shifting agriculture, intensive agriculture or urban expansion) driving deforestation between 2000 and 2019 across the pygmy hippopotamus distribution area. Out of c. 89 600 km^2 in the year 2000, 15 900 km^2 (17%) of forest were lost, primarily to shifting agriculture (14 900 km^2). Côte d'Ivoire and Liberia accounted for 14 900 km^2 (94%) of the net area of forest lost, c. 15 times greater than deforestation in Sierra Leone and Guinea combined (953 km2). Forest loss inside protected areas is pervasive, and it is essential to prioritize conservation efforts in areas where deforestation is still low (e.g., Taï, Sapo and Gola Rainforest national parks). We suggest that the preservation of the UGF will face challenges associated with people's demand for food and income. Continued landscape-scale planning and action to reduce deforestation are urgently needed to limit the impact of shifting agriculture on pygmy hippopotamus habitat.

Human-hippo conflicts around Lake Tana Biosphere Reserve, Ethiopia: Vulnerability of hippopotamus in human-dominated landscape

Kifle, Z., Assefa, W.W. and A. Moges 2023

PLOS ONE, 18(10)

Currently, the demand of the human population for more land, water, and other natural resources from wildlife habitats is increasing all over the world. Such intense human pressure results in conflict with wildlife and the impacts affect both parties negatively. The human-hippo conflict poses a serious problem for both local farmers' livelihoods and hippo conservation. To date, the extent of human-hippo conflict is poorly documented in Ethiopia. Specifically, the extent of human-hippo conflicts around Lake Tana Biosphere Reserve (LTBR) is unknown. Therefore, this study aimed to investigate the extent of human–hippo conflict, and possible mitigation measures proposed by the local people around LTBR, Ethiopia. We conducted a questionnaire interview with the household head, the household head's wife, or other adults ≥ 18 years old. All respondents reported that crop damage was the main cause of human–hippo conflict around LTBR. Livestock grazing competition (17.4%) and human attack (19.5%) were also sources of conflicts in the region. Respondents claimed that hippos destroyed crops including maize *(Zea mays*), teff (*Eragrostis teff*), finger millet (*Eleusine coracana*), and rice (*Oryza sativa*). Most (91.2%) respondents claimed that the severity of crop damage caused by hippos was high in the region. Most respondents (range 90 to 93%) complained about high crop damage suggesting that hippos be eliminated from the region. Local people estimated that the population sizes of hippos comprise an average of 243 individuals; however, we counted 122 hippos during our boat survey in the area. The result of this study showed that human-hippo conflicts cause negative effects on both farmers' livelihood and hippo conservation in the region. To mitigate human-hippo conflict, we suggest that proper land use zonation systems around key areas, broad awareness creation among local people, and alternative crop production should be promoted around the LTBR.

Status of Hippopotamus, *Hippopotamus amphibius* L., in the River Sanaga of the Centre Region of Cameroon

Shidiki, A.A., Rosalie, T.M. and D. A. Ulrich 2023
Sustainable wildlife Management

Wildlife protection and management structures around the world have used protective enclaves often referred to as protected areas to limit pressure on biodiversity. No attention has been paid to species living in unprotected areas often known as free areas. The aim of this study is to contribute to the sustainable management of hippopotamus population in the river Sanaga that is facing threats of being extinct and to also provide information on their status to decision makers. The survey method used during this study was a total count that was carried out using several techniques including foot walk and waterway counts. The results revealed that four hippos were cited in two out of the seven villages in the area. A distance of 32 km was covered in the river. The site with the highest number of hippopotamus was in the village of Tsang with three hippos seen. The main threats to the survival of hippos are poaching, fishing, sand mining and crop farming along the river bank. To lessen these threats on the hippopotamus population, sensitization and awareness campaigns are needed. It is recommended that a hippo sanctuary and a hippo friendly club be created in the study area.

Activity and nocturnal home range size of male common hippopotamus in Kruger National Park, South Africa

Fritsch, C.J.A, Streicher, J.P. and C. T. Downs 2023
African Journal of Ecology, 61(4)

The common hippopotamus (*Hippopotamus amphibius*) is a driver of ecological processes in African savannah aquatic and terrestrial ecosystems. Recent studies have highlighted the ecological impacts of hippos in these systems; however, these lack behavioural data to contextualise their ecological inputs. We fitted global positioning system (GPS) transmitter bracelets on male hippos (n = 3) in Kruger National Park, South Africa. The mean home range size for hippos using Adaptive Local Convex Hull (a-LoCoH) home range (~6 km^2) was smaller than previously documented. This study contributes baseline behavioural data for managing hippos in Kruger National Park and southern Africa.

Responses of *Hippopotamus amphibius* to environmental changes at Bui National Park, Ghana

Bempah, G., Wiafe, E.D., Nartey, M.A., Messenger, K and C. Lu 2023
Acta Ecologíca Sinica, 43(3): 469-479

Many researchers have adopted the use of indicator species to detect changes in the environment and predict future ecological modifications. Irrespective of the popularity of indicator species concept among scientists in recent times, there is less studies on the use of mega semi-aquatic mammals as indicator species, especially in Africa. This study determined the ecological role of *Hippopotamus amphibius* and how the mammal respond to environmental changes in an aquatic ecosystem, focusing on changes in biological diversity (fish and phytoplankton) and environmental factors (temperature, pH, dissolved oxygen, conductivity, total dissolved solids, hydrogen isotope, and oxygen isotope) by comparing pools harboring *H. amphibius* and pools without *H. amphibius* at the Bui National Park, Ghana. The results show that *H. amphibius* play an important ecological role by indicating high productivity in aquatic ecosystem and serving as influencers of the aquatic food web at Bui National Park. The results found significantly higher concentrations of dissolved oxygen in H. amphibius pools than pools without H. amphibius. Significantly higher diversity of fish and phytoplankton species were recorded in pools with *H. amphibius*. Common fish species identified during this study include, *Oreohromis niloticus*, *Labeo coubie*, *Alestes dentex* and *Labeo senegalensis*. Phytoplankton communities were dominated by Chlorophyceae (37.26%), Cyanophyceae (25.21%), and Bacillariophyceae (21.53%). The study results also showed that H. amphibius are sensitive to changes in depth of water, preferring areas with shallow pools. Managerial options for *H. amphibius* populations require strong support because of their socio-ecological benefits including potential ecosystem effects, increasing fishing and tourism value at the Bui National Park.

Drivers of land use changes and impacts on human-hippos (*Hippopotamus amphibius*) interactions in villages adjacent to Lake Babati, Tanzania

Mmbaga, N.E. 2023
Discover Environment, 1(8)

Hippopotamus (*Hippopotamus amphibius*) are victims of land use changes (LUC) due to their semi-aquatic nature. Although human–hippopotamus interactions (HHI) are known to exist in the area surrounding Lake Babati, nothing is known about the LUC in relation to the interactions. The study aimed at assessing the trend of LUC in the last 20 years in relation to time of establishing new settlement and farming seasons in relation to HHI, respondents’ perceptions of HHI, and mitigation measures used by local people against Hippos adjacent Lake Babati. Remote sensing and GIS techniques, questionnaires and focused group discussions were used to assess human perceptions regarding trends of the LUC in the study area. LUC was monitored by using landsat images from the years 1999 and 2019. The findings indicate an increase in settlement while water, agroforestry, and seasonal agricultural lands were decreasing. The time respondents stayed in the village, farm size, and respondents’ perception of HHI trends were observed to vary with the distance from the lake. The presence of LUC on adjacent Lake Babati jeopardized the ecological integrity of Hippos’ habitat and increased tension and overlap between hippos’ and human needs. The findings provide a baseline for managing HHI and recommend proper land use planning that prioritizes the use of alternative crops like fruit trees especially within 3 km from the lake. Human population and settlement expansion patterns should also be monitored in areas closer to the lake for sustaining wildlife conservation and livelihood development in Lake Babati and surrounding areas.

Diseases

Wild boar (*Sus scrofa*) as a potential reservoir of infectious agents in Portugal: a review of two decades (2001–2021)

Jota Baptista, C., Seixas, F., Gonzalo-Orden, J.M. and P. A. Oliveira 2023
European Journal of Wildlife Research, 69(1):1-8

The wild boar (*Sus scrofa*) is a mammal with a broad distribution in the Eurasian territory and a potential reservoir for several zoonotic pathogens. Besides being part of the Mediterranean ecosystem and perpetuating these agents in the environment, this species is usually consumed in the Iberian Peninsula, representing a potential public health threat. Due to its extensive expansion and colonization of new geographical areas, which leads to increasing contact with humans, domestic animals, and wildlife, infectious disease assessments are crucial. During the last two decades (2001–2021), several researchers have studied wild boars to identify, understand, and predict potential health risks and disease outbreaks in animals and humans. North-eastern, central-eastern (mainly because of tuberculosis), and southern Portugal were the regions where most pathogens have been identified. Some agents with zoonotic importance (but with few reported data) should be the focus of future surveillance studies, such as Leptospira spp., Brucella spp., or Trichinella spp. This review aims to summarize the available information on pathogens (bacteria, viruses, and parasites) reported in wild boars, in Portugal, in the last two decades, with a particular focus on agents with zoonotic potential.

Molecular Detection and Epidemiology of Potentially Zoonotic *Cryptosporidium* spp. and *Giardia duodenalis* in Wild Boar (*Sus scrofa*) from Eastern Spain

Martí Marco, A., Moratal, S., Torres Blas, I., Cardells, J., Lizana, V. and M. A. Dea Ayuela 2023
Animals, 13(1):1-16

The protozoans *Giardia duodenalis* and *Cryptosporidium* spp. are common causes of gastrointestinal disease in humans and animals. While both are commonly documented in domestic animals, few studies have analysed their presence in wildlife. To assess the prevalence of both parasites in wild boar (*Sus scrofa*) in the Valencian Community (eastern Spain), 498 wild boar faecal samples were collected from 2018 to 2022. *Cryptosporidium* spp. was detected by performing a nested PCR targeting a 578 bp sequence of the small subunit ribosomal RNA gene (SSU rRNA), followed by sequencing and phylogenetic analysis. For *G. duodenalis*, a qPCR amplifying a fragment of 62 bp from the SSU rRNA was employed. Positive samples were genotyped for glutamate dehydrogenase and B-giardin genes. Different epidemiological factors were considered potential modulating variables in the transmission of both parasites. *G. duodenalis* prevalence was 1.20%, while *Cryptosporidium* spp. Prevalence reached 21.7%. Coinfection was observed in 0.2%. Genotyping of G. duodenalis isolates only detected genotype E. Two species of Cryptosporidium spp. were identified: *Cryptosporidium scrofarum* and *Cryptosporidium suis*. The results of this study demonstrate that the exposure to *Cryptosporidium* spp. in wild boars is high, particularly among young individuals belonging to the Typical Mediterranean climate. Moreover, the probability of infection is dependent on both the season and the density of wild boars. On the other side, exposure to *G. duodenalis* seems scarce and is influenced, in turn, by the climate. Both *Cryptosporidium* species detected in the present study have been reported in humans. Due to wild boar increasing in number and their colonisation of urban and peri-urban areas, this could represent an inherent health risk for the human population.

Trichinella Infection in Culled Wild Boar (*Sus scrofa*) from El Palmar National Park, Argentina, and Exposure Risk in Humans and Dogs Consuming Wild Boar Meat

Tammone Santos, A., Riva, E., Condorí, W. E., Fernández, V., Rodriguez, M. G., Rivero, M. A., Faraco, M., Aguirre, P., Loyza, L., Caselli, A. E., Uhart, M. M. and S. M. Estein 2024
Journal of wildlife diseases

Trichinellosis is a foodborne disease caused by ingestion of raw or undercooked meat containing *Trichinella* spp.larvae. Consumption of wild boar (*Sus scrofa*) meat represents an important source of human trichinellosis worldwide. In El Palmar National Park (EPNP), Argentina, invasive alien wild boars are controlled and meat from culled animals is released for public consumption following on-site artificial digestion (AD) testing. Meat trimmings and offal from the control program are often used as food for dogs (*Canis familiaris*). We evaluated infection and exposure to *Trichinella* spp. in wild boars from EPNP, as well as exposure to Trichinella spp. and associated risk factors in dogs and human consumers of wild boar meat. *Trichinella* spp. larvae were detected in muscle samples from 5/49 wild boars by AD (10.2%; 95% confidence interval [CI], 3.8%–23%), with a mean burden of 0.24 larvae per gram (lpg; range, 0.06–0.95 lpg). Anti-Trichinella antibodies were not detected in wild boar serum samples (n=42). In dogs, 12/34 were seropositive to *Trichinella* spp. (35.29%; 95%, CI, 20.3%–53.5%). Immunoglobulin (Ig) G antibodies were not detected in human serum samples (n=63). Our results reveal the presence, albeit at low prevalence, of *Trichinella* spp. in wild boars and exposure in dogs fed game offal. These findings suggest that the low prevalence and parasitic load in wild boars, together with the best practices applied by EPNP culling program personnel, contribute to keeping the risk of infection in people low. The dog results highlight that the parasite is circulating in the area, and therefore the risk of infection is not negligible. We recommend the implementation of an animal surveillance strategy in order to monitor the evolution of this zoonosis in the study area.

Seroepidemiological and biomolecular survey on *Toxoplasma gondii* in Sardinian wild boar (*Sus scrofa*)

Sini, M. F., Manconi, M., Varcasia, A., Massei, G., Sandu, R., Mehmood, N., Ahmed, F., Carta, C., Cantacessi, C., Scarano, C., Scala, A. and C. Tamponi 2024
Food and Waterborne Parasitology, 34(1):1-6

Toxoplasma gondii is a zoonotic parasite able of infecting all warm-blooded animals. Toxoplasmosis is one of the major foodborne diseases globally. The consumption of wild boar (*Sus scrofa*) meat from recreational hunting has been linked to outbreaks of human toxoplasmosis. The island of Sardinia (Italy) contains a large wild boar population, thus providing an opportunity to assess the distribution of Toxoplasma in this species and the associated risks of transmission to humans. A total of 562 wild boars were screened: heart and meat juice samples were tested for *T. gondii* DNA via nested-PCR and IgG anti-Toxoplasma by commercial ELISA. Anti-Toxoplasma IgG were detected in 24.6% (138/562) of animals, while 37.2% (209/562) of the heart samples were PCR positive. The prevalence of *T. gondii* antibodies and DNA highlights the potential role of wild boar as an important reservoir for this parasite. The study suggests that wild boar could play a significant role in spreading the parasite to humans. As wild boar numbers are increasing throughout their range, their potential role in transmitting toxoplasmosis should be communicated to stakeholders, and the impact of different population control methods on disease transmission should be thoroughly assessed to mitigate potential threats effectively.

Genomic regions associated with pseudorabies virus infection status in naturally infected feral swine (*Sus scrofa*)

Bowden, C. F., Kiser, J. N., Miller, R. S., Buckley, A. C., Boggiatto, P. M., Giglio, R. M., Brown, V. R., Dorian, G., Neibergs, H. L., Piaggio, A. J., Speidel S. E. and J. T. Smyser 2023
Frontiers in Genetics, 14(1):1-12

Pseudorabies virus (PRV)—the causative agent of Aujeszky's disease—was eliminated from commercial pig production herds in the United States (US) in 2004; however, PRV remains endemic among invasive feral swine (*Sus scrofa*). The circulation of PRV among abundant, widespread feral swine populations poses a sustained risk for disease spillover to production herds. Risk–based surveillance has been successfully implemented for PRV in feral swine populations in the US. However, understanding the role of host genetics in infection status may offer new insights into the epidemiology and disease dynamics of PRV that can be applied to management strategies. Genetic mechanisms underlying host susceptibility to PRV are relatively unknown; therefore, we sought to identify genomic regions associated with PRV infection status among naturally infected feral swine using genome–wide association studies (GWAS) and gene set enrichment analysis of single nucleotide polymorphism data (GSEA–SNP). Paired serological and genotypic data were collected from 6,081 feral swine distributed across the invaded range within the contiguous US. Three complementary study populations were developed for GWAS: 1) comprehensive population consisting of feral swine throughout the invaded range within the contiguous US; 2) population of feral swine under high, but temporally variable PRV infection pressure; and 3) population of feral swine under temporally stable, high PRV infection pressure. We identified one intronic SNP associated with PRV infection status within candidate gene AKAP6 on autosome 7. Various gene sets linked to metabolic pathways were enriched in the GSEA–SNP. Ultimately, improving disease surveillance efforts in feral swine will be critical to further understanding of the role host genetics play in PRV infection status, helping secure the health of commercial pork production.

Pig virus imperils food security in Borneo
Meijaard, E., Erman, A., Ancrenaz, M. and B. Goossens 2024
SCIENCE, 383(6680): 267
African swine fever has devastated pig populations in Asia since 2018. On the island of Borneo, which includes the country of Brunei, the Malaysian states of Sarawak and Sabah, and Indonesian Kalimantan, bearded pigs (*Sus barbatus*) were once the most numerous large mammal species, but African swine fever has led to population declines of 90 to 100%. The substantial drop may warrant a conservation status uplisting from Vulnerable to Critically Endangered.. The loss of pigs disrupts food security and ecosystems and threatens other endangered wildlife. In the past, bearded pigs constituted 81% of hunted wildlife weight in villages in East Kalimantan.. The state of Sarawak alone once harvested a million bearded pigs per year, and Sabah's annual hunted pig weight was estimated at 8.6 million kg. Although the Muslim population of Borneo does not eat pork, the pig population collapse affects the livelihoods and cultural traditions of millions of non-Muslim people. The decline of Borneo's pig population also poses unknown ecological effects. Wild pigs are important seed predators that play a substantial role as ecosystem engineers. In addition, in the absence of pigs, local people are likely to shift their focus to hunting endangered species, such as pig-tailed macaques (*Macaca nemestrina*). Although African swine fever has garnered substantial attention in countries with major pork industries, its effects in Borneo have been largely overlooked. Resistance to the disease in domestic pigs in southern Africa has been identified, but the basis for resistance remains unknown, especially in wild pigs. There is no evidence indicating that wild pig populations can fully recover in Borneo or on other islands in Southeast Asia where the disease has taken a toll, including Java, Sumatra, Timor-Leste, and the Philippines. Urgent research and interventions,

with the participation of rural communities, should focus on preventing the spread of African swine fever to other regions where people depend on pigs, such as the island of New Guinea.

The mass mortality of Asia's native pigs induced by African swine fever
Luskin, M.S., Moore, J.H., Mendes, C.P., Nasardin,M.B., Onuma,M. and S.J. Davies 2023
Wildlife Letters, 1(1): 8-14
Asia's wild pigs are ecosystem engineers and a key food for predators and people. The arrival of African swine fever (ASF) in 2018 induced near-100% fatality in domestic pigs and decimated the Chinese pork industry in 2020 but outcomes for wild pigs have been delayed and unclear. Here we report on the mass mortality of native wild boar (*Sus scrofa*) in Peninsular Malaysia. ASF was confirmed at our long-term study site in February 2022 and wild boar carcasses increased >100-fold in June 2022 compared to prior years. Camera trapping revealed an 87% decline in wild boar activity in 2022 compared to five prior surveys. Wild boars retired in old birthing nests and pairs of animals died next to each other in the open. Similar results are being anecdotally reported across the region with immense repercussions suspected on ecology and conservation. We urge a rapid research response to take advantage of this unique natural experiment.

Partial pulpectomy of a tusk fracture with pulp exposure in a North Sulawesi babirusa (*Babyrousa celebensis*)
Dreyer, S., Grund, L., Klein, C., Lawrenz, A., and D. Fischer 2023
Veterinary Record Case Reports, 11(3)
A 6-year-old, male North Sulawesi babirusa (*Babyrousa celebensis*) kept at a zoological institution, suffered a tusk fracture of unknown origin, associated with pulp exposure and a relapse of the fracture after 10 months. In other tusked animals, endodontic therapy has been reported to treat acute pulp exposure and to preserve the growing tusk. Therefore, a partial pulpectomy was attempted in the babirusa, combined with systemic antibiotic and anti-inflammatory therapy. Under general anaesthesia, the partial pulpectomy was performed twice, followed by a direct pulp capping with mineral trioxide aggregate and closure of the coronal pulp opening using glass ionomer cement and composite. Partial pulpectomies have been performed in babirusas before, but using mineral trioxide aggregate as pulp capping is a novel treatment regimen. It was performed without complications, and the tusk continued to grow. Over a follow-up period of 14 months, the tusk was successfully preserved in absence of any relapse or instability.

African Swine Fever Virus Host–Pathogen Interactions
Netherton, C.L., Shimmon, G.L., Hui, J.Y.K., Connell, S. and A.L. Reis 2023
Subcell Biochem, 106:283-331
African swine fever virus is a complex double-stranded DNA virus that exhibits tropism for cells of the mononuclear phagocytic system. Virus replication is a multi-step process that involves the nucleus of the host cell as well the formation of large perinuclear sites where progeny virions are assembled prior to transport to, and budding through, the plasma membrane. Like many viruses, African swine fever virus reorganises the cellular architecture to facilitate its replication and has evolved multiple mechanisms to avoid the potential deleterious effects of host cell stress response pathways. However, how viral proteins and virus-induced structures trigger cellular stress pathways and manipulate the subsequent responses is still relatively poorly understood.

African swine fever virus alters nuclear substructures, modulates autophagy, apoptosis and the endoplasmic reticulum stress response pathways. The viral genome encodes for at least 150 genes, of which approximately 70 are incorporated into the virion. Many of the non-structural genes have not been fully characterised and likely play a role in host range and modifying immune responses. As the field moves towards approaches that take a broader view of the effect of expression of individual African swine fever genes, we summarise how the different steps in virus replication interact with the host cell and the current state of knowledge on how it modulates the resulting stress responses.

Complete genome analysis of African swine fever virus genotypes II, IX and XV from domestic pigs in Tanzania

Hakizimana, J. N., Yona, C., Makange, M.R., Kasisi, E.A., Netherton, C.L., Nauwynck, H. and G. Misinzo 2023
Scientific Reports 13(1):5318
African swine fever (ASF) caused by ASF virus (ASFV) is an infectious transboundary animal disease notifiable to the World Organization for Animal Health causing high mortality in domestic pigs and wild boars threatening the global domestic pig industry. To date, twenty-four ASFV genotypes have been described and currently genotypes II, IX, X, XV and XVI are known to be circulating in Tanzania. Despite the endemic status of ASF in Tanzania, only one complete genome of ASFV from the country has been described. This study describes the first complete genome sequence of ASFV genotype XV. In addition, the first Tanzanian complete genome of ASFV genotype IX and three ASFV strains belonging to genotype II collected during ASF outbreaks in domestic pigs in Tanzania were determined in this study using Illumina sequencing and comparative genomics analysis. The generated ASFV complete genome sequences ranged from 171,004 to 184,521 base pairs in length with an average GC content of 38.53% and encoded 152 to 187 open reading frames. The results of this study provide insights into the genomic structure of ASFV and can be used to monitor changes within the ASFV genome and improve our understanding of ASF transmission dynamics.

Nestedness and beta diversity of gastrointestinal helminth communities in common warthogs, *Phacochoerus africanus* (Suidae), at 2 localities in South Africa

Junker, K., Horak, I.G., Boomker, J. and B. R. Krasnov 2023
Parasitology, 150 (10): 911-921
Few studies have investigated the ecological interactions between wild species of Suidae and their parasites, leaving our knowledge concerning this host–parasite system fragmented. In the present study, we applied network studies to analyse community nestedness in helminth assemblages of common warthogs, *Phacochoerus africanus* (Gmelin) (Suidae). Helminth data were compiled from 95 warthogs, including young and adult males and females, from 2 different conservation areas in Mpumalanga and Limpopo Provinces, South Africa, collected monthly over a period of 1 year each. The aim was to study the effect of host sex, age and season of sampling on the structure of helminth infracommunities harboured by the warthogs and to search for non-random structural patterns in the warthog–helminth interaction networks. Furthermore, we investigated the influence of a warthog's age, sex and season of sampling on beta diversity and dark diversity of their helminth infracommunities. Lastly, we asked whether the effects of host sex, age and sampling season on helminth communities differed between the 2 localities. We found

that helminth communities of warthogs were nested and host–parasite interactions were influenced by all 3 factors as well as combinations thereof. However, the resulting patterns differed at the 2 localities, indicating that local environmental processes are important drivers of community structure.

Preliminary Study on Gastrointestinal Helminths in Warthogs (*Phacochoerus africanus*) at the Mole National Park, Ghana

Owusu, P.J., Oduro, D., Duah-Quashie, N.O., Owusu, E.H. and G. Futagbi 2023
West African Journal of Applied Ecology
Most emerging human infectious diseases originated from wildlife. To find out if warthogs in Mole National Park harbour zoonotic parasites, a total of 39 warthog faecal droppings were sampled and examined. Zinc Sulphate Floatation technique was used in processing the samples for microscopic examination and quantification of parasite eggs. Out of the 39 warthog droppings, 95% were infected with one or more parasite species. At least seven genera of helminths were identified. Nearly 72% of the warthog droppings arboured *Strongyloides* sp and trichostrongyle-type. *Enterobius* sp. was found in 64.1% of the droppings. Other parasitic helminths identified such as *Ascaris* sp., *Taenia* sp., *Monieza* sp., and *S. haematobium* occurred in less than 50% of the animals. Z-tests showed significant variations in prevalence among the various parasites ($p<0.05$). Mostly, the level of infection ranged from moderate ($100<EPG<500$) to high ($EPG \geq 500$) loads of helminth eggs. Forty-two percent of the warthogs had three or more parasites. This study reveals some helminths that are harboured by the warthogs in the Mole National Park. The presence of zoonotic parasites such as Ascaris sp. and Taenia sp. in the warthogs is an indication of potential for transmission of zoonoses in the community.

Faecal Microbiota Characterisation of *Potamochoerus porcus* Living in a Controlled Environment

Scarafile, D. Luise, D., Motta, V., Spiezio,C., Modesto, M., Porcu, M.M., Yitzhak, Y., Correa, F., Sandri, C., Trevisi, P. and P. Mattarelli 2023
Microorganisms, 11(6):1542
Intestinal bacteria establish a specific relationship with the host animal, which causes the acquisition of gut microbiota with a unique composition classified as the enterotype. As the name suggests, the Red River Hog is a wild member of the pig family living in Africa, in particular through the West and Central African rainforest. To date, very few studies have analysed the gut microbiota of Red River Hogs (RRHs) both housed under controlled conditions and in wild habitats. This study analysed the intestinal microbiota and the distribution of Bifidobacterium species in five Red River Hog (RRH) individuals (four adults and one juvenile), hosted in two different modern zoological gardens (Parco Natura Viva, Verona, and Bioparco, Rome) with the aim of disentangling the possible effects of captive different lifestyle and host genetics. Faecal samples were collected and studied both for bifidobacterial counts and isolation by means of culture-dependent method and for total microbiota analysis through the high-quality sequences of the V3–V4 region of bacterial 16S rRNA. Results showed a host-specific bifidobacterial species distribution. Indeed, *B. boum* and *B. thermoacidophilum* were found only in Verona RRHs, whereas *B. porcinum* species were isolated only in Rome RRHs. These bifidobacterial species are also typical of pigs. Bifidobacterial counts were about 106 CFU/g in faecal samples of all the individuals, with the only exception for the juvenile subject, showing 107 CFU/g. As in human

beings, in RRHs a higher count of bifidobacteria was also found in the young subject compared with adults. Furthermore, the microbiota of RRHs showed qualitative differences. Indeed, Firmicutes was found to be the dominant phylum in Verona RRHs whereas Bacteroidetes was the most represented in Roma RRHs. At order level, Oscillospirales and Spirochaetales were the most represented in Verona RRHs compared with Rome RRHs, where Bacteroidales dominated over the other taxa. Finally, at the family level, RRHs from the two sites showed the presence of the same families, but with different levels of abundance. Our results highlight that the intestinal microbiota seems to reflect the lifestyle (i.e., the diet), whereas age and host genetics are the driving factors for the bifidobacterial population.

Intestinal parasites in *Pecari tajacu* and *Sus scrofa domesticus* in the Caatinga from Southeastern Piauí, Brazil

Sampaio, M., Sianto, L., Chame, M., Saldanha, B. and B. Brener 2023
The Journal of Parasitology, 109(4): 274-287
This study identifies gastrointestinal parasites in the feces of *Pecari tajacu* (caititu) and *Sus scrofa domesticus* (domestic pig) in southeastern Piauí, Brazil. The region covers 2 protected areas, Serra da Capivara National Park and Serra das Confusões National Park, and surrounding communities. Fecal samples from 64 animals, 42 from domestic swine and 22 from caititu, collected between 1985 and 2013, were analyzed by optical microscopy. Helminths and/or protozoa were found in 64% of the domestic pig samples and 27% of the caititu samples, totaling 18 morphospecies: Nematoda, Spirurida (2 morphospecies), Trichostrongyloidea, Eimeriidae, *Aspidodera* sp., *Bertiella* sp., *Metastrongylus* sp., *Trichostrongylus* sp., *Moniezia* sp., *Gongylonema* sp., *Trichuris suis*, *Spirocerca lupi*, *Macracanthorhyncus hirudinaceus*, *Globocephalus urosubulatus*, *Strongyloides* cf *ransomi*, *Balantioides coli*, and *Eimeria* cf *scabra*. The highest parasite diversity was obtained in the pig samples, totaling 15 morphospecies, compared to only 6 in caititus, with *S.* cf *ransomi*, *G. urosubulatus*, and *S. lupi* present in both hosts. We discuss the presence of parasites associated with domestic animals around the Protected Areas and potentially zoonotic parasites close to human communities, which raise concerns about the conservation of wildlife, human health, and livestock in the region.

Preparing Collared Peccary (*Pecari tajacu* Linnaeus, 1758) for Reintroduction into the Wild: A Screening for Parasites and Hemopathogens of a Captive Population

Gonçalves da Silveira, J. A., Magela Moreira, S., do Nascimento, A. F., de Oliveira, M. M., Andrade dos Santos, H., Tôrres de Miranda Estevam, L.G., Rodrigues Pereira, C., Guimarães Oliveira, A.G., D'Elia, M. L., de Carvalho Araujo, A. and J. M. Magnino Silva 2024
Pathogens, 13(1):1-16
The reintroduction of captive animals to the wild helps restore endangered species, but it risks pathogen transmission, harming wild populations. Such transmission can impact the genetic diversity and long-term viability of these populations. This study assessed parasite diversity and load in captive *Pecari tajacu*, a species native to the Americas and culturally significant to Brazilian indigenous culture, prior to reintroduction. Samples from 24 peccaries were analyzed for ectoparasites, hemopathogens, and stool parasites with direct and molecular analysis. Findings showed that various parasites were present. Two peccaries (8.3%) were infested by the adult tick *Amblyomma sculptum*. Six (25.0%) tested positive for *Trypanosoma evansi*, four (16.7%) for hemobacteria of the family Anaplasmataceae, twelve (50.0%) for hemotropic *Mycoplasma*, and

seven (29.2%) for *Leishmania braziliensis*. Stool samples indicated multiple parasites, with sixteen (66.7%) peccaries infected by Strongylida order parasites, Spiruridae in three (12.5%), and *Ascaris suum* in one (4.2%) animal. Cysts of *Balantidium* sp. were found in twenty (83.3%), *Entamoeba polecki* in five (20.8%), and *Iodamoeba bütschlii* in two (8.3%) peccaries. To our current knowledge, this is the first global report of *Leishmania braziliensis*, *Iodamoeba bütschlii*, and *Entamoeba polecki* in *P. tajacu*, irrespective of the environment, including both captivity and wild conditions. Some of these parasites are common in domestic animals, and others are zoonotic, indicating potential interspecies pathogen transmission.

SARS-CoV-2 Infection in Captive Hippos (*Hippopotamus amphibius*), Belgium

Vercammen, F., Cay, B., Gryseels, S., Balmelle, N., Joffrin, L., Van Hoorde, K., Verhaegen, B., Mathijs, E., Van Vredendaal, R., Dharmadhikari, T., Chiers, K., Van Olmen, T.J.S., Agliani, G., Van den Brand, J.M.A. and H. Leirs 2023

Animals, 13(2): 316

Two adult female hippos in Zoo Antwerp who were naturally infected with SARS-CoV-2 showed nasal discharge for a few days. Virus was detected by immunocytochemistry and PCR in nasal swab samples and by PCR in faeces and pool water. Serology was also positive. No treatment was necessary.

SARS-CoV-2 Infection in a Hippopotamus, Hanoi, Vietnam

Bui, V.N., Dao, T.D., Tran, L.H., Vu, T.T., Nguyen, T.H., Nguyen, G.H., Tran, K.V.D. Nguyen, H. X., Bui, A.N., Unger, F., Nguyen-Viet, H. and H.S Lee 2023

Emerging Infectious Diseases, 29(3): 658–661

While investigating the death of a hippopotamus at a zoo in Hanoi, Vietnam, we isolated SARS-CoV-2 and sequenced the RNA-dependent RNA polymerase gene from different organs. Phylogenetic analysis showed that the SARS-CoV-2 strain was closely related to 3 human SARS-CoV-2 strains in Vietnam.

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