BULLetin

Journal of the IUCN SSC Asian Wild Cattle Specialist Group

IUCN SSC Species Survival Commission AWCSG Asian Wild Cattle Specialist Group

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Cover Photo

A group of three immature wild water buffalo males in Nepal's Kosi Tappu Wildlife Reserve

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EDITOR'S NOTE

By Corinne Bailey, AWCSG Programme Officer and James, AWCSG Chair

Welcome to the seventh issue of BULLetin, the newsletter of the IUCN SSC Asian Wild Cattle Specialist Group (AWCSG). In BULLetin, we present novel research on the ecology and conservation of Asian wild cattle species, and share stories about their conservation.

This issue profiles some amazing and diverse research about Asian Wild Cattle, including findings from a state-wide study of Bornean banteng populations, research into kouprey genomics, disease risk analysis for potential future translocation of tamaraw and a comprehensive overview of the global *ex*-situ population of anoa and its role in conservation.

This issue also contains an update of the current status of wild water buffalo across its range, and novel research into habitat suitability for Gaur within Thailand.

The eighth issue of BULLetin will be published later in the year and we look forward to receiving your interesting articles and updates. Get in touch via social media, our website or contact Corinne at c.bailey@chesterzoo.org.

We are currently updating membership for the Specialist Group. So please read on if you wish to be a member! The membership of Specialist Groups has a four year cycle, and we are now in the 2021-2025 cycle. So members from the previous cycle have been re-invited automatically by email from SSC titled 'IUCN Commission membership renewal 2021-2025'. If you have not seen this email please check your emails and following the instructions and login and accept membership as soon as possible. If you can't find the email please contact James at jamesaburton@yahoo.co.uk. For people that are interested to become new members please get in touch to let us know your interest in Asian wild cattle and we will review and respond within a couple of months.

We will be conducting Red List Assessments for certain Asian wild cattle species in the coming three years. If you would like to be involved, please contact Tom Gray (tgray@wwf-tigers.org) or myself. We will be reaching out to many of you to ask for your contributions to this process. At the same time we will also be working on a few Green Status assessments. There is more information on this exciting initiative here.

I'm pleased to share with you that our Specialist Group received the IUCN SSC Chair's Citation of Excellence for our work in 2020 in delivering the SSC Species Strategic Plan for that period. Thanks to all of you that are involved with our activities, your contributions helped us achieve this success.

Keep up to date with our activities and other Asian wild cattle news on our website (www.asianwildcattle.org) and social media (Facebook: IUCN Asian Wild Cattle Specialist Group, Twitter: @IUCN_WildCattle and Instagram: @iucn_wildcattle). We hope you enjoy this issue, and look forward to hearing from you.

We hope you enjoy this issue, and thank you for your continued efforts in conserving Asian wild cattle.

NEWS AND UPDATES

Two kouprey genomes and a banteng, gaur, kouprey polytomy

By Mikkel-Holger Sinding, Smurfit Institute of Genetics, Trinity College Dublin

The critically endangered and likely extinct kouprey (*Bos sauveli*) is a large, cattle-like species of wild Asian Bos. If indeed extinct, it is an animal where research can no longer be based on living populations and many details of its nature seems lost.

Among the many fascinating aspects of the kouprey is its evolutionary history and how it may be related to other species, particularly the other wild Asian Bos. This is a topic of controversy in past literature, (Galbreath et al., 2006; Galbreath et al., 2007; Hedges et al., 2007; Hassanin and Ropiquet,2007) and while it is evident the kouprey is a clear and independent species (Hassanin and Ropiquet, 2007), genetic work has been restricted to relatively few markers with limited analytical power.

Therefore, to dig deeper into the evolutionary history of the kouprey and making rare data an available resource, my co-authors and I shotgun sequenced two kouprey specimens from the Natural History Museum of Demark. Resulting in a 3.6x and a 1.8x coverage nuclear genomes, which were analysed alongside available gaur and banteng as well as a broad reference including bison, domestic cattle and yak.

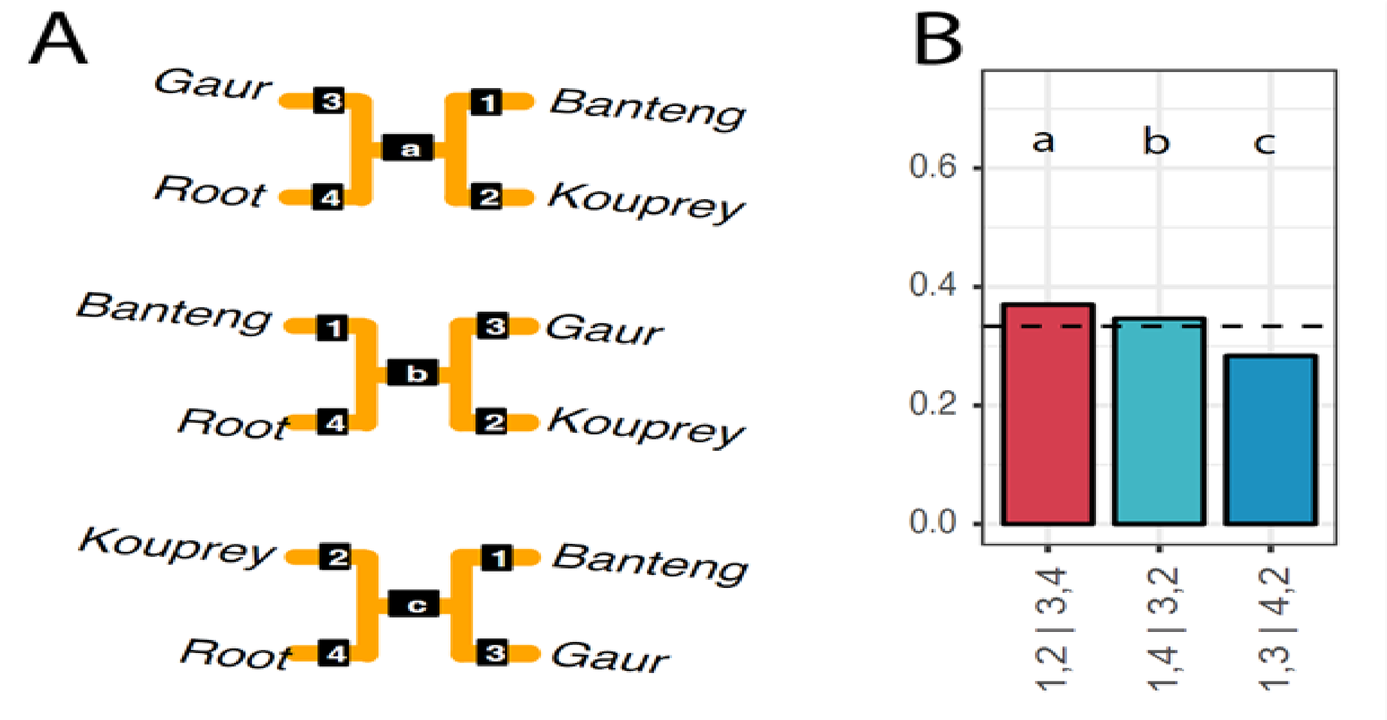

Figure 1 (A) Visualization of alternative topologies. (B) Display of quartet frequencies of the three possible configurations of internal branches in the nuclear phylogeny, when evaluating clades as an underlying unrooted tree. The red bar shows the top score configuration presented in the phylogeny (A), whereas the two blue bars show alternative configurations. Alternative tree configurations are labelled corresponding to branch IDs in (A). The dotted line indicates a level of a one-third bipartition for every quartet, which is the threshold frequency of a true bipartition (Allman et al., 2011).

The affiliation of koupreys is as previously reported as closely related to banteng and gaur (Hassanin and Ropiquet, 2007), interestingly and based on nuclear genome wide diversity, we find it is almost equally close to both. This is not because the kouprey is a hybrid of banteng and gaur, but rather that the three species at the root are extraordinary closely related, with almost equal amounts of incomplete lineage sorting among each pair, compared to the third species. This scenario is compatible with an evolutionary history, where the three species diverged in a polytomic pattern. This also offers an explanation for the puzzling mitochondrial structure of banteng, gaur and kouprey, which show a paraphyletic pattern of lineages in banteng and gaur sub-species, with kouprey nested within which's a compatible with an initial polytomic diversification.

A clear observation from this work is that there is a great need of geographically diverse gaur and banteng genomes, to gain further depth in analysis. I have obtained funding for more work in Asian Bos genomics and re looking for potential collaborators with samples. If you are interested and have access to banteng and gaur tissue (non-faecal), please feel free to contact my email (mhssinding@gmail.com).

The sad reality is that kouprey may be lost, but at least museum specimens offer an opportunity to investigate this animal from molecular perspectives and in doing so, also illuminating the evolution of banteng, gaur and Bos overall. At least now the first kouprey genomes are available (NCBI PRJNA764745).

Read the full paper at Sinding, Mikkel-Holger S., et al. "Kouprey (Bos sauveli) genomes unveil polytomic origin of wild Asian Bos." Iscience 24.11 (2021): 103226. https://doi.org/10.1016/j.isci.2021.103226

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Identifying the diet of wild tamaraw through DNA metabarcoding

By Elyza Tan, Mindoro Biodiversity Conservation Foundation Inc.

The tamaraw (*Bubalus mindorensis*), a dwarf buffalo species endemic to the island of Mindoro, is the largest land mammal of the Philippines (Custodio et al. 1996). However, its population has declined severely over the last century due to hunting and habitat loss (Harper 1945; Schult 2001). With fewer than between 604 individuals left, it is now classified as Critically Endangered (DENR 2015; DENR-TCP 2021).

Tamaraws were thought to occur only in the following areas of Occidental Mindoro in the last two decades: Mts. Iglit-Baco Natural Park (MIBNP), Aruyan-Malati Tamaraw Reserve (AMTR), and Mt. Calavite Wildlife Sanctuary (MCWS) (Long et al., 2018).

Recently, however, a population was reconfirmed in Oriental Mindoro, after years of unconfirmed presence in the area, particularly in Mt. Gimparay. This site varies in its flora compared to known tamaraw sites in Occidental Mindoro (Schütz, 2019; Tabaranza et al., unpubl).

Three habitat types were identified in Mt. Gimparay, namely, the grassland thickets with pandan groves, mossy forest, and tropical sub-alpine forest. In comparison, MIBNP, known to house the largest Tamaraw population across the Mindoro, is mainly composed of grasslands with secondary forest patches.

The difference of habitats in both identified areas where Tamaraws thrive, gave us hope to improve its population to possible establishments of corridors or translocation of individuals. But before that, it is necessary to understand their ecology, including their diet, further. Thus, this project aims to identify the diet of wild Tamaraw through DNA metabarcoding of flora species from the faecal samples collected from Mt.Gimparay and MIBNP.

The results from this project can aid in identifying suitable areas as prospective habitats for the Tamaraw and increase our understanding of the population dynamics of the species with the availability of food in the habitat.

Mt.Gimparay 2018 Tamaraw Verification Survey © Elyza Tan, MBCFI

This project will help to secure the long-term survival of the Tamaraw by providing baselines for future in-situ and ex-situ conservation activities as recommended by the Tamaraw Conservation and Management Action Plan 2019-2028. Despite the ongoing pandemic and strict local restrictions in 2020, Mindoro Biodiversity Conservation Foundation Inc and its partners have conducted the initial activities while following safety protocols. The project has already secured the permit to collect samples. Before the passing of Kalibasib, the first and last successfully bred Tamaraw faecal samples were collected to identify the appropriate kit for metabarcoding analysis. Preliminary testing for metabarcoding analysis is currently being conducted at the University of Philippines-Diliman.

Moreover, dialogues with Indigenous Mangyan Tribes Taubuid and Alangan are being processed to secure safe access in the project areas. If you are interested in supporting and collaborating, please do not hesitate to contact MBCFI: elyza_p_tan@mbcfi.org.ph and info@mbcfi.org.ph.

Collecting samples for preliminary testing © Elyza Tan, MBCFI

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Population of Bornean banteng under threat from poaching

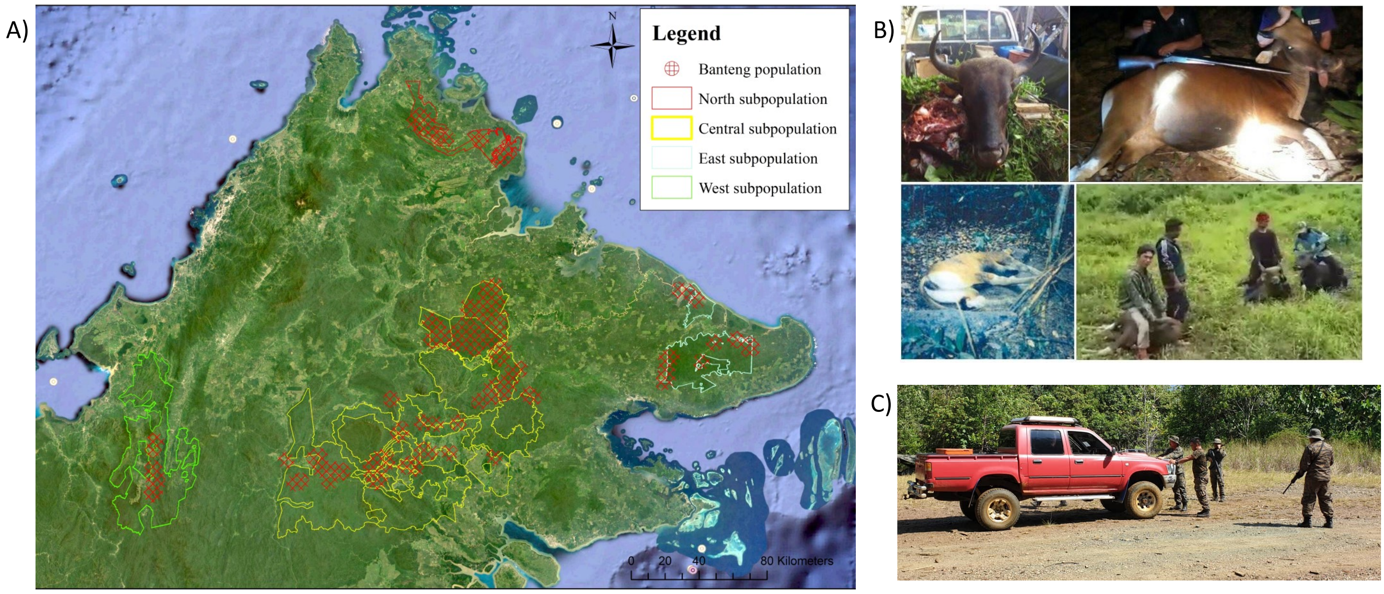
By Benoit Goossens, Cardiff University & Danau Girang Field Centre

Findings from a state-wide study on the Bornean banteng have concluded that it is crucial that poaching of the species needs to cease and that the population is supplemented with captive-bred individuals if we are to ensure its survival and recovery.

In a scientific paper recently published in the journal, Endangered Species Research, scientists and wildlife managers from Danau Girang Field Centre (DGFC), Cardiff University and the Sabah Wildlife Department (SWD) collated the first population parameters for the endangered Bornean banteng by developing population models to stimulate the effect of different hunting offtake rates.

The findings from camera trap and sign surveys were carried out over a period of six years (2011-2015). They suggest that in the Malaysian state of Sabah, the Banteng population is geographically divided into four management units based on connectivity: The Northeast (with Paitan and Sugut Forest Reserves), Sipitang Forest Reserve in the West (Deramakot, Tangkulap, Malua, Kuamut and many other forest reserves) and Southeast (Kulamba and Tabin Wildlife Reserves) which all require active management to prevent further population decline and local extinction.

At an international workshop on the conservation of the Bornean banteng in 2017, the total population of banteng in Sabah was estimated at a minimum of 320 individuals. This workshop conducted a population viability analysis. modelling exercise and it showed that if only 1% of the population was hunted in Sabah, population growth would cease in the smallest Northeast and Sipitang Management units In the Southeast and Central units, growth would cease if 2 and 4% of the population were hunted, respectively. Extinction was estimated at 21 to 39 years if 5% of the population were hunted every year. Due to the size of the Central management unit, this location would probably experience the extinction of banteng last.



A) Banteng distribution in Sabah with the location of the four management units: North, Central, East and West ©DGFC. B) Collage of poaching events that happened between 2017 and 2018 in Sabah's protected areas ©DGFC C) Roadblock by PROTECT rangers ©Sabah Forestry Department

Conservation actions for the Bornean banteng have since included an action plan for Sabah that was drafted and approved by the State Government in 2019. The survey work on the Bornean banteng was in-part funded by the Sime Darby Foundation, and as a follow-up to the action plan, the Foundation continued its support through funding for PROTECT, a boots-on-the-ground enforcement team under the Sabah Forestry Department. As another boost to wildlife enforcement, the US Department of State through its Bureau of International Narcotics and Law Enforcement Affairs (INL) also provided funding to SWD and DGFC in 2019 to set up an intelligence unit and a forensic unit. This funding bolsters the efforts of Sabah government on fighting poaching and illegal trade, and overall will enable the implementation of the action plans for the banteng as well as for other wildlife.

The banteng study was mainly funded by the Sime Darby Foundation, with additional funding from Houston Zoo, Mohamed bin Zayed Species Conservation Fund, Malaysian Palm Oil Council and Woodland Park Zoo, and supported by the IUCN Asian Wild Cattle Specialist Group.

Read the full article: Gardner PC, Goossens B, Abu Bakar SB, Bruford MW 2021. Hunting pressure is a key contributor to the impending extinction of Bornean wild cattle. Endangered Species Research 45: 225.235.

Two banteng bulls displaying along a river in one of the forest reserves in Sabah ©DGFC

Disease risks analysis as a step towards evaluating feasibility of translocation as a conservation option for Critically Endangered tamaraw

By Amit Kumar[a], Mikko Reyes[b], Emmanel Schütz[c], Jeff Holland[d], Malcolm Fitzpatrick[a] and Anthony W. Sainsbury[a]

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[b] *Tamaraw Conservation Program*
[c] *D'ABOVILLE Foundation and Demo Farm Inc*
[d] *Centre of Conservation for Tropical Ungulates*

Tamaraw Conservation and Management Action Plan 2019-2028 (TCMAP) was elaborated in 2019 with stated aim to confer an extinction risk of zero to the tamaraw (*Bubalus mindorensis*), a critically endangered Philippine bovid, over a period of 100 years with multiple populations occupying multiple sites across the Mindoro island (DENR 2019). Proposals are being considered to use reintroductions, reinforcements and establishing an ex-situ population on Mindoro for reviving the isolated and fragmented sub-populations of tamaraw (Boyles et al. 2016, DENR 2019). The aim of these translocations is to increase the number and range of tamaraw sub-populations which currently stand at four (Fig. 1), ultimately contributing to the TCMAP's vision of ensuring long term viability of a tamaraw metapopulation on Mindoro. Several destination sites are under consideration for translocations, such as the sites holding small sub-populations of tamaraw at Mount Calavite Wildlife Sanctuary and Aruyan-Malati, and some of the historical tamaraw ranges on Mindoro.

Also, establishing an *ex situ* breeding population of tamaraw is being explored for which revival of such an erstwhile facility is an option (Fig. 2). Principal conservation benefits desired from the ex-situ population include maintaining an insurance population in the face of extinction threats to wild populations, and to provide animals for any future translocations, which will also contribute to maintain gene-flow across the metapopulation (DENR, 2019). A feasibility study team with international collaboration, drawing experts with experience in ungulate translocations, ex-situ breeding, tamaraw ecology, Philippine government representatives and local veterinarians, is looking into achievability of the whole translocation and captive breeding endeavor. This study will inform the Philippine government decision-making enabling them to proceed with any option under assessment based upon the scientific evidence. An important component of this feasibility study is to analyze disease risks in tamaraw translocations. Taking onboard experts from the feasibility study team as stakeholders, a partial disease risk analysis (DRA) was undertaken for the purpose. We utilized a qualitative method proposed by the Zoological Society of London (ZSL), which utilizes qualitative estimations to assess the risk from each hazard (disease agent), considered of concern to translocation. Briefly, the risk estimation from each hazard involves assessing the likelihood of exposure and infection of translocated tamaraw and other related species in destination sites from a hazard, and the likely magnitude of biological, economic and ecological consequences after such exposure and infection. There is very scant information about diseases in tamaraw, however, it is highly possible that this free-living bovid is susceptible to the infections prevalent in domesticated ungulates in the Philippines. Pathogens *Fasciola* spp., *Pasteurella multocida*, *Trypanosoma evansi*, *Leptospira* spp., bovine ephemeral fever virus and bovine rotavirus have been associated with outbreaks in the related species of cattle/buffalo in Philippines and other Asian countries, with mortalities to a varying extent. *Fasciola* spp. and *Leptospira* spp. have also been detected in tamaraw in the past (Masangkay et al., 1996). We included the above mentioned six infectious agents in the scope of our partial DRA as the hazards of concern, and

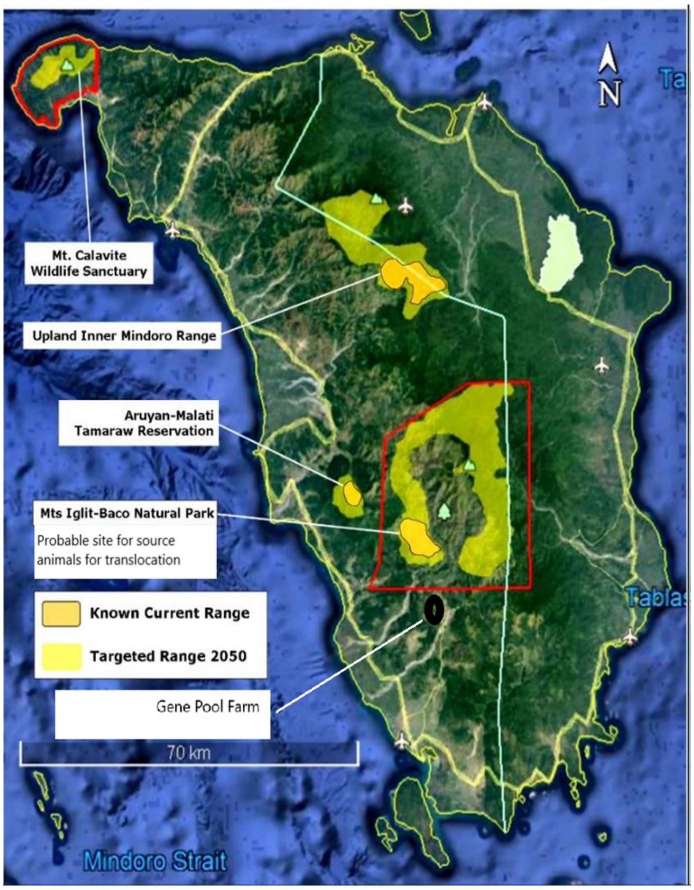

Figure 1: Current distribution of tamaraw sub-populations and projected range till 2050 in the Mindoro (Philippines) as targeted in Tamaraw Conservation and Management Action Plan. Tamaraw sub-population from 2500-hectare Core Zone of Monitoring in the Mount Iglit-Baco Natural Park is the most probable source for animals to be translocated. Also highlighted is the Gene Pool Farm, the site of erstwhile ex-situ breeding sub-population of tamaraw. Adapted from DENR 2019.

analysed the risk they pose to tamaraw translocations using qualitative estimations as per the standardized DRA method of the ZSL.

Logical, reasoned and referenced discussions were held involving experts from the ZSL and feasibility study team at every step of partial DRA. The probable pathway to be followed from capture of the source animals to release in destination/release sites was obtained from concerned experts. Such pathway is of high importance as it clearly lays out at which points hazards can harm the animals being translocated, and/or the populations at destination sites (Bobadilla-Suarez et al., 2017).

If any geographical and ecological barriers are breached in a translocation, the risk of exposure to novel disease agents is increased (Bobadilla-Suarez et al., 2017; Hartley & Sainsbury, 2017). The six infectious hazards of concern were categorized into source, destination, carrier, host-immunodeficiency, transport and population hazards considering the factors such as crossing of ecological and geographical barriers in the translocation, effect of stressors on the host-parasite dynamics and potential impact of hazard on the host population numbers. We undertook release, exposure and consequence assessments separately for the individual hazards, and later combined to qualitatively estimate the overall risk from each hazard (Sainsbury & Vaughan-Higgins, 2012). Briefly, our release assessment described the likelihood/probability of exposure and infection of translocated animals from a hazard, exposure assessment estimated the likelihood of exposure and infection of susceptible animals at destination sites, and consequence assessment laid out the likely magnitude of biological, economic and ecological consequences from a hazard. Thereafter, we assigned a level of negligible, low, medium or high to the overall risk posed by each infectious agent of concern (Bobadilla-Suarez et al., 2017). Each of the six identified hazards of concern was found to be posing a non-negligible risk to the proposed translocations, for which we explored options to

Table 1: Categories, estimated risk levels and chief risk mitigation actions recommended to reduce risk of disease from six hazards to tamaraw translocation.

Hazard of concern	Hazard category	Estimated risk level	Some identified disease risk management options
P. multocida	Carrier	Medium	Avoiding peak rainfall and temperature conditions during translocation, pre-translocation vaccination of the captured animals, minimizing translocation stress, and annual vaccination of eligible ex-situ population.
T. evansi	Carrier and population	Medium	Minimizing contact of the tamaraw with livestock herds at source and destination sites, minimizing translocation stress, and providing designated water sources at the ex-situ facility.
Bovine Ephemeral Fever virus	Population	Medium	Avoiding translocations during or just after rainy season, effective post-release monitoring of ex-situ population, and avoiding excess dung/manure pile-up in the ex-situ facility.
Fasciola spp.	Carrier	Low	Choosing destination sites where water reservoirs are not connected with rice-fields during rainy-season/floods, and periodical flukicide administration for the ex-situ population.
Leptospira spp.	Population	Low	Avoiding selection of destination sites where core tamaraw habitats fall in the flood-prone areas, and minimizing contact of the tamaraw with livestock herds at destination sites.
Bovine Rotavirus	Population	Low	Avoiding translocation of the dams in late gestation or those having expected calving during the next peak winter season, and minimizing contact of the tamaraw with livestock herds at destination sites.

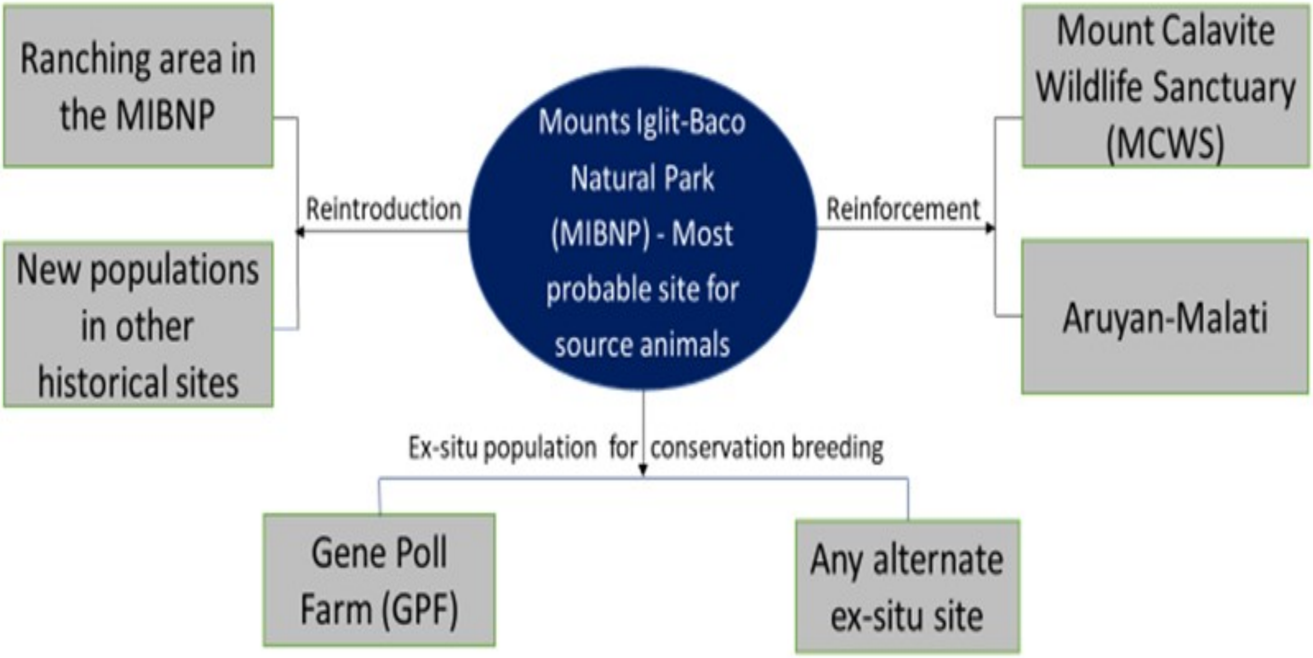

Figure 2. Several options are being considered for translocation of tamaraw from the 2500-hectare Core Zone of Monitoring inside MIPNB, such as the small existing sub-populations at MCWS and Aruyan-Malati, and historical ranges in MIPNB and elsewhere. For ex-situ breeding population, some other sites including erstwhile site GPF are being explored.

reduce such risk based upon the ecology, pathogenesis and risk level from individual hazards (Table 1).

Identified management actions were judged to be important to reduce the risk of disease from hazards of concern. This study will lay the foundation for a complete disease risk analysis for tamaraw translocations when resources can be dedicated and further information is acquired by the feasibility study team regarding prevalent diseases in ungulates at the destination sites. The inputs gathered and inferences drawn will guide the future DRAs for remaining identified hazards.

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Bridging the Gap in *ex situ* and *in situ* population management of anoa

By John Andrews[a], Marcel Alaze[b], and Yohana Tri Hastuti[c]

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Anoa (*Bubalus Sp.*) are the smallest wild cattle species and live wild only on the islands of Sulawesi and Buton in Indonesia. Two species are identified; the lowland anoa (*Bubalus depressicornis*) and the mountain anoa (*B. quarlesi*). Currently, both species are listed as 'Endangered,' (Burton et al. 2016a; 2016b) and face threats of agricultural conversion, hunting and increased mining activities (Rejeki, 2018). Locally known as "demons of the forest," anoa are elusive and secretive. Mountain anoa are thought to be lighter in color than lowland anoa and as the name suggests, one species is thought to be distributed in more mountainous habitat than the other. However, it is not yet well understood whether the distribution of the two species overlap. With these species declining rapidly, conservation of the species on a global level is critically needed. In 2016, a global effort began to conserve anoa as well as babirusa (*Babyrousa sp.*) and banteng (*Bos javanicus*) in Indonesia in a unique One Plan Approach (Byers et al., 2013) of developing a joint *in situ* and *ex situ* conservation plan and incorporating partners involved in both areas.

The One Plan Approach framework initiated in 2016 is called the Global Species Management Plan (GSMP) administered by the World Association of Zoos and Aquariums (WAZA). New GSMPs were started for each of these ungulates, later joined by the long running Sumatran Tiger (*Panthera tigris sondaica*) GSMP, and together this group is known as the Action Indonesia partnership. The goal of this collaborative group is to achieve safe and stable populations of these species in the wild. Action Indonesia aims to contribute to the conservation of these species *in situ* and to achieve genetically and demographically healthy *ex situ* assurance populations, which provide future options for restoration of wild populations.

Zoos and aquariums are often underused resources for species of conservation concern. They have much to contribute to conservation of the species they hold and breed. *Ex situ* populations can be great resources for rich biological data that are sparse for wild populations and valuable resources to observe or discover behaviors and husbandry knowledge that may be hard to glean from the wild.

Assurance populations are those that are maintained and managed in zoos with at least part of the purpose being to ensure a species does not go extinct and can be reintroduced into the wild. Zoo populations of Threatened, Critically Endangered or even Extinct in the Wild species are valuable for this purpose. Guam rails (*Hypotaenidia owstoni*) and Guam Kingfishers (*Todiramphus cinnamominus*) are both extinct in the wild and reintroductions have been supplemented in the past from zoo breeding populations. California Condors (*Gymnogyps californianus*), once close to extinction, were all brought into human care for intensive breeding for reintroduction in zoos and today are roaming wild in California again. Przewalski's horse (*Equus ferus przewalskii*) and Arabian Oryx (*Oryx leucoryx*) are classic ungulate examples of animals that disappeared from the wild and were brought back from well maintained zoo populations. As a stated goal of Action Indonesia, the Anoa GSMP has put in much work to facilitate connections of *ex situ* and *in situ* practitioners, skill sharing opportunities and capacity building of zoo management in Indonesia. Connecting *ex situ* populations with *in situ* conservation can demonstrate the importance of responsible population management of species like Anoa in zoos around the world.

For the Anoa GSMP, there are currently three zoo regions participating and managing *ex situ* populations, including the American Association of Zoos & Aquariums (AZA), European Association of Zoos & Aquariums (EAZA) and the Indonesian Zoological Parks Association (PKBSI). With some additional holdings in some other Asian countries, like Japan or Singapore, the global *ex situ* population of Anoa currently consists of approximately 185 anoa among 42 different zoos and aquariums around the world (Fig. 1A).

The first animal recorded being brought into a zoo from the wild was as early as 1844 with the importation of an anoa into a zoo in Paris, France (Burton et al., 2018). The more modern populations in the other zoo regions are from exports occurring in the late 1960's and mid 1970's. Eleven animals were brought into zoos and aquariums and nine of these make up the genetic founders from which all the AZA and EAZA animals currently descend. Cooperative breeding programs and population management have been present in both EAZA and AZA regions since the 1980's (Faust et al., 2019). These programs focus on managing *ex situ* populations for particular goals among member institutions, sharing data, exchanging animals and being genetically and demographically minded about how to manage animals for long term sustainability. Each region manages their populations regionally, but with the global population in mind.

The *ex situ* population in EAZA consists of 41 anoa across 20 member facilities and is managed in a cooperative program called an EAZA

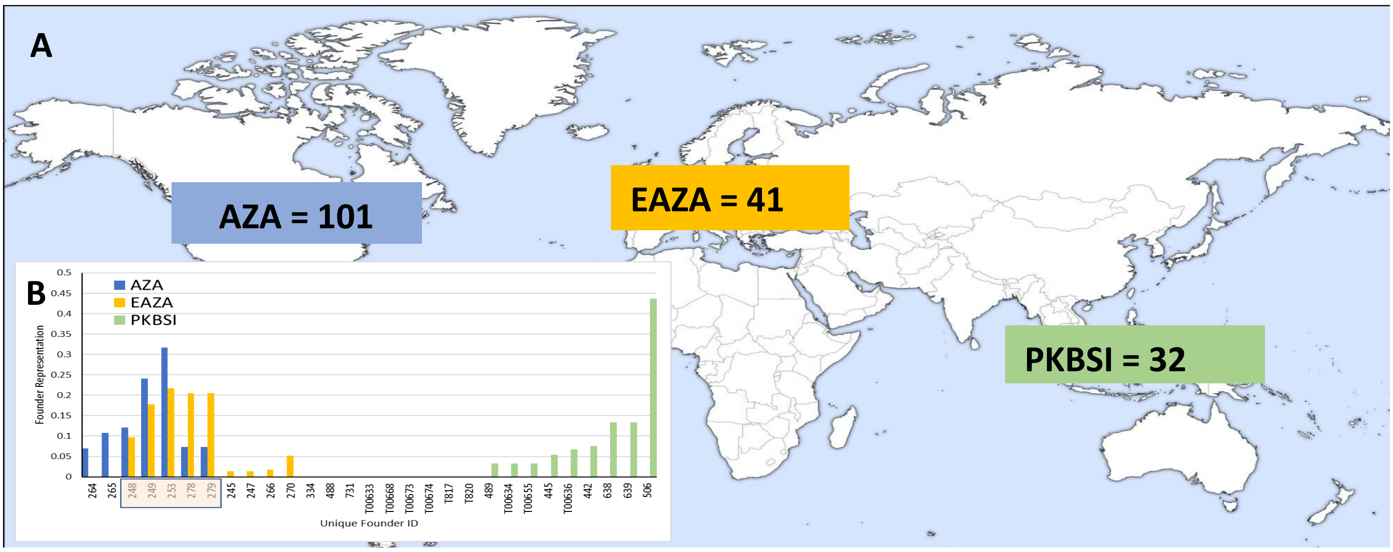

Figure 1: (A) Global depiction with zoo regions labeled in colored boxes and the current size of each regions ex situ population. (B) Inset in the global map, is a representation graph showing how all currently living animals among these three zoo regions are related. In Blue, AZA founder representation overlaps with several EAZA founders in orange, indicating that these two population share many common ancestors. In Green, the PKBSI population founders are noted. For all those founder ID's on the x-axis with no representation represent unique genetics among the global population.

Ex-Situ Program (EEP). With the small size of this population, successful breeding and demographic stability is vital to sustaining anoa long term in European zoos. Recently, this population has been challenged with few births and loss of some breeding aged females (Fig. 2).

To combat recent challenges, the population managers have recommended more transfers than usual to set up new breeding pairs and recruit new zoos to breed and exhibit anoa. Genetically, anoa in this region may be closely related and inbreeding may be difficult to avoid. In cases like this, keeping the population productive and reproducing maintains demographically stable populations. For long term sustainability, this *ex situ* population will need to continue consistent breeding to maintain demographic numbers and then must incorporate new animals with unrelated genetics.

In AZA, anoa are managed in a similar cooperative program called Species Survival Plans (SSPs). Most animals in AZA are related to those in Europe because of historic exchanges of animals between regions. In AZA, the population size is even smaller. Only ten anoa are held at seven AZA facilities currently (Fig. 2). Without more holders, that small population alone is not viable by itself. Interest and support for exhibiting this species is waning in AZA. With increased successes in the global efforts, population managers are hoping to reverse this trend. Interestingly, one private North American facility, specifically for ungulate conservation, holds over 150 anoa. Including this facility, North America contains the largest *ex situ* population of any anoa globally. Gene diversity is still a challenge in all North American anoa as they are all from the same sources as European animals. The North American population needs more zoos to exhibit and promote the species and make space for the population to grow. Like Europe, new unrelated animals from the range country would genetically benefit the population greatly and improve sustainability.

In Indonesia, the zoo population is also small but being closer to the native range of the species, may be more genetically diverse and more distantly related to other regional populations (Fig. 1B). According to the international studbook of Anoa, the zoo population in Indonesia currently consists of 37 anoa across seven zoos and breeding centers. The current *ex situ* population started around 1970 and grew from breeding and

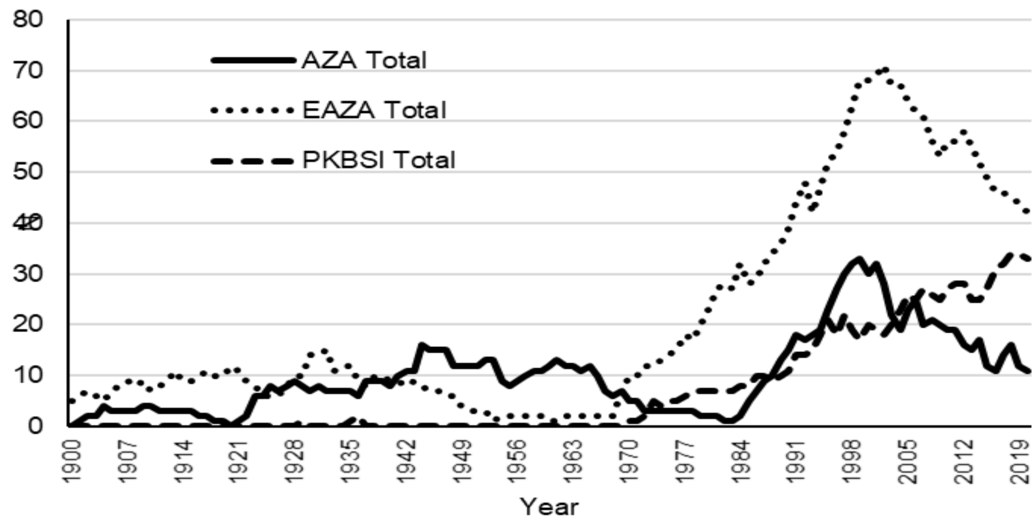

Figure 2: Census of the global ex situ anoa population by zoological region; AZA, EAZA and PKBSI regions from 1 Jan 1900 to 31 Dec 2020

confiscations of animals from the wild to the current size (Fig. 1). The Indonesian Zoo Association (PKBSI) is in the process of building their own version of a cooperative breeding program with anoa and various other species, with the support of Action Indonesia (Burton et al., 2020). Early steps of this process involve data sharing among member zoos and managing data in a national studbook. Data are provided from zoos that hold anoa to a central zoo professional that works at a facility that is a member of PKBSI. For Anoa, Dr. Yohana Tri Hastuti from Taman Safari Indonesia, Bogor is the National Studbook Keeper and is responsible for keeping accurate data to facilitate population management and communicating with Indonesian zoos that hold the species they are managing. While small, the Indonesian *ex situ* population is important because they are potentially the most important source of unique genetic founders in zoos (Fig. 1B). Not only will it be vital for growing the *ex situ* population there to represent different genetic lines more, but exchanges to other regions would infuse much needed diversity in the future. Some facilities in Indonesia are unique and meant for breeding the species or as a rehabilitation facility for confiscated animals. Current challenges for the anoa *ex situ* population in Indonesia are largely space constraints and need for transferring animals. Moving animals around Indonesia is difficult logistically and physically, but mixing up animals to cross blood lines and avoid inbreeding is vital to long term sustainability.

Breeding and transfer recommendations between zoos is a key tenant of cooperative breeding programs in zoos. These recommendations guide which animals should breed to avoid inbreeding and increase gene diversity as well as how to mix animals among zoos so that bloodlines are not overrepresented, zoo needs for exhibit animals or moving offspring are met and demographic stability can be maintained.

The Anoa GSMP group has been working hard to collaboratively build breeding programs among Indonesian zoos since 2016 and has achieved several successes. The first formal analysis was completed of the Anoa National Studbook in 2016. Following this analysis, and workshops held in Indonesia with zoo official attendees from across Indonesia, the first formal written report sharing the *ex situ* population status and breeding and transfer recommendations was produced. This document contained the current gene diversity, demographic status and future recommendations for the population in Indonesia, including a national Indonesian target of increasing the *ex situ* population to 75 anoa individuals. It was then shared with all zoo officials holding anoa, as well as government officials and used to guide breeding in the *ex situ* population. In 2018, a second document was created with updates after changes in the population and following the 2nd Action Indonesia Global Species Management Plan Workshop. In this workshop, 91 participants from 20 Indonesian zoos attended as well as 30 other Indonesian and International institutions. For anoa holders, 17 attendees from 7 zoos who hold anoa were able to attend, discuss and share their experiences and needs at the workshop helping to create better recommendations for everyone. Engaging with such a wide group of people has been key to building cooperation and success in population management. Four births were produced from recommended pairings and one recommended transfer was accomplished following recommendations since 2018. This is a massive success for *ex situ* population management of anoa in Indonesia, but there is more to learn. As we continue to move forward and prepare for the next workshop and next set of recommendations, we continue to learn from the past, and change or build this process with partners in the GSMP.

In addition to these *ex situ* population successes in Indonesia, the Anoa GSMP also develops strategies for maintaining the global population. Each zoological region faces different challenges related to zoo space for new animals, relatedness among populations or need for demographic support. Previous strategies to address these challenges center on the idea of interregional transfers of animals. AZA and EAZA would benefit from more interest and space to increase population numbers in their respective regions, but they would also benefit from new genetic unrelated lines from Indonesia. Conversely, Indonesia could also use more space to grow, but capacity building is needed to build a system of cooperation, and partner with government, zoo and PKBSI officials to make transfers easier in Indonesia.

In addition to building up genetically viable *ex situ* populations to strengthen the genetic diversity of the global metapopulations, the Action Indonesia GSMPs work holistically to raise awareness about the species and their threats, and to support in situ conservation efforts through population monitoring. Conservation education can increase knowledge of species and conservation efforts where they are implemented (Nekaris et al., 2017) and can influence public behavior and connection to nature (Ancrenaz et al., 2018). Educators in the GSMP have been integral to spreading the word and messaging among member zoos around the world, which would intern bolster *in situ* support for rescued animals. Education groups have developed a web platform to focus information for Action Indonesia, implemented the first annual Action Indonesia Day in August 2019, and started Facebook groups to connect educators across the globe. GSMP educators also successfully delivered workshops to Indonesian zoo officials to encourage more education programs, signage and started short term community education outreach projects in partnership with NGOs with communities living with these species (Burton et al., 2020). In the next three years, awareness raising will also occur directly

A female anoa and her calf from Leipzig Zoo in Germany. Credit: Leipzig Zoo to address threats to populations in the wild in Sulawesi and Java.

The Anoa GSMP continues to implement strategies for cooperative breeding and managing the global population sustainably, but *in situ* populations have benefited from zoo, government and *in situ* experts. Experts from Indonesia (and international) zoo staff and government representatives have shared their experience through training Sulawesi protected area rangers on handle and transport of rescued anoa.

Technical support from Indonesia and international zoo experts is ongoing to develop an island wide coordination of the management of rescued anoa by local government offices. Currently, monitoring of anoa populations trends over time in the wild is not consistent between sites and absent for some important populations So work is in development by Indonesian and international experts to achieve greater consistency and start new monitoring to fill knowledge gaps, funded by zoo partners. In the future, it is likely that anoa in the wild may need to be managed as a metapopulation (regional group of connected populations of a species with movement of animals among sub populations) to maintain gene diversity as much as possible. Different *ex situ* populations and the wild populations are likely to become too small to maintain gene diversity. Action Indonesia partners will continue to be vital, even if partners are not zoos exhibiting species in the GSMPs.

Fundraisers, conservation supporters, keepers and educators from zoos, non-profit, academic and government agencies are all active participants with Action Indonesia initiatives for anoa and other species. These partnerships can provide input on future holistic strategies to manage a metapopulation of anoa successfully.

Maintaining gene diversity is vital for sustaining populations of anoa, whether in the wild or in zoos. Wild anoa especially have recently been found to have lost a significant amount of gene diversity in the past few hundred years (Frantz et al. 2018). In zoo populations that are often closed (i.e. no imports or exports), gene diversity will always decline via genetic drift (Lacy, 1997). Population management is what we use to slow loss of gene diversity as much as possible for sustainability and ensure animals are as diverse as possible if ever needed for reintroductions. Understanding the genetic status of assurance wild and zoo populations then becomes more vital for long term conservation. Research is underway to evaluate the level of relatedness among *ex situ* anoa, determine individual geographic origins of animals compared to wild anoa and determine true genetic variability of the zoo population compared to the wild.

Ex situ and *in situ* experts in the Anoa GSMP collaborated with geneticists to help prioritize which zoo anoa to sample for these research questions. Samples will be processed in Indonesia, in partnership with Indonesian scientists. Results from this multidisciplinary study will help give more resolution to the relatedness of zoo anoa and can feed into management recommendations. Zoo populations are highly valuable as assurance populations for future conservation needs and incorporating genetic results can strengthen the sustainability of anoa in zoos.

While much has been accomplished in the first five years of Action Indonesia, the Anoa GSMP has a strong vision of the future. All three regions aspire to grow their regional sub populations and increase the interest of zoos in their regions to house anoa. The GSMP continues to work with *in situ* partners and the donor community around the world to strengthen population monitoring efforts across multiple sites in Sulawesi to inform future management. International zoo donors provide a great deal of support to the Anoa GSMP, especially in development of future *in situ* projects.

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A herd of wild Water Buffalo in Assam's Manas National Park © Anwaruddin Choudhury

Upward trend in numbers of the wild water buffalo (*Bubalus arnee)*

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Abstract

The Endangered wild water buffalo, (*Bubalus arnee)* which has suffered greatly owing to habitat loss, fragmentation and poaching, is slowly making a comeback, especially in Nepal and Assam, India. The Indian state of Assam continues to hold the bulk of the global population. Kaziranga and Manas in Assam, Dibru-Saikhowa and Kosi Tappu in Nepal and Huay Kha Khaeng in Thailand are the key protected areas for the species. Habitat loss and poaching continue to be threats for the species. This article reviews its current status across its range with updated information, comparing an initial assessment from 2010 to 2021.

Introduction

The wild water buffalo *Bubalus arnee* is rare and its range is small and highly fragmented. It has already vanished from most parts of its range. It is the ancestor of all the domestic varieties of buffalo in the world. It has been listed as Endangered (Kaul et al., 2019). The current distribution of wild water buffalo is confined to North-east and Central India and small pockets in Bhutan, Nepal, Thailand and Cambodia, and probably in Myanmar. The wild water buffalo is extinct in Bangladesh and Lao PDR, and is fast approaching this status in some of the above-listed countries. This article is updating that status in 2021, following previous assessments from more that 10 years earlier (Choudhury, 2010; 2014). Perhaps the earliest written documentation is found in *The Babur-Nama* ('Memoirs of Babur') (Babur 1529) and later on a good hunting account is found in the memoirs of the Maharaja of Cooch Behar (The Maharajah of Cooch Behar, 1908).

North-east India

The current distribution of the wild buffalo in this region of India is mainly in the states of Assam, Arunachal Pradesh, Meghalaya and West Bengal. Assam is the stronghold of the wild water buffalo in the world having four-fifth of the known population. Kaziranga National Park has little more than half of the global population of the animal, more than 2,500 (up from 1963 in 2008). Some other key sites in Assam are Manas and Dibru-Saikhowa National Parks. In Manas there is continued increase, well over 500 now (up from 230 in 2008). The numbers in Laokhowa and Burhachapori Wildlife Sanctuaries are also likely to increase as some more habitat is being added to Burhachapori. The population in the unprotected areas of Dibrugarh (Kollolua-Jokai areas) is stable. The current numbers of the isolated herd in Dum Duma Reserved Forest is not known but has not increased.

The main population of Arunachal Pradesh is in D'Eing Memorial Wildlife Sanctuary, which is less than a hundred. Elsewhere the numbers in the *chapories* (riverine islets and tracts) of Dibang and Lohit rivers the small population may be on the decline. The small Meghalaya population which used to occur in Garo Hills and some adjacent areas of western Khasi Hills is nearing extirpation as there are no recent reports. The small population of northern West Bengal survives in eastern part of Buxa Tiger Reserve which regularly moves into Bhutan.

Central India

In Central India the key sites are Indravati National Park, Pamed and Udanti Wildlife Sanctuaries (all in Chhattisgarh) and Kolamarka Conservation Reserve (in Maharashtra). Owing to some disturbance the current status in Indravati and Pamed are not known but there must be some population as the movement of animals across border in Maharashtra indicates. A small population of 16 animals was discovered in Maharashtra state in 2013, which has been given protection by creating the Kolamarka Conservation Reserve. The population was 35 in 2018 as per the census of the Forest Department (Kulkarni, 2019). In Chhatisgarh the numbers could be between 25 and 50. Currently there are a small number of buffaloes taken from Manas in Assam for breeding and potential future reintroduction in Udanti Sitanadi Tiger Reserve. Genetic and detailed morphometric assessment of both translocated and wild buffalo are highly recommended before any release occurs. The case of Maharashtra is an example where the numbers of buffalo is growing. This also indicates that there are populations in Indravati Tiger Reserve as some animals move between these two states. The ecosystem where the buffaloes of Central India live (relatively drier) is different from north-east India and further studies might reveal it to be a separate subspecies as well. Groves (1996) considered the Central Indian and Nepal buffaloes are different from Assam buffaloes and placed them as nominate subspecies. However, the Nepal and Assam buffaloes had population contiguity till early 20th century (Choudhury, 2010) and the type of the species was from northern Bengal (midway between Assam and Nepal) (Harper,1940).

Nepal

The main buffalo area is Kosi Tappu Wildlife Reserve, where there is significant increase mainly due to lack of any natural predation (tiger has been extirpated, and the leopard is also very rare). This year's census showed a significant population of 498 buffaloes (up from 200 in

2010) (Mandal, 2021). Nepal has translocated some animals to Chitwan national park as a second home where currently 12 animals are surviving (Rimal, 2020). The Kosi Tappu population is likely to continue to increase.

Bhutan, Thailand and Cambodia

In Bhutan there is no resident population but herds and individuals regularly occur as they move between Assam and Bhutan (Choudhury, 2008). With the improvement in Manas in Assam the visiting Bhutan population is also increasing. Elsewhere the only key site for the species is Huai Kha Khaeng Sanctuary in Thailand. Unfortunately the numbers are below 50 and there is no sign of any increase. There is also no recent report from Cambodia where a few survived in Mondulkiri province.

Conservation

Choudhury (1994) had estimated a global population of 3,300–3,500 but soon the Manas population of around 1,200 started to decline sharply owing to widespread poaching. As a result, the global estimates for a decade and half later also almost remained same (Choudhury, 2010; 2014), i.e. 3,400–3,500. But with the improvement of protection measures in Manas and owing to rise in numbers in Kaziranga and Nepal, the total population has shown improvement. The current estimate with visible increase in Kaziranga, Manas and Kosi Tappu is about 4,690 (range 4,600 – 4,800), which is a positive sign (Table 1).

However, the buffalo is still threatened with extinction across its range as the population is still not large enough and habitat has remained as it was, with little possibility of increase after some time. More than half of its populations are inside a single protected area (Kaziranga National Park, Assam in North-east India). So far 10+ separate populations/subpopulations have already been formed in what were once largely contiguous populations. Many of these are nonviable and susceptible to genetic degradation. Wild buffaloes have experienced a severe decline due to habitat destruction, poaching for meat, competition and disease transmission from domestic stock, possible hybridization, insurgency and invasion of exotic weeds.

The Wild Buffalo has been declared as the State Animal of Chhattisgarh. At least 13 national parks and sanctuaries across its range protect the species. It is also protected under law in most of the range countries.

Table 1. Estimates of Wild Water Buffalo

Country	Province/State	Number of Wild Buffalo*	
		In Choudhury (2010)	Current estimate
India	Assam	2,800	3,800
	Arunachal Pradesh	200	150
	Meghalaya	50	<40
	Other States	<50	>70
	India Total	**3,100**	**4,070**
Nepal		200	510
Thailand		50	50
Cambodia		<20	<20
Bhutan		<30	<40
	Rest of the World Total	**300**	**620**
TOTAL		**3,400**	**4,690** (4,600–4,800)

A 'big' bull with a cow on the Sapt Kosi River in Nepal's Kosi Tappu Wildlife Reserve © Anwaruddin Choudhury

Recommendations have been made for effective protection and management of the existing protected areas, fencing with metal railings in some areas, control of poaching, involvement of local communities in conservation, detailed surveys in Myanmar, Lao PDR and Vietnam, population estimate and monitoring at regular intervals, genetic study, removal of exotic weeds, reintroduction in select former habitats, check on encroachment, eviction of encroachers, creation of new protected areas, extension of existing protected areas and conservation education (Choudhury, 2010; 2014; Kaul et al. 2019). It is time now for setting a target as done by "Indian Rhino Vision" to attain a wild population of at least 3,000 *Rhinoceros unicornis* by 2020, in case of buffalo to attain a population of at least 7,000 by 2030.

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RESEARCH AND REPORTS

Importance of protected areas in conservation and recovery of gaur (*Bos gaurus*) in Thailand

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Keywords: Distribution, Gaur, Habitat suitability, Large herbivore, Wildlife management

Abstract

Gaur (*Bos gaurus*) listed as vulnerable on the IUCN Red List and is an endangered species in Thailand, one of the wild cattle that play a crucial role in forest habitats. This research is aimed at predicting gaur's suitable habitat within Thailand. Gaur occurrence data were obtained in 2020 by field surveys and recorded gaur signs on wildlife trails, patrol routes, and buffer zones in protected areas. The maximum entropy was used to generate a habitat suitability model. The results of the gaur distribution range showed that gaur occurred in 11 of 17 terrestrial forest complexes which mostly connected in large patch distribution range. Despite its wide distribution range, the result of the suitable area indicated that potential habitat remains in seven forest complexes, with an area of only 8.8% of the mainland found to be suitable habitat for gaur. 80.2% of this suitable area is located inside protected areas, while one of five suitable habitats fell outside protected areas, especially in small forest patches and agricultural areas. The results of this study are important data to provide guidelines for the management and maintenance of gaur habitat in Thailand.

Introduction

Gaur (*Bos gaurus*), the herbivorous wild cattle species, plays an important roles in the quantity control of plants in the ecosystem and as the main prey of large carnivores (Karanth & Sunquist, 1995; Roininen et al., 2007). According to the IUCN Red List, the gaur is a Vulnerable species and its population is decreasing in scattered areas along the 10 range states: Bhutan, Cambodia, China, India, Lao PDR, Malaysia, Myanmar, Nepal, Thailand, and Viet Nam (Duckworth et al., 2016). Meanwhile, the species is listed as endangered in Thailand (Office of Natural Resources and Environment Policy and Planning, 2017) and are protected as listed in the Wild Animal Reservation and Protection Act (2019). The gaur consists of two subspecies (*B. g. readei* and *B. g. hubbacki*) which can be found in the north and south of the Isthmus of Kra, respectively (Lekagul & McNeely, 1977). They were widespread in the 13 forest complexes (46 protected areas) with high abundance in the Eastern, Dong Phayayen-Khao Yai, Khlong Sang-Khao Sok, and Western Forest Complex, respectively (Kanchanasaka et al., 2010).The forest area in Thailand has decreased from 43% in 1973 to 32% in 2019 (Royal Forest Department, 2018), and with the degradation, fragmentation and transformation of suitable habitat, the populations of gaur are low in abundance or are currently extirpated in many protected areas (Kanchanasaka et al., 2010; Prayurasiddhi et al., 2013). On the other hand, the gaur population is increasing in some places, such as in Khao Pang Ma Non-hunting Area, a part of Dong Phayayen-Khao Yai Forest Complex, where they have increased from 30 individuals in 2001 to 271 individuals in 2017 (Bidayabha, 2001; Laichanthuek et al., 2017).

In Thailand, holistic data for the suitable habitat of gaur have been lacking. This data is necessary to inform an action plan for guidelines for gaur conservation. Therefore, the understanding of gaur habitat, especially suitable areas, is very important to maintain and manipulate that habitat. The objective of this research was to assess the habitat suitability for gaur in Thailand. The results will provide guidelines on habitat management and effective conservation planning for gaur and their habitat.

Materials and methods

Study area

This study was conducted in protected areas (PAs) in Thailand, located between 5°37′–20°27′ N and 97°22′–105°37′E. The total 402 PAs covered 116,860 km^2. These are established to protect and buffer of wildlife habitat, covering 22.8% of the country. These PAs are comprised of 60 wildlife sanctuaries (37,377 km^2), 155 national parks (70,651 km^2), 96 non-hunting areas (7,704 km^2), and 91 forest parks (1,128 km^2) which are grouped into 19 forest complexes (17 terrestrial and two marine forest complexes). The survey areas covered 211 protected areas (105,173 km^2) consisting of 60 wildlife sanctuaries (37,377 km^2), 133 national parks (63,616 km^2) and 18 non-hunting areas (4,180 km^2).

Species occurrence data

Gaur occurrence data were obtained from the Department of National Parks, Wildlife and Plant Conservation. The presence data were recorded from the signs survey and also included direct sightings by the Smart Patrol Monitoring Center in 2020. The survey team recorded the presence of gaur along wildlife trails, patrol routes, and buffer zones in PAs across Thailand. Gaur signs in one 30-minute survey time period corresponded to one presence record. There were 4,629 records of presence. The presence records and trails were standardized by creating 1km^2 grid cells to analyze the study area, which covered all forest types and elevations. The survey covered 72,428 grid cells, or 68.8% of the survey area.

Environment variables

The habitat suitability was generated based on 14 variables including the ecological variables (forest type, forest canopy height, distances to the nearest intact forest landscape [IFL], and distances to the nearest stream), topographic variables (elevation and slope), and climatic variables (annual mean temperature (BIO1), mean diurnal range (BIO2), isothermality (BIO3), temperature

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seasonality (BIO4), maximum temperature of the warmest month (BIO5), annual precipitation (BIO12), precipitation seasonality (BIO15), and precipitation of warmest quarter (BIO18)).

Four ecological variables were included. Firstly, the forest type in 2018 was used to generate the model. The forest areas covered 31.7% of Thailand (Royal Forest Department, 2018). It was classified from satellite imagery into 15 categories namely tropical rain forest, dry evergreen forest, hill evergreen forest, coniferous forest, peat swamp forest, mangrove forest, fresh-water swamp forest, beach forest, mixed deciduous forest, dry dipterocarp forest, bamboo forest, secondary forest, grassland, vegetation on a rock platform, and non-forest area (agricultural area and abandoned agricultural land). This data was obtained from Royal Forest Department (2018). Secondly, the forest canopy height in 2019 (Potapov et al., 2020) was used to generate the habitat suitability model. Thirdly, the IFL around 17,333 km2 (16% of PAs) in 2016 was used to predict the suitable habitat which extracted from www.intactforest.org. Lastly, the stream was created from the topographic map at 1:50,000 scale in 2018 which obtained from Royal Thai Survey Department.

The topographic variables consist of the elevation and slope which extracted from www.worldclim.org (version 2.1). For the climatic variables, the climatic data period 1970-2000 was predicted the modeling which extracted from www.worldclim.org (version 2.1). The band collection statistics tool in ArcGIS was used to select 8 variables (BIO1, BIO2, BIO3, BIO4, BIO5, BIO12, BIO15, BIO18) that correlated less than 0.8 ($r < 0.8$) for predicting habitat suitability (Trisurat et al. 2015; Ebrahimi et al. 2017).

Habitat suitability model

The Maximum Entropy Species Distribution Modeling (Maxent) version 3.3.3 was used to analyze habitat suitability (Phillips et al., 2006; Phillips & Dudik, 2008; Ebrahimi et al., 2017). Maxent was chosen because the data set was presence-only data. The maxent generated pseudo-absence data which covered the whole area in Thailand. A randomly selected sample of 75% of occurrence data was used as train data and 25% as test data (Cianfrani et al., 2010; Trisurat et al., 2015). All environmental layers were resampled to the same cell size as 1 km2 covering 511,000 km2 of the mainland. For identification of the area of habitat suitability, the probability of presence value (0-1) was cut off by using the logistic threshold of maximum training sensitivity plus specificity to identify the suitable area and equal

Table 1 Distribution of gaurs in Thailand

Forest complex	Area (km^2)	Number of grid (1 km^2/grid)	
		Survey grid	Gaur presence grid
Srilanna-Khun Tan	9,879	5,619	13
Phu Miang-Phu Thong	5,167	3,686	26
Phu Khieo-Nam Nao	8,347	5,904	199
Phanom Dongrak-Pha Tam	3,146	2,669	9
Dong Phayayen-Khao Yai	6,587	2,049	427
Eastern	3,695	1,861	100
Western	19,816	14,669	678
Kaeng Krachan	5,056	2,763	96
Chumphon	2,630	1,866	55
Khlong Saeng-Khao Sok	5,563	3,879	520
Hala-Bala	2,474	861	2

training sensitivity and specificity to identify the core area (Trisurat et al., 2015; Planisong et al., 2018; Silva et al., 2020).

Results

Distribution

Gaur occurred in 11 terrestrial forest complexes (Fig. 1 and Table 1). The distribution range of gaur covered 41,198 km^2 over 59 PAs. The distribution area mostly connected to the large patch habitat except the Srilanna-Khun (1), Tan and Hala-Bala (11) Forest Complexes. The largest distribution range was located in the Western Forest Complex (7).

The gaur occurrence data was distributed in eight forest types including dry evergreen forest, mixed deciduous forest, moist evergreen forest, hill evergreen forest, dry dipterocarp forest, secondary forest, grassland, and non-forest area (agricultural area and abandoned agricultural land). The gaur distributed in different forest canopy height, elevation, and slope (Fig. 2). The results showed gaur mostly positively associated in the habitat less than 28m of forest canopy

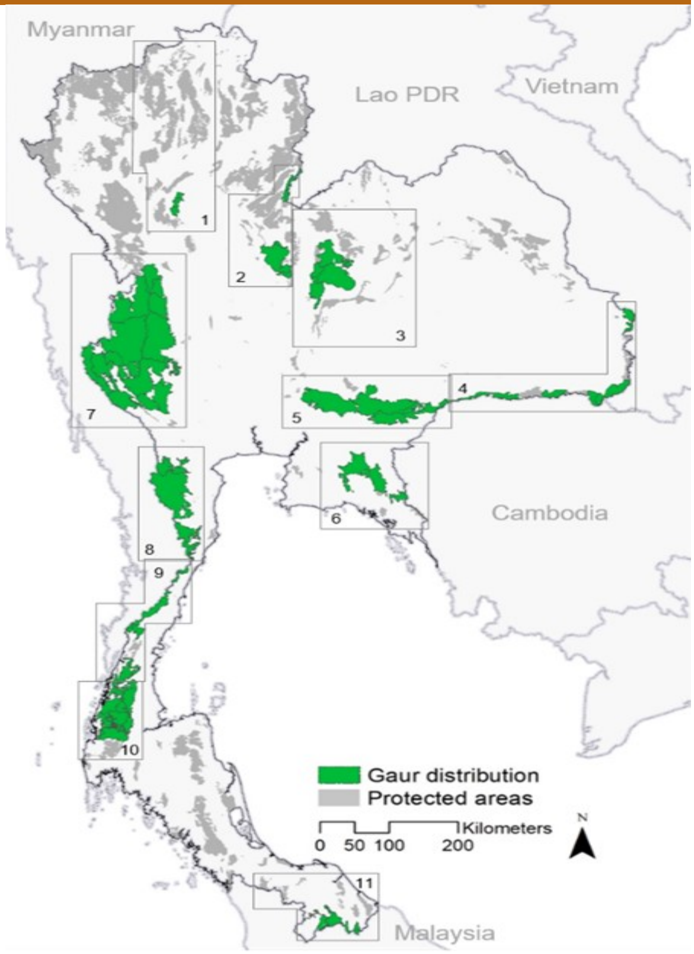

Figure 1 Gaur distribution in Thailand, where outlines of boxes indicate forest complex management units: (1) Srilanna-Khun Tan, (2) Phu Miang-Phu Thong, (3) Phu Khieo-Nam Nao, (4) Phanom Dongrak-Pha Tam, (5) Dong Phayayen-Khao Yai, (6) Eastern, (7) Western, (8) Kaeng Krachan, (9) Chumphon, (10) Khlong Saeng-Khao Sok, and (11) Hala-Bala Forest Complex

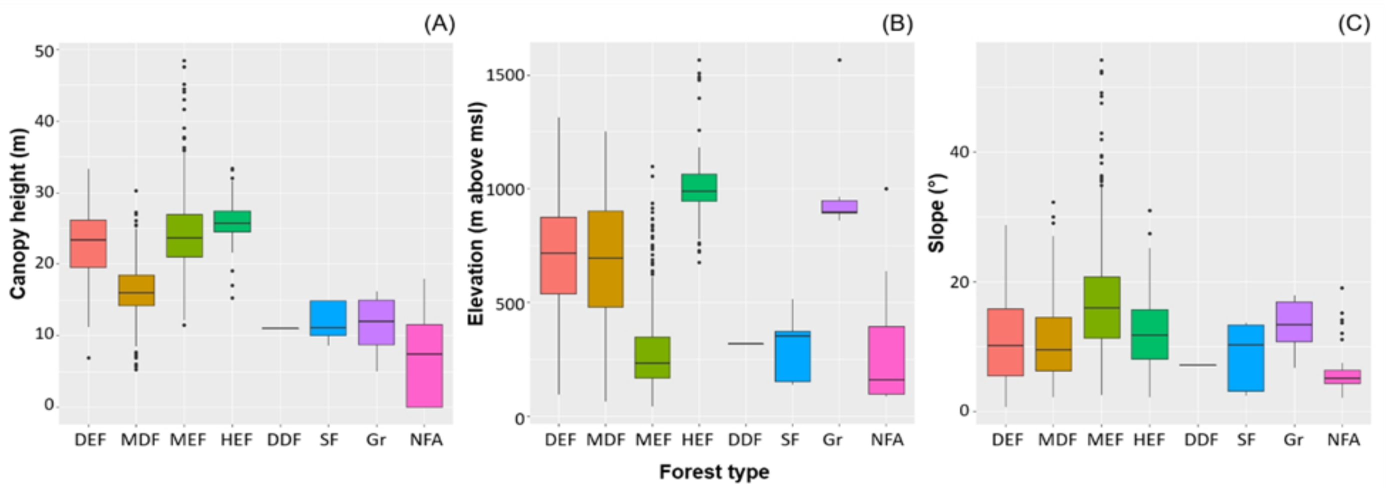

Figure 2 Gaur distribution between different forest type and (A) forest canopy height, (B) elevation, and (C) slope (DEF = dry evergreen forest, MDF = mixed deciduous forest, MEF = moist evergreen forest, HEF= hill evergreen forest, DDF = dry dipterocarp forest, SF = secondary forest, Gr = grassland, NFA = non-forest area i.e. agricultural area and abandoned agricultural land)

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height, 1,100m above mean sea level (msl), and 20 degree of slope .

Habitat suitability

The habitat suitability model showed a high degree of accuracy (AUC = 0.9). The intact forest landscape had the highest relative percentage contribution for gaur suitable habitat, followed by forest type, precipitation seasonality, and forest canopy height, respectively (Table 2). The gaur probability of presence increased when nearest the IFL. The mixed deciduous, dry evergreen, and moist evergreen forest had the highest probability of presence, respectively. The jackknife test of variable importance for the gaur habitat suitable model indicated that the IFL was the highest gain when used in isolation, followed by forest type, forest canopy height, and max temperature of warmest month, respectively (Fig. 3).

Table 2 The relative percentage contributions and permutation importance for environmental variables used in modeling of gaur habitat suitability

Environmental variable	Relative percentage contributions	Permutation importance
Ecological variable		
Distance to intact forest landscape	73.0	15.6
Forest type	12.9	1.9
Forest canopy height	2.6	2.2
Distance to stream	0.1	0.1
Topographic variable		
Elevation	0.5	1.5
Slope	0.2	0.5
Climatic variable		
BIO1: Annual mean temperature	2.2	16.4
BIO2: Mean diurnal range	0.2	1.0
BIO3: Isothermality	2.0	6.2
BIO4: Temperature seasonality	1.0	28.8
BIO5: Max temperature of warmest month	1.3	2.3
BIO12: Annual precipitation	0.2	2.3
BIO15: Precipitation seasonality	3.4	18.6
BIO18: Precipitation of warmest quarter	0.5	2.6

The gaur habitat suitability showed the high probability of suitable habitat located with the large patch area (Fig. 4A). The potential habitat for gaur covered 45,008 km^2 or only 8.8% of the mainland, while the core areas located in suitable area remained 21,415 km^2 (4.2% of the mainland). 36,089 km^2 (80.2% of gaur suitable area) was located inside the PAs, while the around 8,929 km^2 (19.8% of suitable area) was located outside PAs, especially in small forest patches, agricultural area, and abandoned agricultural land (Fig. 4B and Table 3). The results indicated the potential habitat remained in seven forest complexes consists of the Western, Dong Phayayen-Khao Yai, Khlong Saeng-Khao Sok, Kaeng Krachan, Phu Khieo-Nam Nao, Eastern, and Phu Miang-Phu Thong Forest Complex, respectively.

Although the gaur occurred in 11 forest complexes, only seven forest complexes were suitable. Moreover, 20% of the suitable habitat area fell outside PAs and bordered PAs (Fig. 5). Most of these areas were connected to become large patches of area which were probably large enough for gaur to inhabit, although some of these patches were fragmented and small, nearly destroyed areas.

Table 3 Suitable habitat and core area of gaur in Thailand

Gaur habitat	Logistic thresholds	Area (km^2)	Percentage of Thailand[b]	Percentage of PAs[c]	Area located inside PAs	
					Area (km^2)	% of Area
Suitable area	0.2054	45,008	8.8	41.9	36,089	80.2
Core area	0.4415	21,415	4.2	20.0	20,239	94.5

[a]Logistic threshold cut-off value; [b]Mainland area 511,000 km^2; [c]Total PAs area in the mainland 107,458 km^2 (excluding forest parks

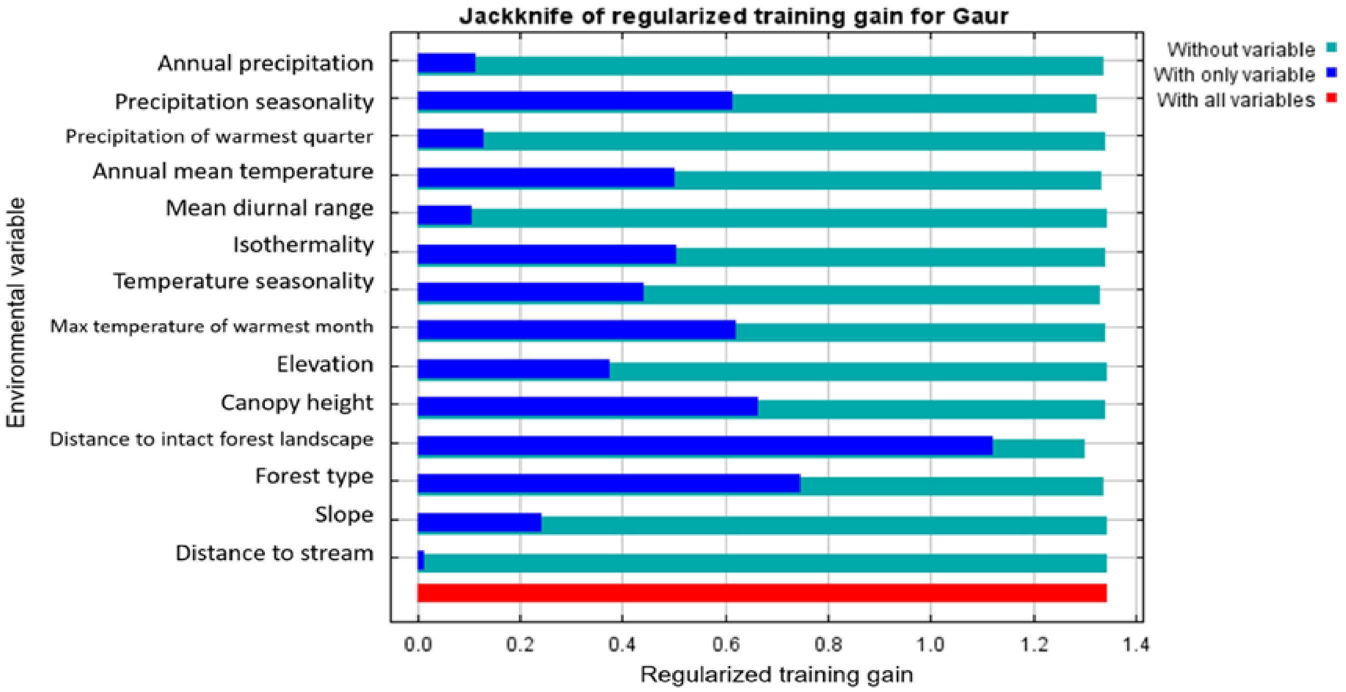

Figure 3 Jackknife analyzed individual predictor variables important in the development of the model to the overall model quality (regularized training gain). The dark-blue bars indicate the gain achieved when including only that variable and excluding the remaining variables; light-blue bars indicate the gain is diminished without the given predictor variable.

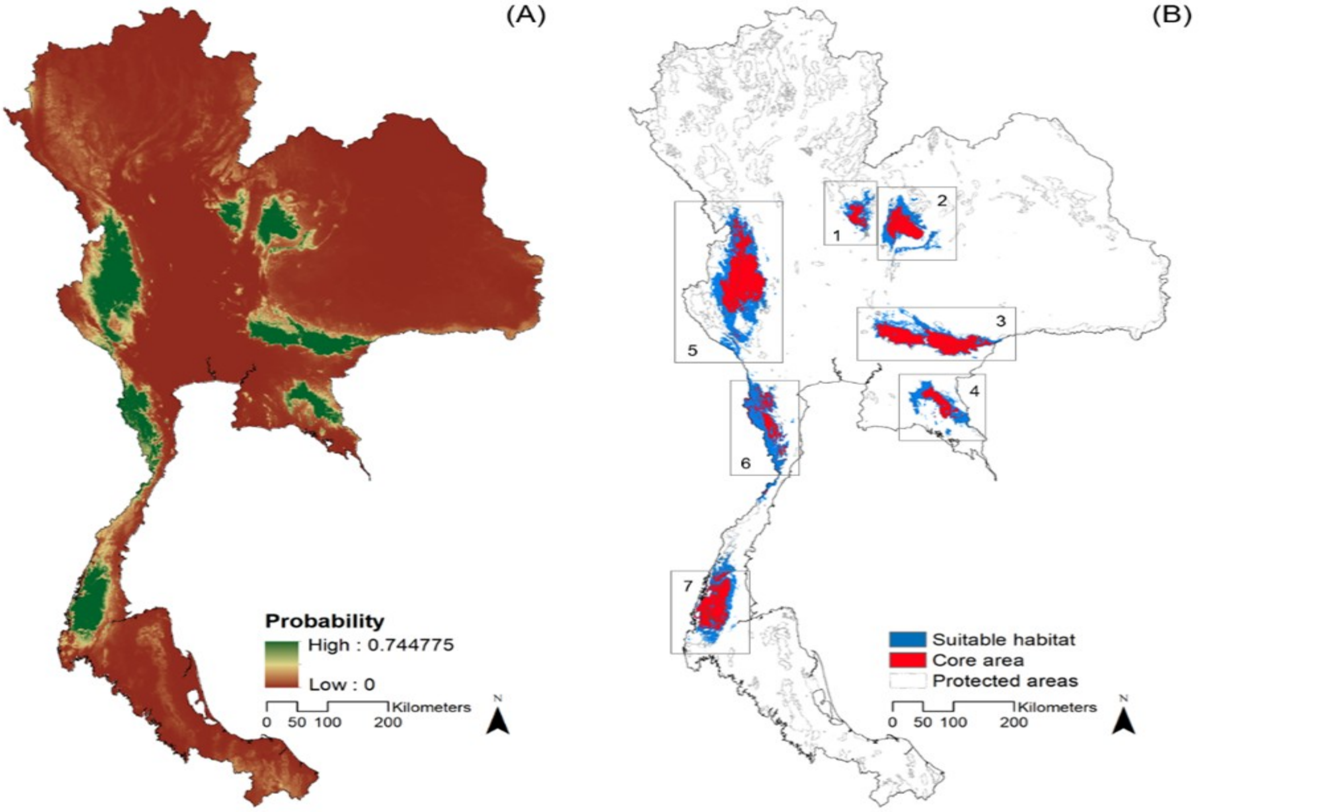

Figure 4 Habitat suitability for gaur (A) Habitat suitability (B) Habitat is classified as suitable habitat and core areas: (1) Phu Miang-Phu Thong, (2) Phu Khieo-Nam Nao, (3) Dong Phayayen-Khao Yai, (4) Eastern, (5) Western, (6) Kaeng Krachan, and (7) Khlong Saeng-Khao Sok Forest Complex

Discussion

Distribution

Currently, gaur occur in 11 forest complexes, which is a decrease from 13 forest complexes in 2010. However, the number of PAs occupied by gaur has increased from 45 in 2010 to 59 in 2020 (Kanchanasaka et al., 2010). This new occurrence could be from the dispersal of gaur population from the adjacent PAs. Another possible reason for the additional areas is the increased protection and patrolling of PAs (National Parks, Wildlife and Plant Conservation Department, personal communication). Presently, gaur are distributed more widely than in the past, but are extirpated from some northern and southern PAs where they were found in 2010. Additionally, Kanchanasaka et al. (2010) reported that gaur increased in abundance in large PAs connected to large habitat patches. The highest abundance within forest complexes were Eastern, Dong Phayayen-KhaoYai, Khlong Saeng-Khao

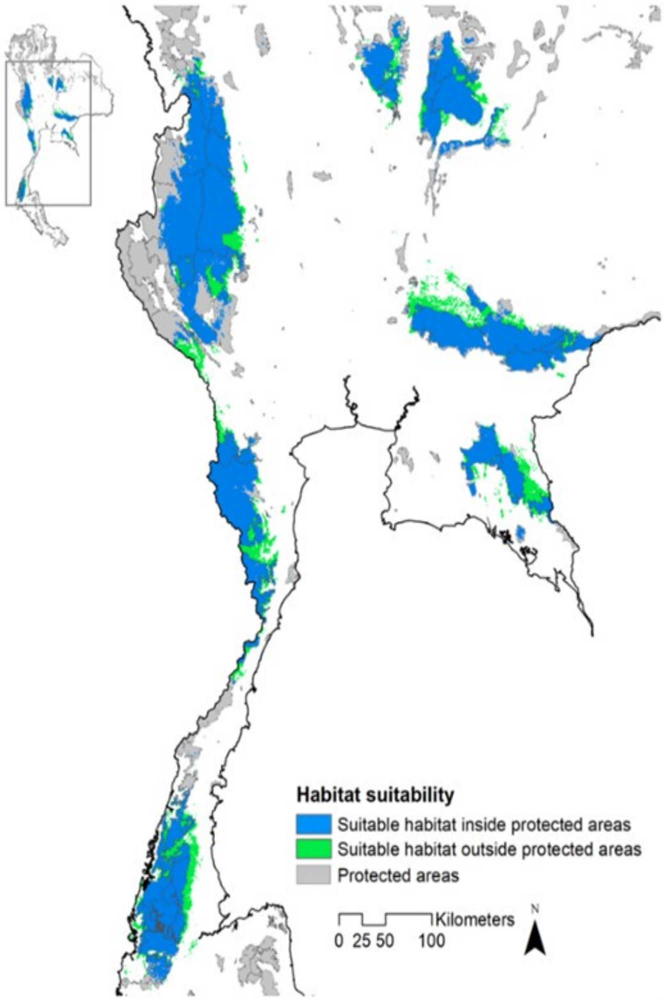

Figure 5 Gaur suitable habitat inside and outside protected areas

Sok, Western, Phu Khieo-Nam Nao, and Kaeng Krachan Forest Complex, respectively. Additionally, a small group of Gaur inhabited areas outside of PAs.

Habitat suitability

Gaur inhabited several forest types and elevations. According to these results, gaur used many elevation levels from 100 m up to 1,100 m above sea level (asl), while the habitat suitability model predicted the highest probability of presence appeared in 900–1,000 m asl. In addition, this research showed the land cover variables (IFL and forest type) are more important than bioclimatic variables for gaur habitat. Meanwhile, Trisurat et al. (2015) discovered the strongest variables associated with gaur presence in northern Thailand were composed of the temperature variables (mean, maximum, and minimum temperate), precipitation of coldest quarter, and distance to road, respectively. However, according to the results of suitable habitat in the Western Forest Complex, gaur are likely to inhabit areas of the shallow slope, closer to the ranger stations and streams, and further from villages (Trisurat et al., 2010). Kanchanasaka et al. (2010) showed that environmental factors were significant to the habitat selection of gaur in Thailand. The suitable area consists of less sloped areas (0–27 degrees), near salt licks, and close to the water sources (less than 6 km distance). The data indicated the gaur's probability of presence was increased when nearest to streams and gaur avoided human disturbed areas. Moreover, the effects of loss of suitable habitat showed that deforestation had a stronger impact than climate change (Trisurat et al., 2015).

Habitat management concern

According to the results of suitable area analysis, huge suitable areas were located outside PAs in agricultural areas and small forest patches in the potential forest complexes for gaur habitat (i.e. Dong Phayayen-Khao Yai, Eastern, Western, Khang Krachan, and Khlong Saeng-Khao Sok Forest Complex). Around 19.8% of the suitable habitat for gaur is at risk because it is located outside PAs which did not proceed to protect the areas. Moreover, the local communities used these areas and natural products in border forest lands and the buffer zones between PAs and villages. Therefore, suitable gaur habitats located outside of PAs were nearly destroyed. Nowadays, agricultural areas have surrounded the edges of PAs and in some places have disturbed the forest areas at the edges of PAs. Additionally, the expansion of agricultural areas, settlements, and roads in Thailand has caused many wildlife habitats to become fragmented, degraded and transformed, especially in the lowland forest (Prayurasiddhi et al., 2013, Namkhan et al., 2020). These landscape changes cause suitable gaur habitat to decrease and as such threaten the gaur populations. The suitable area outside PAs can be an important part of and add great value for gaur conservation. Future gaur habitat management planning should therefore include these areas to manage and maintain the habitat for effective gaur conservation in Thailand.

Acknowledgements

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AUTHOR GUIDLINES

Aim & Scope

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- Materials and methods
- Results
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- Acknowledgements (optional)
- References (Harvard style)
- Figures and tables, presented alongside individual captions (please also send photos and figures in separate files in the highest available resolution)

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The metric system should be used for all measurements and weights with a space between the number and the unit of measurement. Temperature should be expressed as degrees Celsius (^{o}C). Numbers from one to nine should be spelled out except when used with units; e.g. one anoa but ten banteng and 3 km.

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Please use common English names of plants and animals, and adhere to the taxonomy used in the IUCN Red List. At first mention in the main text, give both the common and scientific names (in italics). If possible, also add the local name of the species in the area where you work.

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