TAXONOMY AND CONSERVATION STATUS OF THE SUIFORMES - AN OVERVIEW

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The Suborder Suiformes consists of three extant families: the Suidae, Dicotylidae and Hippopotamidae. These are now thought to comprise at least 19 living species, of which all but three species- the collared peccary *Tayassu tajacu*, the red river hog *Potamochoerus porcus* and the bush pig *P. larvatus* - are threatened to varying degrees, either throughout their ranges or because they include one or more threatened subspecies. Even the widely distributed and often locally abundant Eurasian wild pig (*Sus scrofa*), common warthog (*Phacochoerus africanus*) and white-lipped peccary (*T. pecari*) all have threatened subspecies, which merit increased conservation attention. By comparison, the status of a few taxa, such as the pigmy hog (*S. salvanius*), the recently recognised Visayan warty pig (*S. cebifrons*) and the Nigerian race of pigmy hippo (*Hexaprotodon ivoriensis heslopi*), are critical; whilst others, like the enigmatic Vietnam warty pig (*S. bucculentus*), may already have followed the three species of Madagascar dwarf hippos (*Hippopotamus laloumena*, *H. lemerlei* and *Hexaprotodon madagascariensis*) and the Cape race of the "desert" warthog (*P. a. aethiopicus*) into extinction. Recent revisions of the taxonomy of these animals are summarized in table 1 and the present known conservation status of all currently recognized taxa are summarized in table 2.

Table 1. Taxonomy of living and recent suiformes.

Total: superfamilies 2, families 3, subfamilies 3, genera 9, species (provisionally 22 (of which 3, possibly 4, are extinct), subspecies (provisionally) > 65 (of which at least 1, but possibly 2 or more, are extinct).

Order: Artiodactyla (comprising three suborders: Suiformes, Tylopoda, and Ruminantia)
Suborder: Suiformes (comprising two superfamilies and three families, as follows):

Superfamily: Anthracotheroidea

Family: *Hippopotamidae*
(no separate subfamilies, but two genera and two living and three recently extinct species, as follows):

Genus: *Hippopotamus*	**Species**: *H. amphibius* (5 ? ssp) - Common Hippo
	H. laloumena - Madagascan Hippo (extinct)
	H. lemerlei - Madagascan Dwarf Hippo (extinct)
Genus: *Hexaprotodon* (=*Choeropsis*)	**Species**: *H. liberiensis* (2ssp) - Pygmy Hippo
	H. madagascariensis - Madagascan Pygmy Hippo (extinct)

SuperFamily: Suoidea (comprising two families, seven genera and ≤ seventeen species, as follows):

Family: Dicotylidae (no separate subfamilies, but two genera and three species, as follows):

Genus: *Tayassu*	**Species**: *T. tajacu* (14 ? ssp) - Collared Peccary
	T. pecari (c. 5 ssp) - White-lipped Peccary
Genus: *Catagonus*	**Species**: *C. wagneri* (0 ssp) - Giant or Chacoan Peccary

Family: Suidae (comprising three subfamilies, five genera and ≤ fourteen species, as follows):

Subfamily: Suinae - the "true" pigs	
Genus: *Sus*	**Species**: *S. scrofa* (c. 17 ssp) - Eurasian Wild Pig
	S. salvanius (0 ssp) - Pygmy Hog
	S. bucculentus - Vietnam Warty Pig (extinct ?)
	S. verrucosus (2 ssp) - Javan Warty Pig
	S. barbatus (3 ssp) - Bearded Pig
	S. cebifrons (0 ? ssp) - Visayan Warty Pig
	S. philippensis (? ssp) - Philippine Warty Pig
	S. celebensis (0 ? ssp) - Sulawesi Warty Pig
Genus: *Potamochoerus*	**Species**: *P. larvatus* (>3 + ? ssp) - Bushpig
	P. porcus (0 ssp) - Red River Hog
Genus: *Hylochoerus*	**Species**: *H. meinertzhageni* (4 ssp)- Forest Hog
Subfamily: Phacochoerinae - the warthogs	
Genus: Phacochoerus	**Species**: *P. aethiopicus* (2 ssp, 1 extinct) - Desert Warthog
	P. africanus (c. 4 ssp) - Common Warthog
Subfamily: Babirousinae - babirusa	
Genus: *Babyrousa*	**Species**: *B. babyrussa* (4 ? ssp, 1 possibly extinct) - Babirusa

Table 2. Summary of present conservation status of Suiformes.

Taxon	Current Conservation Status
Family Hippopotamidae	
Hippopotamus amphibius	2*
Common Hippopotamus	
(subspecific taxonomy requires review)	
Hippopotamus laloumena	Extinct
Madagascan Hippopotamus	
Hippopotamus lemerlei	Extinct
Madagascan Dwarf Hippopotamus	
Hexaprotodon liberiensis	
Pygmy Hippopotamus	
H. l. liberiensis	4
H. l. heslopi	Indeterm. (prob.6)
Hexaprotodon madagascariensis	Extinct
Madagascan Pygmy Hippopotamus	
Family Dicotylidae	
Tayassu tajacu	1-2*
Collared Peccary	
(subspecific taxonomy requires review)	
Tayassu pecari	
White-lipped Peccary	
T. p. ringens	3
T. p. spiradens	3 - 4
T. p. equatorius	Indeterm.
T. p. pecari	1 - 2
T. p. albirostris	1
Catagonus wagneri	5
Chacoan Peccary	
Family Suidae	
Phacochoerus aethiopicus	
Desert Warthog	
P. a. aethiopicus	Extinct
*P. a. delamerei***	4
Phacochoerus africanus	
Common Warthog	
(subspecific taxonomy provisional)	
P. a. africanus	1
P. a. aeliani	Indeterm. (prob. 5)
P. a. massaicus	1
P. a. sundevallii	1 - 2
Hylochoerus meinertzhageni	
Forest Hog	
H. m. meinertzhageni	3 - 4
H. m. rimator	3 - 5
H. m. ivoriensis	5
H. m. ssp. (S. Ethiopia)	Indeterm.
Potamochoerus larvatus	
Bushpig (subspecific taxonomy provisional)	
P. l. hassama	2
P. l. (?) *somaliensis*	2
*P. l. koiropotamus***	1
P. l. larvatus (introduced ?)	1 - 2
P. l. hova (introduced ?)	1 - 2

(**Family Suidae**, continued)

Potamochoerus porcus Red River Hog	1
Sus scrofa Eurasian Wild Pig	
S. s. *scrofa*	1
S. s. *meridionalis*	2 - 3
S. s. *algira*	2
S. s. *attila*	1
S. s. *lybicus*	1 - 2
S. s. *nigripes*	1
S. s. *davidi*	1
S. s. *cristatus*	1
S. s. *affinis*	1
S. s. ssp. (Bopeta, Sri Lanka)	Indeterm.
S. s. *sibiricus*	1
S. s. *ussuricus*	1
S. s. *leucomystax*	2
S. s. *riukiuanus*	4 - 5
S. s. *taivanus*	2 - 3
S. s. *moupinensis*	1
S. s. *vittatus*	1
Sus salvanius Pygmy Hog	6
Sus bucculentus Vietnam Warty Pig	Extinct ?
Sus verrucosus Javan Warty Pig	
S. *v. verrucosus*	4
S. *v. blouchi*	4
Sus barbatus Bearded Pig	
S. *b. barbatus*	2
S. *b. oi*	3
S. *b. ahoenobarbus*	3
Sus cebifrons Visayan Warty Pig	5 - 6**
Sus philippensis Philippine Warty Pig	3**
Sus celebensis Sulawesi Warty Pig	1 - 2**
Babyrousa babyrussa Babirusa	
B. *b. babyrussa*	5
B. *b. celebensis*	4
B. *b. togeanensis*	5
B. *b. bolabatuensis*	Indeterm. (Extinct?)

Key:

* = Future taxonomic reviews likely to result in one or more subspecies being included in a more threatened category.

** = Additional taxonomic material from selected areas likely to indicate taxon comprises/includes two or more subspecies.

Status category definitions:

1 = '**Widespread and abundant**';

2 = '**Known or believed relatively secure**' (*i.e.* widespread at low density, but abundant in some areas or limited distribution but abundant and not thought to be threatened, and/or well represented in protected areas);

3 = '**Potentially at risk or Rare**' (*i.e* not thought to be immediately threatened, but has restricted distribution or is widespread but nowhere abundant, but occurs in some protected areas);

4 = '**Known to be at risk or Vulnerable**' (*i.e.* has restricted distribution an/or limited ecological tolerance, known to be threatened by habitat destruction/disturbance, hunting pressure or other factors, over the majority of its range, and/or is inadequately represented in reserves);

5 = '**Seriously threatened or Endangered**' (*i.e.* highly restricted and/or fragmented distribution; all known population declining and status likely to become critical in the near future);

6 = '**Critically endangered**' (*i.e.* only one or a very few, small populations, which are unlikely to survive unless urgent action is taken to redress causative factors);

Extinct = '**Extinct**'.
Indeterm. = Indeterminate: '**Taxa considered to be Threatened**' (*i.e.* status categories 3 to 6 above, but available data insufficient to determine appropriate categorisation.

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All data modified after
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CONSERVATION GENETICS OF THE GENUS Sus

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Abstract: Recent technical advances in biochemical and molecular biology make it possible to study the population genetics and phylogenetics using biological samples collected undestructively during field researches, or collected from museum specimens. Applications of conservation genetics of the genus *Sus* range from the definition of a molecular phylogeny of the Suiformes to the description of boundaries between species and subspecies and the identification of the origins of wild, feral, domestic or cross-breeded populations. In this paper I review information on the genetic structure of west European wild pig populations, and present recent findings on nucleotide variability of mitochondrial DNA genes. The amplification of DNA through the polymerase chain reaction and following nucleotide sequencing of selected mitochondrial DNA genes, are effective methods which can be applied to describe patterns of within- and among- species genetic variability in the Suidae.

Keywords: *Sus scrofa,* Suidae, Molecular biology, Populations, Hybridization, Mitochondrial DNA.

IBEX J.M.E. 3:6-12

1. Introduction

The Suidae comprise a number of species of great biological interest and economical value. Suids interact with human activities, because they are domesticated, reared, crossed, translocated, hunted, eated, and in certain cases, venerated or persecuted. They have a place in many traditional cultures and in the everyday life of millions of humans. Such notwithstanding, the biology of many species is still poorly known, and their management and conservation cannot take advantage of the necessary basic information.

Conservation genetics, the application of population (and in particular small populations) genetic models and biochemical and molecular technologies to conservation biology, is aimed to preserve biodiversity at the different levels it is organized (genes, populations, species, evolutionary lineages), and can be applied to address a wide range of still open questions about the biology of the Suidae.

First of all we need to develop a molecular phylogeny of the Suidae, which must integrate non-molecular knowledges, and constitute the background within which to describe the time scales and patterns of their evolution. This framework is necessary to delineate species (as well as subspecies and populations) boundaries and relationships. Just to mention a few examples: the wild pig fauna of entire regions (e.g., the Philippines) is poorly known, and species/subspecies boundaries have not been clearly delineated so far (Oliver *et al.*, 1993). The patterns of speciation and partitions of genetic diversity among populations of the African suids await description (Grubb, 1993), as well as it is not known the extent of genetic divergence among the 3 (or more ?) subspecies of the babirusa (Macdonald, 1993). Captive breeding is frequently mentioned as a necessary option to secure the preservation of some endangered suids (first of all, the highly endangered Pygmy hog, *Sus salvanius*; Oliver & Deb Roy, 1993). Captive propagation with the perspective of reintroduction in the wild, needs the preservation of the largest possible fraction of the species' gene pool. Quantification of existing gene diversity within small populations, breeding plans aimed to retain the maximum possible gene diversity and to avoid inbreeding and inbreeding depression are efforts required to reconstitute viable populations in the wild.

Suids represent a resource for human populations. Two species have been domesticated (*Sus scrofa* and *S. celebensis*; Groves, 1981), and other are easily bred in captivity (National Research Council, 1983). Most populations of the Eurasian wild pig are intensively exploited and managed, but the genetic, demographic and ecological impacts of intense hunting pressure and animal translocations are still poorly known. In selected cases it will be important to determine the origins of feral pig populations, and evaluate eventual genetic peculiarities, because, besides the obvious problems they pose as pests in exotic habitats, they could have some value for conservation and as possible source of human incomes (Brisbin, 1990), once appropriately managed and controlled.

2. Population genetics of *Sus scrofa.*

Multilocus Protein (enzymes and non-enzymatic proteins) Electrophoresis (MPE) is an inexpensive and simple technique, widely used to study population genetics and phylogenetics of many animal species. Proteins migrate in an electric field because some aminoacids are charged. If a point mutation (or a deletion, an insertion) changes the aminoacid composition of a protein, it will change (in about 30% of the cases) its net electric charge, and its rate of electrophoretic migration will be different and distinguishable from the original molecular form. Appropriate staining recipes will, then, reveal allelic variation at single structural loci. Therefore, it is possible to identificate and count genotypes and alleles, compute within-population estimates of gene diversity, between-population genetic distances, and work up a number of population genetic models like Hardy-Weinberg equilibrium, linkage disequilibrium, gene flow, geographical population structuring, and so forth. Limitations of protein electrophoresis derive from the low mutation rates at structural loci, and from possible selective value of some allelic variants. lt is not expected any aminoacid substitution in populations which were recently separated, and the recovery of heterozygosity is slow after a recent bottleneck (Lande & Barrowclough, 1987). In some cases proteins may be not sufficiently variable to allow discriminating among recently isolated populations.

Some populations of the Eurasian wild pig have been recently studied, using karyotype mapping (Bosma *et al.*, 1984), blood groups (Kurosawa *et al.*, 1979) and MPE (Tanaka *et al.*, 1983; Randi *et al.*, 1989). Results concordantly showed the existence of an east-west clinal variation in allele frequencies, which produced dendrograms separating the eastern from the western phenotypically recognized subspecies (Kurosawa *et al.*, 1979). Studies of restriction fragment length polymorphism of the mitochondrial DNA (Watanabe *et al.*, 1986; Lan & Shi, 1993) supported these conclusions. The observed genetic gap is roughly correspondent to the distributions of the two prevalent karyotypes, 2n = 36 and 2n = 38 (Bosma *et al.*, *op.cit.*). An insufficient sampling of wild pig populations along an east-west transect from central Asia to central Europe prevents us to understand the origins of these concordant patterns of genetic variation: the apparent clinal variation, and the apparent main genetic gap could be the results of recent dispersal from different and anciently isolated centers of origins, and/or of isolation by distance acting on populations with restricted (at least across some areas) gene flow. Multivariate morphometrics of skull measures indicated a more or less linear north-east to south-west dimensional cline, perhaps mainly due to environmental effects and adaptations to food availability on growth rates and adult body size (Randi *et al.*, 1989). Blood groups and MPE showed comparatively greater genetic distances between Asian and European-American domestic pig breeds (Tanaka *et al.*, *op.cit.*), supporting the idea of polyphyletic domestication (Oliver *et al.*, 1993). Some of the modern pig breeds originated from Asian stocks or possibly from crosses between Asian and European pig strains (Ollivier & Sellier, 1982). These informations can be used to investigate the population genetic structure and the putative origins of local wild pig populations, particularly in cases where translocations and/or introductions could have originated populations of uncertain origins or unknown genetic make up. We have used MPE to describe genetic variability in some west European wild pig populations (*S.s. scrofa*), and to assess the genetic structure of the formerly described ltalian subspecies (*S.s. meridionalis*, the Sardinian wild pig, and *S.s. majori*, the Maremma wild pig; Randi *et al.*, 1989). Clustering multilocus pairwise genetic distances indicated small divergence among *S.s. majori* and other west European wild pig populations (Fig.1). These results prompted us to reject the validity of the subspecies *S.s. majori*, which must be considered, at best, an ecotype phenotypically adapted to a Mediterranean type habitat. Within relatively short geographic distances, and in contrast with the presence of significant body size differences, allozyme variability is often not structured enough to evidence significant population gaps. We have recently studied genetic variability in some Bulgarian wild pig populations sampled in localities where were described (Genov *et al.*, 1991) the existence of different morphological phenotypes: a larger one living in the northern plains, and a smaller one occurring in the southern mountains. MPE showed results concordant with morphometrics (Fig. l), but allele divergence among northern and southern populations was small (Randi *et al.*, 1992). Such small distances are not necessary attributable to genetic isolation and absence of gene flow, but most probably to genetic disequilibrium and drift, with consequent ran-

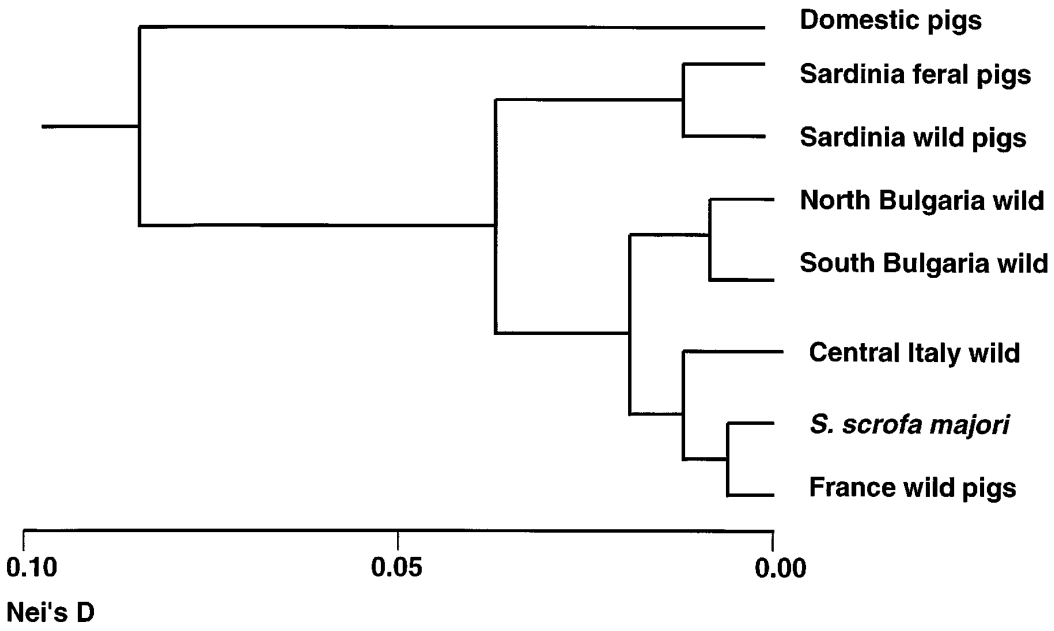

Figure 1 - UPGMA dendrogram obtained by clustering allozyme Nei's genetic distances among some west European wild, feral and domestic pig populations.

dom fluctuations in allele frequencies, due to the genetically small effective size of recently established populations. We observed greater genetic distance values separating wild and feral Sardinian pigs from other west European wild pig populations, thus validating the subspecies *S.s. meridionalis* (Fig. 1). The locus 6PGD is a possible marker of hybridization between wild and domestic pigs. This locus was polymorphic in almost all the studied pig breeds (Franceschi & Ollivier, 1981), while it was monomorphic in all the studied west European wild pig populations (Randi *et al.*, 1989). It was monomorphic in Sardinian ferals, as well as in the Smoky Mountains pigs (USA), which originated, at least in part, from introduced European wild pigs (Smith *et al.*, 1980).

We hypothesized that 6PGD is polymorphic in Asian wild pigs and that this polymorphism was introduced in modern pig breeds through hybridization (Randi *et al.*, 1989). This hypothesis has been supported by Kurosawa and Tanaka's paper (1991) showing extensive 6PGD polymorphism in *S.s. leucomystax* and *S.s. riukiuanus* (with some monomorphic populations, possibly due to recent bottlenecks and isolation), and *S.s. taivanus*. 6PGD and other allozyme polymorphisms (PGM, PGI) are linked to artificially selected meat production characters (e.g., in the linkage group PGI-HAL-6PGD; Rasmusen, 1983), and can show allele frequency divergence among wild and domestic pigs. These enzyme loci could be used to locate the geographic origins of certain wild pig stocks, and to detect hybridization and introgression of domestic genes at the population level.

3. Mitochondrial DNA nucleotide sequencing

Using Restriction Fragment Length Polymorphisms (RFLP) we can estimate rates of nucleotide substitutions through restriction endonuclease digestions of purified target DNA, followed by detection of restriction fragments by hybridization with a cloned labelled probe. The main advantage of this method (as well as of most DNA methods) is given by the possibility to choose the appropriate target DNA sequence to be studied. DNA is not a homogeneous strip of nucleotides, but is a structured macromolecule with single copy structural genes and repetitive DNA, with genes evolving at a low pace, or hot spots of mutation and recombination, *i.e.*, sequences with high rates of molecular evolution. Using cloned hypervariable sequences as probes, it is possible to identificate the single individual (DNA fingerprinting), while using slowly evolving sequences as probes (*e.g.*, RNA genes), it is possible to study phylogenetic relationships among very divergent taxa. The main drawback of RFLP method is the need of good quality and abundant target DNA, which cannot so easily be obtained during field work or undestructively collected from endangered species. Recently direct nucleotide sequencing has become feasible at the population level, thanks to the discovery of the possibility to amplificate DNA using the polymerase chain reaction (PCR). The target DNA sequence is amplified *in vitro* using two oligonucleotide primers (synthesized *in vitro*). One primer is complementary to the sequence flanking one end of the target DNA, while the other primer is complementary to the other flanking sequence. The presence of free nucleotides and of a thermostable DNA polymerase, results in the extension of both primers, which copy the target DNA sequence. PCR is performed in an automated machine, the thermal cycler, which controls a 3-temperature cycle: DNA denaturation, primer hybridization, DNA extension. This cycle can be repeated 20-50 times, doubling the quantity of target DNA each cycle, and producing, at the end, a million times the amount of target sequence present initially. This pure DNA can be directly sequenced. Nucleotide sequences produce enormous amounts of genetic information: the single nucleotide is the character (with four possible states), and sequences are exactly comparable through different laboratories. Sequences are cumulative information, and DNA databases are exponentially growing.

One of the most informative application of both RFLP and PCR in population and conservation genetics is the study of mitochondrial DNA (mtDNA). MtDNA is present in the mitochondria, it is maternally inherited (through the oocytes), it is haploid and does not recombine. MtDNA shows (at least in mammals) an average rate of molecular evolution 5-10 times faster than average single copy nuclear DNA. This makes mtDNA the molecule of choice to study genetic divergence among conspecific populations, and to determine maternal phylogenies. We are running a project to sequence selected mtDNA genes in the Suidae, with the aim: 1) to identificate reliable slow-evolving regions, which can retain unambiguous phylogenetic signals and which can allow reconstructing the evolutionary patterns of taxa within the Suiformes; 2) to identificate fast-evolving hypervariable regions, which can be used to describe patterns of genetic variability at the interface between conspecific and intraspecific populations. We have designed oligonucleotide PCR primers to amplificate and to sequence the entire mitochondrial cytochrome b (CYB), a protein-coding gene, with intermediate rate of sequence evolution in mammals, and the mitochondrial control region (D-LOOP), a non-coding region involved in the replication of the mtDNA, and usually evolving at high rate in mammals. We have sequenced about 600 bp of the CYB and 500 bp of the D-LOOP in several species of the Suidae and in samples of different populations of west European wild pig. The main results (Fig. 2) indicate that:
1) CYB showed low sequence variation in *S. scrofa*, and divergence among species was due to point mutations only. Preliminar calibration of the CYB molecular clock agrees with presumed paleontological information, and other molecular findings, on times of speciation within the Suiformes, and suggests that CYB is a suitable gene to obtain reliable phylogenetic signals at the ordinal level. 2) D-LOOP showed extensive sequence reorganization among different species, due to both point mutations and duplications of repeated motifs, as well as to insertion or delection of single bases. Therefore, D-LOOP seems to be an unreliable source of phylogenetic information in the Suidae. West European wild pig samples showed a surprisingly low level of sequence variation at the D-LOOP. Most populations shared the same (CYB + D-LOOP) mtDNA haplotype, including domestic pigs, and some Sardinian wild and feral pigs. Sequence divergence within west European *S. scrofa* (wild and domestic) is less than 1%, and we have not found any mtDNA fixed sequence difference between wild and western domestic pigs. About 60% of the studied Sardinian wild pig specimens showed a different mtDNA haplotype (0.3% nucleotide divergence from the common haplotype), which supports the indications of genetic peculiarity of the Sardinian pig population, and further confirms his subspecific status.

4. Conclusions

The analysis of patterns of nucleotide sequence divergence, both among- and within-species, is a preliminar step, necessary to identificate mtDNA genes which could be used as a relia-

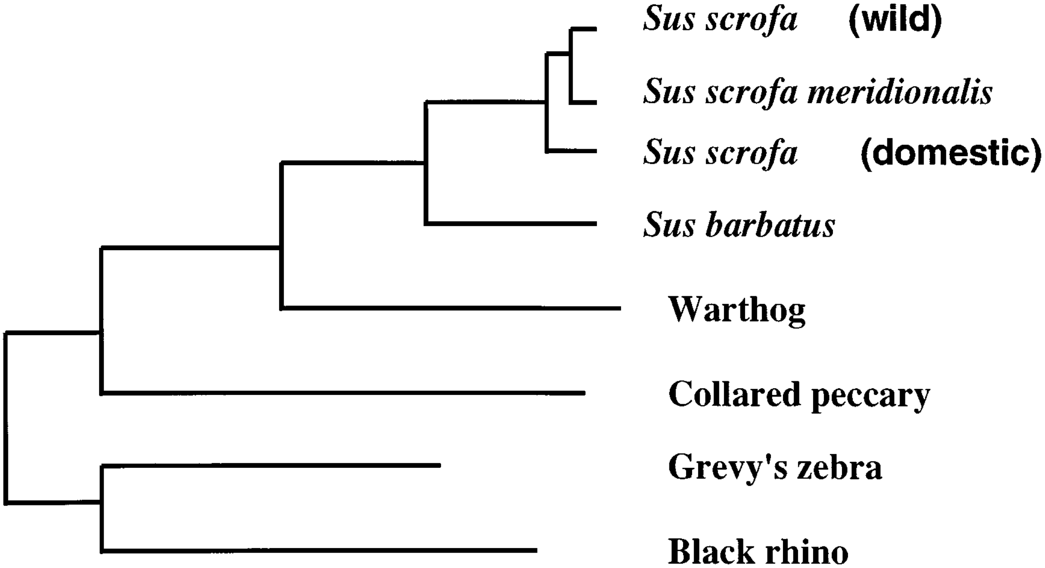

Figure 2 - Neighbor-joining tree showing phylogenetic relationships among Suiformes, obtained using nucleotide sequences of the mitochondrial DNA cytochrome b gene.

ble source of information for intraordinal phylogenetics or population genetics studies in the Suiformes. The mtDNA CYB is a protein-coding gene, and as expected it is structurally conserved across species, as consequence of evolutionary constraints. In the Suiformes CYB seems to evolve at approximately 2% nucleotide substitutions per million year, accordingly with the average rate of mtDNA molecular evolution in mammals. Our findings suggest that CYB can be reliably used to describe times of evolution and pattern of phylogenetic divergence in the Suiformes. CYB will be particularly useful to individuate phylogenetic gaps due to pre- or post-Pleistocene isolation of evolutionary lineages, and could be successfully applied to disentangle species relationships in areas, like the Philippines, of particular biogeographic complexity. The D-LOOP appears to evolve at a faster rate in the Suiformes. It is mainly a non-transcribed region, with lower constraints to both genome size and structural reorganization. Correct alignment of reorganized D-LOOP regions could be difficult in anciently separated taxa, and consequently the D-LOOP could be reliable to track phylogeny at lower ranks only.

Some portions of the D-LOOP should be hypervariable within species, and therefore should be informative for the description of phylogeographic relationships among conspecific populations or clusters of closely related species. The 500 bp of the D-LOOP we have sequenced in west European wild pig samples, so far, showed a surprisingly low rate of nucleotide variability. Genetic variability among populations was concordantly low at nuclear allozyme loci, mtDNA CYB, as well as at mtDNA D-LOOP, supporting the idea of a recent colonization of western Europe by *S. scrofa* populations which survived a relatively intense bottleneck. These findings furtherly stress the existence of high phenotypical plasticity in *S. scrofa*, which favours great adaptability to very different habitat and food conditions, and suggest caution in using morphometry as a tool for intraspecific taxonomy. Within such a framework, it is noteworthy the presence of a peculiar mtDNA haplotype in about 60% of the studied Sardinian wild pigs. Pigs (as well as most of the present large vertebrates) were most probably introduced by man in Sardinia (Groves, 1989). The observed genetic heterogeneity of the Sardinian pig population could have been originated from multiple introductions of pigs of different geographic origins. The peculiar mtDNA Sardinian haplotype has not been detected in any other west European wild pig population, so far. lt could represent the original mtDNA haplotype introduced in Sardinia, probably through semi-domesticated pigs from the Middle East. The other mtDNA haplotype detected in the Sardinian pig population is the common west European pig mtDNA haplotype, which could have been introduced in Sardinia later. This hypothesis points out to two problems. First of all we wish to track the geographic origin and distribution of the Sardinian mtDNA haplotype, with a particular attention to the status of the wild pigs of Corsica and Andalusia, which are currently described as *S.s. meridionalis* (Groves, 1981). The second one has more relevant implications for conservation. The Sardinian pig population is a genetically mixed one. lt is probable that the actual Sardinian pig population is a patchwork of ancient feral pigs (probably originated in the Middle East), which have been introgressed with recent western domestic pigs. If so, we need to analyse this patchwork, mapping haplotypes occurence and frequencies, and enforce the preservation of ancient Sardinian pigs (the true *S.s. meridionalis*) in the areas which will be eventually discovered to be unpolluted.

Concordantly with karyotypes, protein markers and mtDNA RFLP, we expect that mtDNA nucleotide sequences will show greater divergence among Asian and European wild pig populations, as well as domestic pig breeds (work in progress). The individuation of fixed mtDNA sequence differences between different wild pig populations, or between wild and domestic pig breeds will greatly aid the analysis of the genetic origins of managed wild pig populations, as well as the individuation of wild x domestic crosses.

MtDNA is maternally inherited and can characterize maternal ancestries only. PCR can be used to perform a very sensitive fingerprinting analysis through the amplification of microsatellites. Microsatellites consist of 10-50 copies of 1 to 6 bp repeats, which are randomly interspersed in all eucariotic DNAs. There is an enormous number of microsatellites and, as many microsatellites have 4 or more alleles of different length (generated probably by asymmetrical crossing-over), they can describe an enormous amount of variability. These repeats are flanked by DNA with unique sequences, which can be used for locus-specific priming for PCR amplification. Microsatellites can be used as fingerprinting, to detect hybrids if parentals are fixed for different alleles, and for population genetics, if population divergence has been very recent. We can take advantage of the great number (probably more than 400) microsatellite loci which have been described in the domestic pig (Rohrer *et. al.*,1994), and that work perfectly on wild pigs' DNA (unpublished results).

One of the most important advantages of PCR is that it makes possible to amplify very small quantities of DNA (in theory starting from a single DNA molecule), also if recovered in very bad conditions. DNA suitable for PCR can be obtained from almost any kind of small samples (one drop of blood, one hair root, a few square millimeters of skin biopsy), also if in very bad state of preservation (old museum skins, old bones, archaeological remains). Fresh and old samples can be preserved at room temperature in absolute ethanol, without necessity to frozen them. It is therefore possible to collect samples for PCR amplification and DNA sequencing as by-product of many field work projects, as well as from museum specimens.

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DATA ON THE BIOCHEMICAL-GENETICAL POLYMORPHISM OF WILD BOAR IN HUNGARY

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Keywords: Wild boar, *Sus scrofa,* Suidae, Polymorphism, Enzymes, Isoenzymes, Morphometry, Europe.

IBEX J.M.E. 3: 13-14

1. Introduction

Relatively few data are available on the relationships between morphometrical parameters and biochemical-genetical attributes of Wild boar (*Sus scrofa*). Mostly the growing patterns of different parameters were analysed and few results were presented on the correlations and allometry of these characteristics. Better management of Wild boar populations requires more data about the morphological and especially about the genetical characteristics of this species. For this it is important to map the genetical structure of different free-living stocks and to designate the most valuable ones.

The purpose of this study was to evaluate the biochemical variability and differentiation of Wild boar populations in Hungary. The research program covered the following areas:

- Evaluation of biochemical methods for the analysis of enzyme-polymorphism in Wild boar.
- Search for polymorphic enzymes in Wild boar populations to detect the most polymorphic enzymes and investigation of frequent allele variations. The year-to-year variability of enzyme-polymorphism and morphological parameters were also surveyed.
- The relationships between morphological parameters (body weight-body length, body weight-height at shoulder, body weight-circumference of chest) and comparison of sex- and age-dependent variations were estimated by statistical methods.

2. Material and Methods

Body weight, body length, height at shoulder and circumference of chest data of shot animals (n=188) from both sexes were collected in the 1991/92 and 1992/93 hunting seasons. Heart, liver and kidney tissue samples were taken from the animals during evisceration and the samples were stored deep frozen until the laboratory processing.

The following enzymes were investigated: Malic-enzyme (ME, E.C. 1.1.1.40), Isocitrat-dehydrogenase (IDH, E.C. 1.1.1.42), Acid-phosphatase (ACP, E.C. 3.1.3.2), Catalase (CAT, E.C. 1.11.1.6), Hexokinase (HK, E.C. 2.7.1.1.), Glucose-dehydrogenase (GDH, E.C. 1.1.1.47). Electrophoretic and staining procedures were completed according to routine methods described in the literature (Hartl & Höger, 1986 *modified by* Ernhaft, 1991). Polymorphism and heterozygosity were determined by horizontal starch-gel electrophoresis and enzyme-specific procedures for five isoenzymes.

3. Results and discussion

The routine electrophoretic and staining methods used in Red deer studies proved to be appropriate for Wild boar. Similarly to Red deer the homogenization could be omitted which quickened the laboratory processes.

Polymorphic alleles were found in the ME-1, IDH-2, LDH-2, ACP-1, ACP-2 and HK loci. ME-1 and IDH-2 were the most variable isoenzyme loci studied. No polymorphic differences were found between the samples of 1991/92 and 1992/93 seasons.

The most important correlations are presented in table 1. No morphometrical differences were shown between the samples of 1991/92 and 1992/93 season.

On the basis of the isoenzymes the biochemical and genetical characteristics of Wild boar and domestic pig were also compared. Lower biochemical-genetical variability of domestic pigs was found and the allelic variation of ME-1, IDH, GDH, ACP-1 in Wild boar was higher than in domestic pigs.

Table 1. Regression slopes and correlation coefficients for body size parameters.

Parameters	Slope of regression (b)		Correlation coefficient (r)	
	1991	**1992**	**1991**	**1992**
Body weight - body length	0.53	0.49	0.79	0.74
Body weight - height at shoulder	0.20	0.23	0.41	0.48
Body weight - circumference at chest	0.46	0.52	0.84	0.80

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GENETIC CHARACTERIZATION OF SOME POPULATIONS OF WILD BOAR (Sus scrofa scrofa) IN PIEDMONT (ITALY)

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Abstract: Electrophoretic data were obtained from 200 wild boars hunted in Piedmont mountains and were compared with those from other feral populations.

Keywords: Wild boar, *Sus scrofa scrofa,* Suidae, Population genetics, Biochemical genetics, Polymorphism, Europe, GPI, PGD.

IBEX J.M.E. 3:15-16

1. Introduction

In Piedmont, following dramatic environmental modifications, the Wild boar diffused rapidly since the early sixties also as a consequence of absence of predators, decrease of cultivation, and transformation of cattle, sheep and goats breeding techniques, particularly in mountain zones. Some role is also due to introduction for hunting purposes of crosses with domestic pig and of wild boars from Eastern Europe. Therefore we have now a well adapted animal which sometimes presents biometrical traits similar to those of domestic pig. However, biometrical traits, being multifactorial, are only in part expression of gene activity, being heavily influenced by environment. Instead biochemical polymorphisms are useful markers to study the genetic structure of a population, because they are controlled by genes on which the environmental influence is almost null.

2. Material and methods

The samples (liver, heart, kidney and diaphragm) come from 197 wild boars hunted during 1990-1992 in different mountain areas of Piedmont and from 26 domestic pigs from a slaughterhouse as a control. By means of horizontal starch gel electrophoresis the loci GPI, PGD, LDHA, LDHB, ADA1, ADA2, ME1, ME2, MDH1, MDH2, IDH1, IDH2, SODA, SODB, HK, ACP were analyzed. The results have been compared with those relative to *Sus scrofa scrofa* from Austria (Hartl & Csaikl, 1987), from peninsular Italy (Apollonio *et al.*, 1985) and with those of *Sus scrofa meridionalis* from Sardinia (Apollonio *et al.*, *op. cit.)*.

3. Results

GPI system has been found polymorphic as in Austrian Wild boar (GPI*A .24, GPI*B .76); in domestic pig the frequency of GPI*B varies from .30 to .97.

PGD system showed a single allele (PGD*A) as it has been observed in other Wild boar populations. In domestic pig the system is polymorphic and the frequency of PGD*A varies from 0.30 to 0.83.

ADA1 and ME1 were monomorphic in our sample in contrast with Austrian populations. The remaining systems were monomorphic.

4. Discussion and conclusions

All the wild boars of the Western Europe so far examined are similar, although coming from different zones. The constant trait is the monomorphism of PGD locus wich is polymorphic in domestic pig and in some populations of Asian Wild boar (Kurosawa & Tanaka, 1991). This seems to indicate that the alleles PGD*B and PGD*C arose from mutation when *Sus scrofa scrofa* was already differentiated. In this case, if in a population of Wild boar one of these two alleles should be present, the occurence of crosses with domestic pig or of individuals of Asian origin could be hypothesized, although conclusions from a single locus can not be absolute. However, karyotype analysis (Macchi *et al.*, in press) evidenced that chromosome polymorphism is absent in individuals from the same mountain zones, where the present material has been collected. It seems reasonable to accept that in the Piedmont mountains is present the typical Western Europe

Wild boar (*Sus scrofa scrofa*), on which introduction of crosses or wild boars of other subspecies did not have notable influence. Anyway, it seems to be useful to control all the Wild boar centers existing in Piedmont both with karyotype and biochemical polymorphism examination because, if differences from wild population should be found, it would be possible to detect at least one of the sources of illegal introduction.

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CYTOGENETIC VARIABILITY IN THE WILD BOAR (Sus scrofa scrofa) IN PIEDMONT (ITALY): PRELIMINARY DATA

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Abstract: The authors have carried out a cytogenetic study on the Wild boar (*Sus scrofa* L.) in Piedmont in order to assess the origin of the population. The existence of some polymorphism in the diploid number indicates that Piedmont's animals may have different origins. The modified technique we used proved satisfying.

Keywords: Wild boar, *Sus scrofa,* Suidae, Europe, Population genetics, Karyotype.

IBEX J.M.E. 3:17-18

1. Introduction

The cytogenetic studies point out a chromosomal polymorphism in the Wild boar (Bosma *et al*., 1984; Nombela *et al*., 1990). The diploid chromosome number of the West European subspecies is 2n=36, the Eastern European populations have 2n=38, while in the subspecies of Central and Far East Asia it ranges from 36 to 38. The domestic pig has always 2n=38 and its karyotype is identical to that of wild boar with 2n=38.

The aim of this research is to characterize, under the cytogenetic point of view, the populations of *Sus scrofa* living in Piedmont.

2. Material and methods

We analyzed 14 blood samples, drawn from the femoral vein of wild boars trapped and anesthetized in mountainous and plain areas, and 4 blood samples from pigs.

Two methodologies were used: the first is the standard one on whole blood (Moorhead *et al*., 1960), the second is derived from the standard modified by us and using separated blood.

Here we describe the latter because it gave better results.

- Separate the blood using 1 ml of Emagel for 1 ml of blood, leave it for 30 minutes.
- Centrifuge the supernatant for 10 minutes, at 900 revs per minute (RPM), with the same quantity of RPMI-1640.
- Remove and discard the supernatant with a pipette.
- Add 6 ml of RPMI-1640 Dutch modification, 2 ml of fetal bovine serum, 0.2 ml of phytohaemaglutinin, 0.1 ml of antibiotics and 0.1 ml of heparin (100 U/ml).
- Put the cultures in thermostat for 72 hours (37°C).
- 2 hours before the cell collection add 0.3 ml of Vinblastina sulphate (0.5 µg/ml); wait 1 hour then add 0.5 ml of Actinomycin D (100 µg/ml).
- Centrifuge at 900 RPM for 10 minutes.
- Remove and discard the supernatant with a pipette.
- Add a hypotonic solution (KCL 0.075 M) pre-warmed for 15 minutes at 37°C.
- Centrifuge at 900 RPM for 10 minutes, remove and discard the supernatant with a pipette.
- Add 5 ml of Acetic acid (5%).
- Leave it for 5 minutes at room temperature.
- Centrifuge at 900 RPM for 5 minutes.
- Remove and discard the supernatant with a pipette.
- Add 10 ml of fixative (1 part of glacial acetic acid + 3 parts of methanol).
- After 30 minutes centrifuge at 900 RPM for 10 minutes, remove and discard the supernatant with a pipette, add the fixative, centrifuge again at 900 RPM for 10 minutes, remo-

ve and discard the supernatant with a pipette and prepare the slides.

The classic banding technique of Caspersson *et al.* (1970) and Zech (1973) for the Q bands was used.

3. Results

Karyological analysis enabled us to show the chromosomal polymorphism represented by 3 variants 2n=38, 2n=37, 2n=36.

The karyotype 2n=38 consisted of 5 submetacentric chromosomal pairs (1-5), 2 subacrocentic pairs (6-7), 5 metacentric pairs (8-12), 6 acrocentric pairs (13-18) and 2 gonosomes (submetacentric X-chromosome and a small metacentric Y).

The karyotype 2n=37 presented a Robertsonian translocation between a chromosome 15 and a chromosome 18, that gives a submetacentric chromosome, while the two homologous corresponding are free, according to Popescu *et al.* (1980).

Finally the karyotype 2n=36 is homozygotic for the Robertsonian translocation 15-18.

Among the 14 samples analysed, the 6 collected in mountainous areas (4 males and 2 females) had 2n=36. Among the 7 coming from flat areas, 3 subjects (2 females and 1 male) had 2n=38, 2 males 2n=36 and 2 females 2n=37. All the 4 domestic pigs (3 females and 1 male) had 2n=38.

4. Conclusions

The diploid chromosomal number in the subjects coming from mountainous areas is 2n=36, in agreement with the results of Mauget *et. al.*(1984) and Popescu *et al.*(1980).

The chromosomal polymorphism found in the subjects from the plain area lets us suppose that there were in plain arca animals of unknown origin, *i.e.* released for restocking.

From the obtained results we may conclude that the technique we developed is efficient, thus a wider sample will allow us to obtain more precise information on the populations of this species.

Our hypothesis that mountainous areas, where natural selection is stronger, prevent the reproductive success of reared animals (some of which are illegally released) could be tested in the future.

We seek for a greater collaboration from the public administrations in the collection of other samples and in the control of all Wild boar farming in order to prevent a proliferation of animals with unclear chromosomal set. The release of such animals in the wild could cause great negative effects on agriculture and modify the genetical structure of the truly wild population of *Sus scrofa*.

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THE PIG MITOCHONDRIAL GENOME

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Abstract: Restriction analyses, cloning and partial sequencing of pig mitochondrial DNA were performed. Restriction data confirm the previously described differentiation of Asian and European mtDNA types and demonstrate the presence of Asian type mtDNA in one European breed. Samples from wild boars show the same restriction patterns as European domestic pigs.

Keywords: Pig, Wild boar, *Sus scrofa,* Suidae, Mammals, Mitochondrial DNA.

IBEX J.M.E. 3:19-20

1. Introduction

Mitochondria of animal cells contain an autonomous genetic system. The genome itself is a double stranded circular DNA molecule approximately 16-17 kilobase pairs long in most higher vertebrates. Its gene order and content is highly conserved among mammals. This organelle genome possesses the genetic information for two ribosomal RNAs, 22 tRNAs and 13 proteincoding genes. All genes are tightly packed with no or only a few bases between them as spacers. The only major noncoding region is the so called D-loop, located between the genes for the tRNAs for Phenylalanine and Proline. In this region control elements for the transcription and translation processes are located. The origin for L-strand replication however is placed within a cluster of tRNA genes between the genes for Cox1 and ND2. Mitochondrial DNA is widely used to infer phylogenetic relationships and variability patterns among populations. Here we report on preliminary data from a sequencing project, designed to determine the complete nucleotide sequence of the pig mitochondrial genome.

2. Material and Methods

Mitochondrial DNA (mtDNA) from a single animal has been purified and cloned into pUC vectors. Recombinant clones were propagated in *E. coli* and sequenced by the dideoxy method, either using the sequenase kit (USB) or by an automated procedure on an ABI sequencer. Gap filling was accomplished by synthesizing oligonucleotides as sequencing primers. Restriction enzyme analysis was used to refine a previously published restriction map (Watanabe *et al.*, 1985) and to search for RFLPs among 42 animals of different origin, including animals of Asian maternal origin, European wild boars and different domestic breeds. All methods were performed according to standard procedures or suppliers instructions.

3. Results and Discussion

The pig mitochondrial genome is approximately 16,750 base pairs long. Up to now we have sequenced 15,722 bases and report on analysis of up to 13,674. Complete nucleotide sequences have been determined for the following genes: ATPase subunits 6 and 8, Cytochromeoxidase subunits 1, 2 and 3, NADH dehydrogenase subunits 1, 4 and 6, 12s ribosomal subunit, tRNAs for Arg, Asp, FMet, Glu, Gly, Ileu, Leu, Lys, Ser, Trp, Tyr, Val. Homology comparisons to sequences from other vertebrates (Anderson *et al.*, 1981; Bibb *et al.*, 1981; Anderson *et al.*, 1982; Desjardins & Morais, 1990) demonstrate that the pig mitochondrial genome exhibits the same gene order and content as other mammals. Results of homology comparisons are depicted in table 1. Homology is highest between pig and cow, whatever subgroup of sequences is compared. Differences in similarity between pig and mouse and pig and man are marginal. Sequence homology between pig and chicken is lowest, which is not astonishing, as the chicken has to be regarded as an outgroup among this species. As expected, the higher conservation of aminoacid sequences as compared to nucleotide sequences is due to the redundancy of the genetic code especially for the third codon position. This is demonstrated for the pair pig/cow in table 1.

Despite the high similarity between cow and pig sequences, the pig genome is roughly 400 base pairs longer. This is due to the presence of

Table 1: Homology comparisons between pig and other vertebrates.

Pig		Cow	Mouse	Man	Chicken
Total Sequence (13,674 bases)		78.2	73.5	70.9	63.2
Proteingenes (7 genes)		80.0	74.8	73.3	69.0
12sRNA gene		80.9	74.2	75.1	66.1
tRNA genes (12 genes)		86.3	81.8	81.7	72.1
Aminoacidsequences (8 genes)		89.5			
Codonposition	1	88.5			
	2	95.8			
	3	54.2			

additional sequences in the D-loop of the pig. A part of the pig D-loop region consists of a tandem repeat of the sequence CGTGCGTACA. This is a purine/pyrimidine alteration, characteristic for Z-DNA. Our data confirm the presence of this tandem repeat, which is so far unique among mammals except the rabbit (Mignotte *et al.*, 1990), whose D-loop is sequenced. Putative promotor and/or signal sequences have also been assigned to certain positions in the D-loop. Additionally, we identified a sequence as possible origin of L-strand replication by homology analysis. The sequence reads CTCCCGCCGCAGGAAAAAAAGGCGGGAG. Position 22 to 29 is an inverted repeat of positions 1 to 8. This can be regarded as characteristic for loop forming structures, while the inverted repeat forms a stem, the sequences spacing them from the single stranded loop. This structure is thought to be created, when in the process of H-strand replication the L-strand becomes singlestranded at that position. The loop could then act as signal sequence or substrate for a factor initialising L-strand replication.

Our restriction enzyme analyses confirm the previously reported differentiation of Asian and European mtDNA types (Watanabe *et al.*, *op. cit.*) and demonstrate the presence of Asian type mtDNA in the Hampshire breed. Further the Belgian Landrace displays a polymorphic HincII site. Sequence comparisons among pigs yield 98.2% homology for the cytochrome b gene between the gene sequence published by Irwin *et al.* (1991) and our data.

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CONSERVATION AND RESEARCH PRIORITIES FOR THREATENED SUIDS OF SOUTH AND SOUTHEAST ASIA

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Keywords: Suidae, *Sus* spp., *Babyrousa babyrussa,* Asia, Conservation.

IBEX J.M.E. 3:21-25

1. The situation in the region

The eight suid species and numerous subspecies native to South and Southeast Asia constitute the highest diversity within this family found in any region of the world. Groves (1981) has gone a long way toward clarifying the taxonomy of these animals, but recent reviews of the Philippine pigs (Oliver *et al.*, 1993; Groves & Grubb, 1993) have shown that further taxonomic revisions are required as new material becomes available. With few exceptions, we have little detailed knowledge of the natural history of suids in the region, although during the past decade field surveys have begun to provide a better idea of the distribution, status, and habitat preferences of many of the taxa. An International Union for Conservation of Nature and Natural Resources (IUCN) action plan drawing together the existing knowledge and proposing conservation strategies (Oliver, 1993) is the source of much of the data summarized in the present paper. Several of the native suid species and subspecies have been classified as threatened and require conservation action to save them from extinction. Because these threatened taxa occur in a wide variety of habitats and interact with many varied human cultures, each faces a unique set of problems. Nevertheless, uncontrolled hunting and habitat destruction have been identified as the two predominant threats. Consequently, in most situations creation and management of protected areas combined with development and enforcement of sound hunting laws are solutions requiring high priority.

Understanding what needs to be done is a major step toward successful conservation action. Unfortunately a series of factors often make it difficult for the necessary policies to be implemented.

Perhaps the most important constraint is the limited funds which governments of the region are able or willing to commit to the conservation of protected areas and wildlife in general. The World Bank calculates that direct government funding for protected area management in all of Asia is about US $ 30-35 million annually, roughly one third of the amount IUCN estimates is needed as a bare minimum to support only the routine expenditures (Braatz, 1992). As a percentage of total annual national budgets, funding for protected area management is especially low in those countries most important for suid conservation. For the Philippines the figure is only 0.01%, the lowest in Asia. India and Indonesia provide their parks with only slightly higher proportions of 0.03% and 0.06% respectively. By way of comparison, Bhutan with a figure of 0.29% ranks highest in Asia in this respect.

In many societies negative attitudes toward pigs make it difficult to garner public and government support for their conservation. All pigs are despised and avoided by devout Muslims who refuse to eat or even touch any part of the animals, and Islam is the predominant religion in Indonesia and Malaysia. Additionally, farmers who suffer losses from crop raiding pigs are understandably reluctant to heed laws aimed at conserving species they regard as pests.

A somewhat paradoxical complication for suid conservation is that wild pigs are often an important protein source for indigenous societies which obtain much of their subsistence from hunting and gathering in the forests. This may endear the pigs to conservationists who see them as ideal sustainable "non-timber forest products". But where governments are more interested in converting the forest dwellers to plantation workers or agriculturalists living in permanent villages, conserving wild pig populations for hunting is not a priority. To survive by hunting wild animals is viewed as backward, and, in the short term, there are more profitable ways to exploit forests than to maintain them as support systems for a relatively few people who want to continue with a disappearing way of life.

As conservationists we must understand these attitudes and monetary constraints and search for ways to overcome them, or to at least minimize them in each situation. Among other approaches, this may involve public education, training of local wildlife conservation professionals, encouraging conservation of biodiversity rather than species' conservation, promoting controlled hunting of wild pigs, or captive breeding. In addition, basic ecological research on virtually all threatened suid taxa is still needed. Much of the funding for these activities will need to be sought from international aid agencies and non-governmental organizations.

2. Threatened native suids (Tab.1)

Table 1: Threatened Southeast and South Asian Suids

Taxon/Status	**Threats**
Sus scrofa riukiuanus (V or E)	Hunting (pest/food), Disease, Genetic contamination
Sus salvanius (Critically E)	Habitat loss, Hunting (food), Political unrest
Sus v. verrucosus (V)	Poisoning, Hunting (pest/food)
Sus v. blouchi (V)	Hunting (pest)
Sus barbatus oi (R)	Habitat loss
Sus b. ahoenobarbus (V)	Hab. loss, Hunting (pest/food)
Sus philippensis (R)	Hab. loss, Hunting (pest/food)
Sus cebifrons (E)	Hab. loss, Hunting (pest/food)
Babyrousa babyrussa (V or E)	Hunting (food), Habitat loss

E = endangered; V= vulnerable; R= rare

Sus scrofa riukiuanus: Vulnerable or Endangered according to population

S. s. riukiuanus, the smallest and the only threatened subspecies of *Sus scrofa*, is endemic to the Ryukyu Islands south of the main islands of Japan. Numbers are declining rapidly, largely as a result of overhunting, and it is thought to be endangered on at least four of the six islands of the Ryukyu chain. Pigs are killed both for consumption and as agricultural pests, and commercial traders export carcasses to gourmet markets in Osaka. The subspecies is also threatened by a severe skin disease which has spread throughout the population on one island, and genetic contamination through contact with free ranging domesticates. On Iriomote Island there are plans to build a road through a national park, increasing access by poachers who had already reduced pig numbers by half since the park was created.

Due to widespread governmental and local attitudes ranging from ambivalence to hostility toward the pigs, the most effective way to conserve them is by supporting existing or proposed programs directed toward the conservation of biodiversity. In addition, preliminary or repeat status surveys are needed on all six islands in the Ryukyu chain.

Sus salvanius: Critically Endangered

The Pygmy hog (*S. salvanius*) is now known to exist in only two isolated populations in the tall grasslands of northwestern Assam, India, and is considered to be one of the most endangered of all mammals. Its extremely reduced body size (males weigh only about 8.5 kg) makes it potentially a highly valuable genetic resource. The continuing decline in Pygmy hog numbers is attributable to loss of its grassland habitat to human settlements, agricultural encroachment, commercial forestry, and flood control schemes. Annual burning of the tall grasses concentrates the hogs in the small remaining unburned areas where they are particularly vulnerable to hunters. The survival of the species is crucially dependent on the integrity of the Manas Wildlife Sanctuary, which is under threat from high numbers of illegal immigrants and an armed rebellion of local tribals.

The strategy for the conservation of the Pygmy hog places paramount priority on promoting whatever actions are necessary to restore and maintain the Manas Wildlife Sanctuary and its buffer reserves. Field surveys of areas known or suspected to harbor pygmy hogs need to be undertaken, and detailed studies are needed on the behavior and ecology of the species to establish management criteria. A properly structured captive breeding program should be established to provide animals for eventual reintroductions to protected sites within its recent known habitat.

Sus verrucosus verrucosus: Vulnerable

The Javan warty pig (*S. v. verrucosus*) is confined to the island of Java where it is sympatric with the Indonesian subspecies of the Eurasian wild pig (*S. scrofa vittatus*). It occurs at altitudes below 800 m and prefers disturbed habitats and teak plantations to closed canopy forests. Although not uncommon in some areas, the remaining Javan warties are in isolated populations and are subjected to uncontrolled hunting and, in some cases, poisoning. They are killed both by sport hunters and by farmers protecting their crops. There is evidence that hybridization with *S. s. vittatus* occasionally occurs in the wild, but at current levels it is probably not a threat to the genetic integrity of the species.

Javan warty pigs are poorly represented in existing protected areas, and proposals to create three new nature reserves and expand two existing reserves of importance to the taxon need to be implemented soon. Poisoning must be stopped, and surveys of the extent of market hunting should be undertaken with the objective of formulating means to regulate or eliminate the practice. Sport hunters from the cities provide a source of income to rural people acting as guides, and Javan warty populations outside of protected areas should be managed to allow this activity on a sustainable basis. Captive animals need to be administered under a properly structured plan for the long term genetic and demographic benefit of the species.

Sus verrucosus blouchi: Vulnerable

S. v. blouchi, a smaller race of the Javan warty pig than the nominate form, is confined to the 200 sq km Bawean Island in the Java Sea where it is the only suid present. The Muslim population of the island does not hunt the pigs for food, but crop raiders are snared and killed. Much of the habitat of this subspecies consists of forests and teak plantations located within a 4,500 ha wildlife reserve which was created primarily for the benefit of the endemic deer *Axis kuhli*. But because of its very restricted range the subspecies cannot be considered secure, and a survey to determine its current status and conservation requirements is urgently needed.

Sus barbatus oi: Rare

This race of the bearded pig is confined to Peninsular Malaysia and the island of Sumatra in Indonesia where it is sympatric with *S. scrofa vittatus*. It is known to travel over great distances in large herds of sometimes hundreds of individuals, and was widespread throughout the formerly unbroken rain forests characteristic of its range. Today forest fragmentation has disrupted these movements and reduced the subspecies' numbers. For example *S. b. oi* has been extirpated from the southern end of Sumatra, the portion of the island where deforestation has been heaviest during the past 40 years. These habitat changes have almost certainly favored *scrofa* over *barbatus*. Hunting does occur, but apparently not intensively enough to be a major threat. In Peninsular Malaysia, sport hunters are said to prefer the taste of Eurasian wild pigs to that of bearded pigs (Pan Khang Aun, pers. comm.). The subspecies is found in several protected areas in Sumatra and in the Taman Negara National Park in Peninsular Malaysia. Current knowledge of *S. b. oi* is too limited to enable formulation of practical management recommendations, and priority must be given to field surveys and other basic research to determine where they still occur, where and why they migrate, and whether they can survive in logged over forests. A properly structured captive breeding program should also be initiated.

Sus barbatus ahoenobarbus: Vulnerable

The Palawan bearded pig (*S. b. ahoenobarbus*) is endemic to Palawan and the smaller islands of Balabac and the Calamians in the Philippines. This pig is not known to undertake the long migrations for which the other two races of bearded pig are famous. Because it has a restricted range undergoing rapid deforestation, is known to be found in only one small protected area, and is subjected to heavy hunting pressure, the Palawan bearded pig is the most threatened race of its species. The field status survey recently initiated in the Calamian

Islands needs to be continued throughout the range of the race with a view to the development of recommendations for the enhanced future protection of selected populations. Management of the pigs in non-protected areas should be designed to enable their continued harvest on a sustainable basis.

Sus philippensis: Rare

The Philippine warty pig (*Sus philippensis*) is fairly widespread in most of the few remaining forests on the larger islands of the eastern Philippines. However deforestation coupled with uncontrolled hunting have already extirpated it over a large proportion of its former range and continue to threaten the species. As a first step to its conservation, field surveys and research into habitat requirements, population dynamics, and response to hunting pressure and commercial logging are needed. Local conservation education projects should be implemented to make the public aware of the importance of their native wildlife and forests in general, and their wild pigs in particular.

Sus cebifrons: Endangered

This most threatened of the Philippine suids, the Visayan warty pig (*S. cebifrons*), has been eliminated from four of the six islands where it was known to exist. On Negros and Panay it survives in a few small, isolated populations which are still hunted intensively. Forest destruction continues to reduce and fragment their remaining habitat. The overwhelming priority for the conservation of this species is the early declaration and effective future protection of the proposed Panay Mountains National Park; other smaller areas with remnant populations should also be given protected status. This can be done in the broader context of protecting the whole range of critically threatened species endemic to the Visayan faunal region. Data on the present status of the species are required from several islands. A properly structured captive breeding program needs to be developed, and public education projects should be initiated to raise local people's awareness of their natural heritage, including the uniqueness of their wild pigs.

Babyrousa babyrussa: Vulnerable or Endangered according to subspecies

Three extant subspecies of babirusa are currently recognized, all found in Indonesia: *Babyrousa babyrussa celebensis* from Sulawesi, *B. b. togeanensis* from the Togian Islands and *B. b. babyrussa* from the Sula Islands and Buru in the Moluccas. It has been extirpated from much of Sulawesi and is still threatened there and throughout its range by hunting and habitat loss. The babirusa inhabits tropical rain forests, and in recent years large-scale commercial logging has posed a major and increasingly serious threat. They are one of the first animals to become locally extinct after logging or land opening. On Sulawesi 12,000 sq km of land have been declared as wildlife protection areas, but as yet there are no national parks or other wildlife reserves within the ranges of the other two subspecies.

Effective conservation will require field status surveys to develop management recommendations for the enhanced protection of the species, particularly the least known but potentially most threatened races, *B. b. togeanensis* and *B. b. babyrussa*. The government should be assisted in its efforts to establish national parks on islands where these animals occur and require further protection. Hunting for subsistence and commercial purposes should be investigated with a view to its control or elimination. Captive breeding programs should be initiated for the two most threatened races, and fresh blood-stock should be introduced from the wild into the existing captive population of *B. b. celebensis*.

3. Non-native suids of conservation interest (Tab.2)

Introduced and feral pigs should generally be regarded as exotic pests which should be controlled or eradicated wherever possible, however some populations warrant in-situ conservation because they are representative of extinct or endangered taxa, are of anthropogenic or socioeconomic significance, or are of unique genetic importance. There are three such suid taxa in Southeast Asia.

Babyrousa b. babyrussa: Endangered

Although discussed above with the other races of babirusa, this distinctively long haired form may have been introduced to the Sula Islands and Buru Island from southern Sulawesi where it is now extinct. No matter what its origins, the race is severely threatened and in need of conservation action.

Table 2: Non-native SE Asian Suids of Conservation Interest

Taxon/Location/Status	Remarks
Babyrousa b. babyrussa Buru and Sula Island Endangered	Otherwise extinct form probably introduced from southern Sulawesi, threatened by logging and settlers from Java; two reserves proposed
ex-*Sus scrofa* Andaman Island-Endangered Nicobar Islands-Indeterminate	Feral, introduced 2,000 yrs ago; small (35-40 kg); primary food for native tribes; threatened by deforestation and immigrant poachers
ex-*Sus celebensis* Simeulue Island Several island in Moluccas and Lesser Sundas	Feral on Simeulue, brought by settlers whose language related to Buginese; reserve proposed; little known of situation on other islands

ex-*Sus scrofa:* Endangered - Andaman Islands
Indeterminate - Nicobar Islands

These small pigs have descended from feral stock introduced at least 2,000 years ago, and have evolved as an integral component of their insular ecosystems. Both the Andaman and Nicobar populations were formerly assumed to be endemic and are protected under Indian law. They are a primary food source for the isolated tribal societies inhabiting these islands, and may also have ritual and religious significance. A recent influx of immigrants has led to high levels of deforestation from logging, agricultural encroachment and other developments. The pigs are also threatened by immigrant poachers who use more efficient hunting techniques than the tribals, including firearms, snares and dogs. A joint zoological-anthropological survey is needed to ascertain the present distribution, status and threats to the pigs, and to understand their role in the culture of the aboriginal tribes. Based on these findings, recommendations should be made for the pigs' enhanced future protection, taking into account the legitimate rights and needs of the original human inhabitants.

ex-*Sus celebensis:* Indeterminate

On Simeulue Island, northwest of Sumatra, the presence of a highly modified form of S. *celebensis* gives clues to the origins of the island's human inhabitants whose language is most closely related to Buginese or other southern Sulawesi dialects. Thus apparently sometime in the past, settlers arrived at Simeulue from distant Sulawesi, bringing with them the pigs they had domesticated from the forests of their homeland. Other populations of wild pigs referred to as feral S. *celebensis* are known from several islands in the Moluccas and Lesser Sundas. Field studies and surveys are needed to clarify the distribution, status and systematic affinities of these pigs. Anthropological components of such studies should investigate relationships between the ethnic origins of local tribal groups and the distribution patterns of wild pigs of varying derivation, as well as the cultural and socioeconomic importance of these animals. Protected areas need to be established, but management plans should also address the possibility that measures may need to be taken to control the population numbers of these feral pigs.

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THE TAXONOMY, DISTRIBUTION AND STATUS OF PHILIPPINE WILD PIGS

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Abstract: Recent studies have revealed that there are three species and at least two subspecies of wild pigs in the Philippines, of which two species and one subspecies are endemic.This is a larger number of endemic suid taxa than any other country, with the exception of Indonesia. Within the country, the distribution of the native and endemic suids follows broadly predictable lines, with divisions equating to the major "faunal regions" of late Pleistocene islands. Thus the "warty" pigs east of Wallace's Line in Luzon and Mindanao (including Samar, Leyte and, probably, Bohol), *i.e. S. philippensis,* and those of the West-central Visayas Islands (Panay, Negros, Cebu and, probably, Masbate), *i.e. S. cebifrons,* are endemic at the species level; whereas those of Palawan and associated islands, *i.e. S. b. ahoenobarbus,* are closely related to the "bearded" pigs of the Sundaic Region (Borneo, Sumatra, Malaysian Peninsular, etc.) and are endemic only at the subspecies level. There is also evidence that the range of the nominate form of the bearded pig from Borneo, *i.e. S. b. barbatus,* extends to the small islands of Tawitawi and Sibutu in the Sulu Archipelago. If this is the case, these are the only non-endemic wild pig populations in the Philippines.
Unfortunately, however, the generally extreme levels of deforestation on most islands on which they occur, coupled with intense hunting pressure, inadequate legal protection and the poor enforcement of existing legislation even within most protected areas, have resulted in the systematic decline of all Philippine populations of these animals. These factors are especially apparent in the (west) Visayan region, where the endemic warty pig, *S. cebifrons,* is already extinct or close to extinction on at least four (Masbate, Guimaras, Cebu and Sequijor) of the six islands in which it is known or believed to have occurred. It now survives only in a few small, isolated areas on Negros and Panay, where all remaining populations are declining as a result of continued habitat destruction and intense hunting pressure. These populations are also potentially seriously threatened by "genetic contamination" through interbreeding with free-ranging domestic and feral pigs (unpubl. data). By comparison, *S. philippensis* remains relatively widely distributed in most still-forested areas on the larger islands of Luzon, Samar, Leyte and Mindanao, where it occurs in all of the principal national parks. It probably also still occurs on a number of the smaller islands within these regions, but is certainly threatened or extinct on some others. Further studies are likely to reveal genetic differences between some of the principal populations of this species, which is currently (but probably incorrectly) regarded as monotypic.

Keywords: Wild pigs, Suidae, Bearded pig, Warty pig, *Sus barbatus, Sus celebensis, Sus philippensis,* Asia, Karyotype.

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1. Taxonomy and distribution

Following Sanborn (1952), the wild pigs of the Philippines have generally been attributed to two, more widely distributed species, namely: the bearded pig, *Sus barbatus*, and the Sulawesi warty pig, *S. celebensis*. Thus, the wild pigs of the west Philippine islands of Balabac, Palawan and the Calamian Group, which form part of the Sunda Shelf, are most closely related to the bearded pigs of Borneo, Sumatra and the Malaysian Peninsular, whilst those of the central (Visayas Islands) and eastern (Luzon, Mindanao and associated islands) Philippines, which form part of the Wallacean Region, were lumped with the Sulawesi pig.

In a major review of the genus *Sus*, Groves (1981) confirmed the close relatedness of the west Philippine pigs with *S. barbatus*, but reaffirmed their separation as an (endemic) subspecies, *S. b. ahoenobarbus*. However, Groves also argued that the affinity of the central and eastern Philippine pigs with *S. celebensis* was purely superficial and that these populations were also more closely allied to *S. barbatus*; a view later endorsed by Mudar (1986). Groves (1981) also asserted that the central (Cebu and Negros) and eastern (Luzon, Mindoro, Mindanao and Jolo) Philippines populations were not only distinct from those of the western Philippines, but were also distinct from each other. These regional populations were therefore reassigned as two separated subspecies of *S. barbatus*, namely *S. b. cebifrons* and *S. b. philippensis*, respectively (Groves, 1981).

Even so, it was stressed that these were tentative assignations owing to the dearth of museum specimens from the Visayas Region (where only two skulls were available for examination from Cebu, only one from Negros and none from the other Visayan islands of Guimaras, Panay and Masbate) and the complete absence of any comparative cytogenetic data, precluded a definitive assessment of the systematic relationships of these populations.

To a large extent this situation still obtains, though there have been some important developments in our understanding of the systematic relationships and genetic diversity of the Philippine suids in recent years. These developments include the acquisition of a series of skulls and mandibles from Negros (*cebifrons*) and Samar (*philippensis*) which, together with the first photographs revealing the external characters of the Visayan animals, not only led Groves (1991) to reaffirm his assertion that the central and eastern pigs are more closely allied to *barbatus* than to *celebensis*, but also to suggest that these are sufficiently different from *barbatus* and from each other to warrant separation as distinct species, namely *S. cebifrons* and *S. philippensis*, respectively (Groves, 1991; Oliver, 1991,1992). A description of these small (*S. cebifrons*) to medium (*S. philippensis*) sized pigs is provided by Groves and Grubb (1993), who treat both species as monotypic, but acknowledge that *S. philippensis* appears to be regionally variable in some characters and may ultimately prove polytypic.

The first studies of karyotypes and banding patterns of Philippine wild pigs have also yielded important new information. In 1992, blood samples were collected from seven individuals of known origin (including two F1 captive-bred hybrids), representing five islands - Palawan, Culion, Mindoro, Luzon and Mindanao - and the results were compared with those from similar studies of other species of *Sus* which have also been undertaken in recent years. The diploid chromosome number of the domestic pig and Asian and South-East Asian populations of the Eurasian wild pig (*Sus scrofa*) is invariably 38. The same number has been found for *S. barbatus*, *S. celebensis*, *S. verrucosus* (the Javan warty pig) and *S. salvanius* (the pigmy hog). The preliminary results from the Philippine pigs are therefore of considerable interest. Of the seven pigs sampled, three pigs (a boar from Luzon and two sows from Mindanao) had 2n = 36 chromosomes, with a centric fusion between chromosomes 13 and 16 in the homozygous condition, and two pigs (both sows, one each from Culion and Mindoro) showed 2n = 38 chromosomes, with chromosomes 13 and 16 separately present. This type of translocation is new, both to the domestic pig and to the wild species of *Sus* karyotyped so far. The remaining two (hybrid) pigs (one from each of the latter sows but both sired by the Luzon boar), each showed 2n = 37 chromosomes, with the same centric fusion of chromosomes 13 and 16 in the heterozygous condition (for details see: de Haan *et al.*, in press).

These results strongly support Groves' suggestion that *philippensis* is a valid species, endemic to Luzon, Mindanao and associated islands. They also refute the assertions of earlier workers that the Philippine wild pigs east of Wallace's Line should be attributed to *S. celebensis*, which has 2n=38 chromosomes. However, new questions have been raised about the systematic relationships of the wild pigs from Mindoro, since these results indicate that the Mindoro population is closely allied with the bearded pig of Palawan and associated islands (including Culion), *i.e. S. b. ahoenobarbus*, rather than with *S. philippensis* from neighbouring Luzon. However, these results also contradict other evidence, based on craniomorphological comparisons and the external appearance of most Mindoro wild pigs, which indicate their close affinity to *S. philippensis*.

In any event, the recognition of (at least) 3 taxa of wild pigs, means that the Philippines have a larger number of endemic suids than other country with the exception of Indonesia, which has (at least) 5 species and 8 subspecies, of which 3 species and 5 subspecies are endemic. The inclusion of pigs from Jolo in the Sulu Archipelago with *S. (b.) philippensis* (Groves, 1981) is also of interest in this context, since it implies the westward colonisation of these islands by wild pigs from Mindanao, rather than eastwards from the Bornean mainland (Sabah). However, there is increasing evidence that "typical" bearded pigs (*S. barbatus spp.*) also occur in the South-westernmost islands (Sibutu and Tawitawi) of the Sulu chain. There are numerous, apparently reliable, accounts of wild pigs crossing the channel between Sabah and Sibutu, where they have sometimes been killed by fishermen. An officer in the Philippine Navy reported seeing some of these animals whilst on a tour of duty in c. 1970, and a large number of swimming animals are reputed to have been used for target practice by a U.S. Navy battleship, which encountered them whilst on patrol (R. Hilado, pers. comm.). It therefore seems likely that a fourth (non-endemic) taxon of wild pig, the Bornean *S. b. barbatus*, should be added to the Philippine list, and that the Sulu Archipelago has been colonised by different populations/taxa of these animals from the South-west (Sabah) as well as the North-East (Mindanao) (Fig. 1).

2. Present distribution and conservation status

Wild pigs are known or reported from all of the larger, and many of the smaller, offshore islands in the Philippines. As previously indicated, their distribution may be broadly divided into the major biogeographic regions west (Sundaic) and east (Wallacean) of Wallace's Line, each of these being further divided into two sub-regions, *i.e.*: Palawan (including

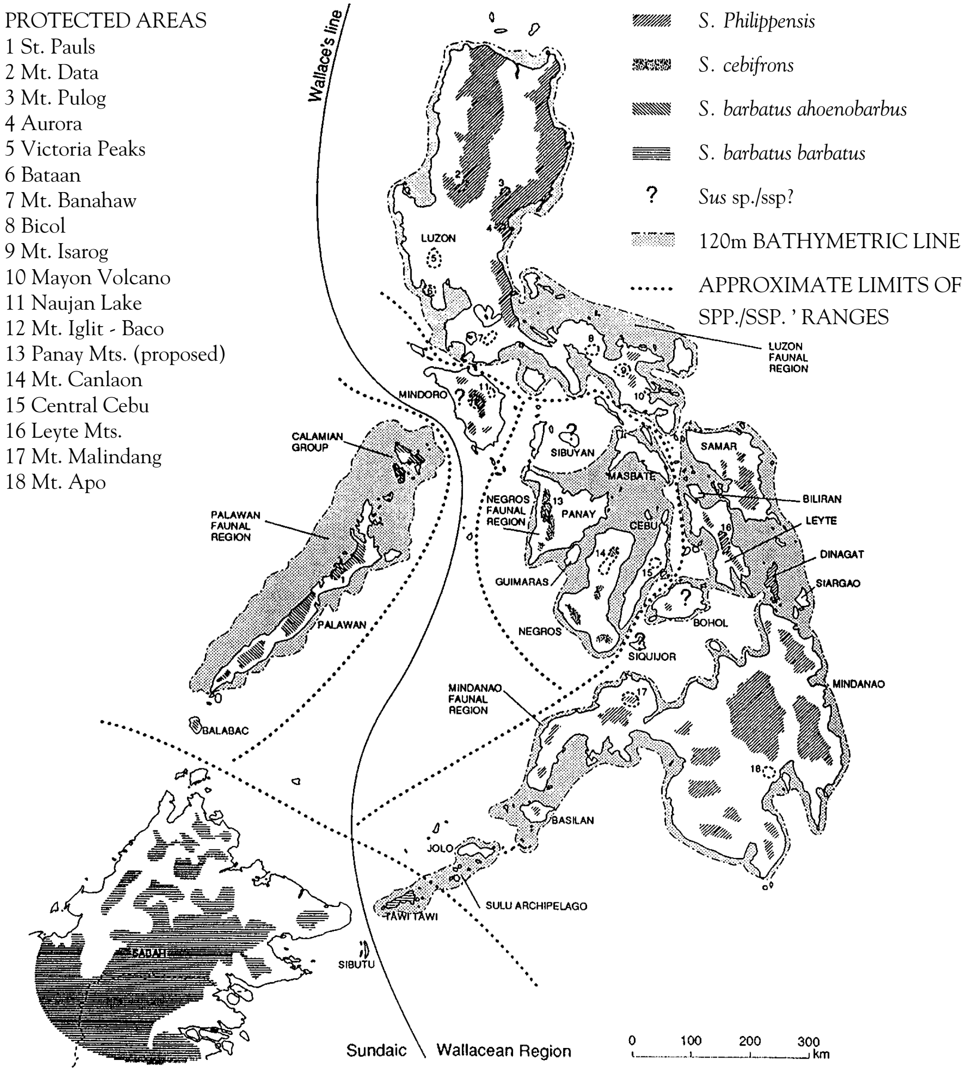

Figure 1 - Presumed former and present known distribution of wild pigs in the Philippines (modified after Groves, 1981; Cox, 1985; Heaney, 1986; Forest Management Bureau, 1988).

Table 1 - Present known distribution and status of wild pigs (*Sus* spp.) in the Philippines.

Taxon	Status	Distribution
S. b. ahoenobarbus (endemic ssp.)	Rare and declining	Balabac, Palawan and Calamians (Busuanga, Culion and Coron Is.)
S. b. barbatus (non-endemic ssp.)	Locally rare (but widespread in Borneo)	Sibutu and Tawitawi only?
S. cebifrons (endemic sp.)	Endangered to extinct	Panay, Guimaras (extinct) Negros, Cebu (extinct) and Masbate
S. philippensis (endemic sp.)	Rare and declining	Luzon, Catanduanes, Samar, Biliran, Leyte, Mindanao, Jolo* and ? other islands*
Sus spp./spp. ?	Rare to extinct	Mindoro (rare), Sibuyan, (rare), Bohol (critical), Sequijor (extinct)

* = no recent data

Balabac and the Calamians Group) and Tawitawi and Sibutu, and the west-central Visayas Islands (comprising Negros, Cebu, Masbate, Panay and Guimaras) and the larger, eastern islands of Luzon, Samar, Leyte, Mindanao and associated smaller islands. Wild pigs are known to occur (or to have occured until recently) on all of these islands and many of the smaller islands and island groups (e.g. Mindoro, Sibuyan, Sequijor and the Sulu Archipelago), though the affinities of some of these populations are not yet known (Tab. 1).

As indicated in table 1, recent data on the wild pig populations on many islands, particularly the smaller islands, are lacking and their present status can only be inferred from the extent of remaining forest over their known ranges. Thus, *S. b. ahoenobarbus* is probably the most threatened subspecies of "typical" (or Sundaic) bearded pig (Caldecott *et al.*, 1993) and is "presumed" to be at greater risk than *S. philippensis*, because it has a relatively smaller range and because the isolated populations on the islands of Balabac (Oliver, in press) and the Calamians are unlikely to remain securely established. This subspecies is thought to be still relatively widely distributed on Palawan, where it may be locally common in some areas, but it is intensively hunted (McGowan, 1986 and pers. comm.) and the surviving forests on Palawan are being rapidly depleted by uncontrolled logging and agricultural encroachment (Quinnell & Balmford, 1988).

By comparison, *S. philippensis* has almost certainly been extirpated over a greater proportion of its former range than *S. b. ahoenobarbus*, but this range is also considerably larger and includes some still relatively extensive tracts of forest on the larger islands of Luzon, Samar, Leyte and Mindanao. On all of these islands the species is reported to remain quite widely distributed wherever significant amounts of forest remain (Cox, 1985, 1987a; Rabor, 1986; L. Heaney, pers. comm.). By comparison, far less forest remains on Catanduanes (Heaney *et al.*, 1991) and Biliran where, by 1985, this species was reported to have declined to the point that viable populations were unlikely to survive for much longer (Cox, 1985, 1987a). *S. philippensis* is also reported from Jolo and it is presumed to occur, or to have occurred formerly, on Basilan and on some of the other smaller islands in the Mindanao and Luzon faunal regions, but recent information from these areas is lacking. Wild pigs are reported to remain locally common in some still-forested areas of Mindoro (Rabor, 1986; Cox, unpubl.), though the identity of these animals, and those of Sibuyan, where pigs were reported for the first time in 1992 (S. Goodman, pers. comm.) are not yet known (Tab. 1).

The distribution and status of wild pigs on Samar, Leyte, Biliran and Bohol were collected during a field survey in the central Philippines in 1985. This was primarily intended to assess the status and future management needs of *S. cebifrons* and the Philippine spotted deer (*Cervus alfredi*), which were assumed to occur on these islands (Cox, 1985, 1987a). However, although all of these islands are included within the Visayas (geopolitical) Region, they are actually a northward extension of the

"Mindanao faunal region", as defined by Heaney (1986) on the basis of the 120 m bathometric line (Fig.1). Thus, although Cox's survey revealed that Samar and (to a lesser extent) Leyte continued to support the largest populations of wild pigs in the "Visayan Islands", these populations are undoubtedly *S. philippensis*, as Groves (1991) has confirmed, rather than *S. (b.) cebifrons*, as was assumed at the time (Cox, 1985, 1987a; Oliver, 1991; Oliver *et al.*, 1993).

Conversely, the recognition that *S. cebifrons* was confined to the west-central Visayan Islands of Cebu, Negros, Guimaras, Panay and (probably) Masbate (or "Negros-Panay faunal region"; Heaney, 1986), profoundly influences any assessment of its conservation status. This taxon is undoubtedly more gravely threatened than previously supposed, or indicated by its current "Vulnerable" designation in the *IUCN Red list of Threatened Animals* (IUCN, 1990). As it is, the species is certainly "Endangered" according to the terms of these status categories (Oliver, 1991; Oliver *et al*, 1993).

The reasons for this are based on Cox's (1985; 1987a) revelations that wild pigs are now extinct on the islands of Guimaras, Cebu and Sequijor, all of which have been virtually deforested (Cox, 1985; 1987a; D. Kho, pers. comm.). A similar situation obtains on Bohol, where the last remaining populations of wild pigs in the Rajaha Sikatuna National Park were said to be close to extinction by 1985 (Cox, 1985; 1987a; A. Alcala, pers. comm.; D. Kho, pers. comm.) and on Masbate, where only two small populations were surviving by 1993, though both of these were subject to continued, intense hunting pressure (Oliver, in press). However, it is not known whether the Bohol or Masbate pigs are allied to *S. cebifrons* or *S. philippensis*. In either event, potentially viable populations of *S. cebifrons* are now confined to the western mountains of Panay, where their numbers are certainly declining, and to scattered fragments of surviving forest on Negros. This range is essentially identical to that of the critically threatened Philippine spotted deer (*Cervus alfredi*) and, in common with the latter species, all of the few surviving pig populations are subject to intense hunting pressure and the continued attrition and fragmentation of their remaining habitat.

The survival prospects of these pigs are therefore intimately linked with efforts now being made to conserve the spotted deer, which has been adopted as a "flagship" species for conservation action in the west-central Visayas (Oliver *et al*, 1991; Oliver, in press). To these ends, a new national park (>40,000 ha) has been proposed for the Mt. Madja-as/Mt. Baloy area of West Panay, in order to protect the single largest and more important tract of forest remaining in this region and, hence, the largest and most important surviving populations of these animals and diverse other Visayan endemic species. A preliminary management plan has been drafted in consultation with the relevant authorities (Cox, 1987b) and it is hoped that this park will be formally gazetted in the near future (W. Dee, pers. comm.). In addition, captive breeding projects have been initiated recently on Panay (at the West Visayas State University) and Negros (at Silliman University, Dumaguete City), under the aegis of formal agreements between the Department of Environment and Natural Resources (DENR), Government of the Philippines and the Zoological Society of San Diego, U.S.A..

On Negros, wild pigs are known to occur on Mt. Silay and the Mangdalangan Mts. (collectively comprising the Northern Negros Forest Reserve, c. 45,000 ha) and Mt. Canlaon National Park (24,600 ha; Tab. 2) in the north and in scattered forest fragments in the south, including the environs of Mt. Talinis/Mt. Guinsayawan/Lake Balinsasayao (c. 20,000 ha), near Dumaguete City. However, in all of these areas wild pigs are subject to intense hunting pressure as well as the continued attrition of their remaining habitat through illegal logging activities. In addition, the close proximity of outlying human settlements to most of the remaining forest fragments on Negros, poses a potentially severe risk of disease transmission and/or genetic contamination to wild pig populations through increased likelihood of their contact with free-ranging domesticates. The latter factor, in particular, has recently been revealed as a serious threat to the few remnant pig populations in the south of this island, where five of six wild-caught piglets collected in late 1992/early 1993 for the captive breeding project at Silliman University proved to be of hybrid origin (E. Alcala, pers. comm.).

These problems and any future conservation efforts directed towards any of the Philippine wild pigs are exacerbated by the negative attitudes of most local people towards these animals. They are most frequently encountered when they are hunted in the forest fragments or when they emerge from the shelter of those fragments to forage in neighbouring cultivation areas or "kaingins". In some areas farmers build bamboo fences to protect their crops or even go to the trouble of surrounding whole clearings with sharpened staves planted obliquely outwards to prevent the entry of wild pigs (Rabor, 1977). Nonetheless, the damage caused to agricultural smallholdings can be severe. For this reason, no special conservation measures have been introduced to protect these animals, which are generally regarded as agricultural pests and, hence, a legitimate target for hunting activities. In the 1960's, government officials distributed poison to farmers on Sibutu to destroy wild pigs (R. Hilado, pers. comm.), and some officers from the (former) Bureau of Forest Development (BFD) even suggested that wild pigs should be hunted down and killed wherever possible (Cox, 1987a).

Table 2: Existing and proposed national parks known or presumed to support populations of wild pigs.

Species/Area	Size (ha)	Location	Comment
S. b. ahoenobarbus			
St. Pauls	360	Palawan	Intact lowland rainforest; area soon to be extended to c. 50,000 ha.
Calauit Island	3,400	Calamians	Whole island declared a game reserve and sanctuary in 1976 to protect released hoofstock from Africa, but now threatened by human resettlements.
S. cebifrons			
Mt. Canlaon	24,557	Negros	Mostly relatively intact montane rainforest, but now isolated; wild pigs present, but hunted.
Panay Mts. (proposed)	40,000	Panay	Proposed to protect last area of remaining forest on this island; probably supports single largest pig population, but hunting is widespread.
Bulabog-Putian	850	Panay	Mostly deforested, wild pigs extinct in area.
Central Cebu	11,894	Cebu	Virtually deforested and heavily encroached; wild pigs extinct on island.
Sudlon	700	Cebu	Virtually deforested, wild pigs extinct on island.
S. philippensis			
Mt. Data		Luzon	Mostly pine forest; no recent information on pigs.
Bataan	23,853	Luzon	Monsoon forest; pigs (and hunting pressure) reported.
Quezon	535	Luzon	Remnant tract of lowland rain forest; pigs reported in 1978, but no recent information.
Mt. Isarog	10,112	Luzon	Wild pigs (and hunting pressure) reported in 1978; no recent information.
Leyte Mts.	c. 42,000	Leyte	Mostly montane and semi-evergreen forest, though some parts threatened by encroachment; prob. still supports a good pig population.
Mt. Apo	72,184	Mindanao	Formerly montane and lowland rain forest, but most of latter lost to encroachment; wild pigs definitely present.
Mt. Malindang	50,000	Mindanao	As Mt. Apo (above)
Sus sp./ssp ?			
Rajaha Sikatuna	9,000	Bohol	Wild pigs reported to be close to extinction.
Mt. Guitinguitin (proposed)	?	Sibuyan	Proposed to protect main watershed and most remnant forest; affinities of wild pigs are unknown (no museum specimens exist).
Mt. Iglit-Baco	75,445	Mindoro	Formerly mostly montane rain forest, but now largely disturbed or degraded; wild pigs said to be common in some places.

3. Acknowledgements

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OBSERVATION ON THE RECENT HISTORY, NATURAL HISTORY AND MANAGEMENT OF THE PIGMY HOG (Sus salvanius)

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Keywords: Pigmy hog, *Sus salvanius*, Suidae, Endangered species, Conservation, Burning, India, Asia.

IBEX J.M.E. 3: 33-36

One early morning in 1964 I was trying to negotiate a large marshy area on elephant back in south eastern part of Manas Wildlife Sanctuary (now a National Park), when the "Mahut" Baneswar excitedly showed me a small animal in a burnt patch of grassland and whispered: "Tukuri Barah". The animal looked like a miniature Wild boar, but despite my inexperience, I noticed that the animal did not have any stripes or markings on its body, which was almost black with a faint brownish tinge. The animal was standing still in some burnt grassland and shortly afterwards suddenly volted. Its movement was fast and lithe, which clearly indicated that the animal, which had the size of a piglet of about three months age, was actually a mature animal and naturally was not a *Sus scrofa*.

I was told that the animal was the "smaller" pig, which had become very rare and not easily sighted any more. Since the animal had such a markedly different appearance to the Wild boar and I strongly suspected that this could be the Pigmy hog (*Sus salvanius*), which had recently been declared extinct by E.P. Gee in his book named "Indian Wild Life", published in 1958, I tried to track the animal but failed. My next sighting of pigmy hogs came about some 3 months later in the same area when we saw only one animal, which was also running away. Naturally, identification remained uncertain. However, about one month later I saw a sounder of three. A male and two females were foraging togheter when we sighted them and soon the three trotted away. But before they left, they stood still for a brief while, which offered me the chance to have a clear, if brief, observation.

Meanwhile I studied whatever literature that was available on pigmy hogs as well as a mounted head and shoulder trophy at Gauripur. I had now no doubt that Pigmy hog survived in Manas. I contacted E.P. Gee, but he was not prepared to accept my unconfirmed identification. I invited him to come to Manas to see for himself, but although he promised to do so, the trip never took place before his sudden death in 1966.

Subsequently, I sighted pigmy hogs repeatedly in the same area at Manas, east of Bhuyapara, near Digjari stream and I am quite sure only a few sounders were alive in that area at that time. In 1969 I sighted pigmy hogs near Latajhar and also near Kuribeel. I also found some old nests, which proved they had colonised this area and, more importantly, they were breeding. In later year, I sighted the species or found conclusive evidence of its presence in many other areas, east of the Beki River, also known as the Manas River.

1. Clue to a successful propagation

As far as I can understand, the main reason for the disappearance of the pigmy hogs over most of its former range is the loss of habitat and poaching of the animal for its meat, which is reported to be extremely palatable. This is a highly specialised species, found only in the tall grass habitat of the Terai Bhabar belt in the sub-Himalayan tract. Though I had once found a dead pigmy hog being carried out by some hunters in the Cachar district of southern Assam, I could not find any other conclusive evidence of the existence of this animal in that area. In any case, the grassland in such areas of sub-Himalayan tract came under tremendous pressure of the rising population since the 1940's. Most such areas have been converted to agricultural land. In addition, the few remaining grasslands are utilised for grazing for domestic cattle and the commercial extraction of various forestry products, notably thatching grasses for roofing houses. The adjacent areas are inhabited by mostly plains tribal people of Bodo community and these people are traditionally heavily dependent on the forest resources. They collect various fruits, tubers, roots, etc. from these areas as food and also utilise various plants as medicines. As a result, the available habitat for this species was greatly disturbed and poaching was rampant. Besides, shooting of animals, traps and snares are used for poaching, which mostly went undetected.

Another factor of biotic interference also caused great harm to all the grassland animals in general and pigmy hogs in particular. This was deliberate burning of these grasslands. During the dry season, when the grass dried up in the high alluvional areas, the areas were set to fire from end of December till the advent of the monsoon showers, that come in early April. Burning even more that once during each dry season was extremely common, since burning would invariably produce a new flush of succulent fodders for domestic stock during these periods. However such "hot" burnings are extremely harmful for all types of wild animals due to loss of cover and the very intensive disturbance caused by movement of cattle and human beings. In addition, besides, illegal poaching was greatly facilitated through the concentration of game in the few remaining areas left unburnt.

Unfortunately, the breeding season of Pigmy hogs also coincided with this period, when their natural habitat was ransacked. As a result was that the animals had barely any chance of nest-building, essential for the protection of newborn litters, even if they could have survived and mate.

The Digjari area, where I first sighted the pigmy hogs, was situated quite close to some villages located near the southern boundary of the Sanctuary, where the intervening area was a large swamp, typical of the Terai. This swamp was quite extensive and impassable. As a result the high alluvional grassland on the north (Digjari area) was hardly utilised by the domestic stock and was spared the worst of this burning and other biotic interference. This is where the pigmy hogs managed to survive.

Since 1964 I managed to stop domestic stock grazing within the limits of the Manas Wildlife Sanctuary. We also attempted to cut off other human intrusion for various use. But we had very little manpower and other resources to accomplish these objectives. However, people of the surrounding villages, though resentful, realised that they cannot enter the area at will and damage the habitat. This was possibly the turning point because by 1969 the pigmy hogs were sighted in some other areas, as mentioned earlier.

There was also a marked improvement in this situation since 1975, after the inception of the Project Tiger, when Manas was made into a Tiger Reserve. More resources were available and it became possible to take anti-poaching activities more seriously and to ensure protection of the habitat more rigidly. Sustained hard work by a band of dedicated field staff made it possible to provide a more secure ecological environment for the wild animals, which was reflected by a marked upward trend of the animal population of many species.

In the concept of management, no human interference to nature was envisaged in the Project Tiger areas. But in this regards I made a small adjustment, which I feel needs to be mentioned. The area of Manas contains grassland and tree forest in the approximate proportion of about 45% and 55%. There are a large variety of habitat types available in the area with very pronounced edge effects and influence of ecotones. Manas thus holds 22 of the principal endangered species of wild Indian mammals, which is a greatest number than any other reserve in the sub-continent and gives an indication of the extreme biodiversity it supports. Naturally maintaining the diversity in habitat types is of extreme importance in the management of this area. But the soil and rock formation with the hot monsoon climate prevailing in the zone will not allow the grassland to persist for long, if totally left to the natural ecological processes. The climatic climax of this area is semi-evergreen to moist deciduous forest, as dictated by the local microclimate. If left to nature the grassland (except the swampy reeds bets) on the alluvional soil will gradually be transformed into the climax type of high forest. The entire area thus will be covered by tree forest in course of time, which will ultimately result in the loss of many of the grassland fauna.

A very pertinent question thus arises as to how the existing grasslands (covering over 40% of the Sanctuary area) are normally mantained. In fact, the most likely explanation is human induced burning of these areas, which has been undertaken since historical times. The burning presents the re-colonisation of the tree species on the one hand and on the other helps to promote vigorous growth of grass. A close look at any patch of grassland in Manas will show that tree seedlings, specially of the fire hardy types, are trying to invade and colonise the grassland near the edges, where the grassland merges with the tree forest. Unless the grassland was burnt, these seedlings would become established to replace the grass in course of time.

This circumstance has prompted the Park authorities to adopt annual grass burning as a management tool, though the normal practice of burning the grass when the entire area becomes dry at the end of December, was discarded. Instead rigidly controlled "early " burning was meticulously planned and practised. Such burning would start immediately after the monsoon (within a fortnight) from end of October or early November, as the case may be and continue till the onset of pre-monsoon showers. Since extensive areas of dry grassland are not available at these times, only small patches can be burnt. Every day during this period antipoaching patrolling parties would crisscross the area on elephant back and put fire to small patches which they may find to be dry enough to burn.

Naturally such burning would never be extensive and would never be very "hot". Even within the burnt areas many unburnt patches are likely to remain, as such patches were not dry enough to burn.

Such induced and forced burning would therefore mantain a chequered, irregular shape with a lot of intervening unburnt and partially burnt areas and would provide excellent cover conditions for both the herbivores and the carnivores alike. Such a practice also maintains sufficient succulent fodders for the herbivores during the lean period, as within 2 or 3 weeks of burning fresh and vigorous grass sprouts. In fact, recently burnt areas attract a large number of animals.

Loss of wildlife during burning has not been reported, though some loss of insects and rodents cannot be ruled out. However, I supervised burning on many sessions, when I kept a strict vigil and yet no loss of wildlife had been noticed by me.

The Manas area has a rather high water table and the area contains ground water in ample measure. Loss of ground moisture or dessication therefore appears to be marginal.

This practice of controlled, early burning of the grass produced excellent results. The percentage of grassland and tree land remains approximately the same even now, as in the early 1960's. There has been a steadily rise in the population of various species, of grassland species of wild animals in particular. All the species like Hog deer (*Axis porcinus*), Swamp deer (*Cervus duvauceli*), Pigmy hog (*Sus salvanius*), Hispid hare (*Caprolagus ispidus*), Rhino (*Rhinoceros unicornis*), etc., have shown marked improvement in status. Besides some species of birds, like the Bengal florican (*Eupodotis bengalensis*), the Swamp partridge (*Francolinus gularis*) and the Peacock (*Pavo cristatus*) have increased considerably in numbers. There are indications that things had been going in the right direction. There is, however, scope for finding out the best way to maintaining the grassland for the survival of *Sus salvanius* with some other endangered species for which detailed research is called for. Research is also warranted to find out biological facts of the life cycle of *Sus salvanius*, as very little is yet known about this elusive animal.

But some facts which have been observed and found from the limited literature may be interesting to discuss. It seems the status of the species, even at the best times, had been "sparse". The largest sounder I came across was of 5 animals. Usually these animals are commonly found in two or three only. The litter size is also small, 3 or 4 *per* litter.

The species occupies a habitat, which supports large variety of predators, large and small, including several raptors or birds of prey, who can easily lift a sub-adult and even an adult specimen. The species seems to have hardly any defence against the varied predators, except sharp instincts, aided by excellent eyesight, olfaction and hearing. The animal freezes on sensing danger and suddenly bolts at high speed. The thick tall grass they occupy, the grass tunnels they use for their movements and their crepuscular activities, all seem to aim at avoiding predation. But even so, the subadults are much more prone to predators because of their tiny size (mean weight only about 200 g at birth) and lack of protective capability of their mothers. I have observed such piglets being taken by birds of prey and even by a Monitor lizard (*Varanus salvator*). The percentage of survival of even one individual per litter is doubtful. In fact I have come across only one case where two yearlings were following their mother. It is a very delicate species and requires very careful handling.

Besides, in Manas National Park (upgraded in 1990) the species definitely occurs at a small wildlife sanctuary, named Barnadi, situated at a distance of about 70 km to the east. This small sanctuary is also included within the buffer zone of the Manas Tiger Reserve. Pigmy hogs had been captured by some tea garden people in 1971 for the first time on the edge of this sanctuary and the species is known to occur here till now, though the status here is indeterminate. Some sporadic reports had been received now and then about occurrence of the species and even sightings of the species from some other parts, which prompted William Oliver to request a survey to be conducted by Assam Forest Ranger, S.K. Sarma, who had known this species well. Unfortunately Sarma could not complete the study in 1987, though he had visited the more likely areas of probable occurrence of the Pigmy hog in northern Assam. However, he could not find any proof of the present existence of the species anywhere except in Manas and Barnadi Wildlife Sanctuary.

2. The future

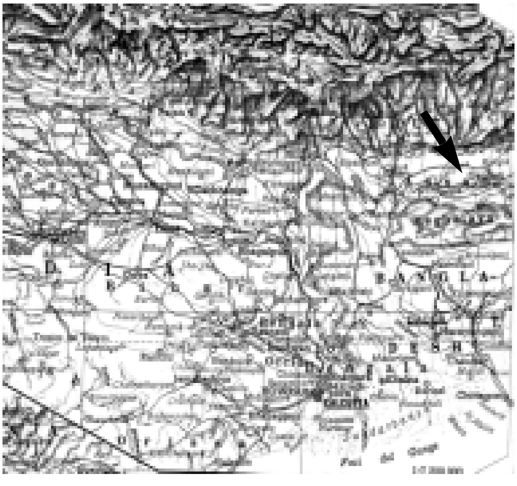
The future of this species seems to be hanging in precarious balance. The Manas area, in my estimation, appears to be the last bastion of this exacting and delicate species, where it made a definitive come back. But the future of Manas itself is covered by a thick cloud of uncertainty, arising out of a militant political movement taken up by the plain tribesmen in demand for a separate self-governed state (province). The militants have raided the Park on several occasions and terror reigned among the wildlife field staff. Nearly a dozen wildlife staff from the isolated interior areas have been withdrawn.

In effect the management authorities have lost any effective control over the area. Wild animals of economical value like the rhino, elephant and tiger have been killed by opportunist poachers. As far as I know, no appreciable damage to the pigmy hogs has been caused so far. Meanwhile possibilities of some settlements of the political imbroglio appears to become brighter in a decade.

The forest area in the State of Assam is under tremendous pressure from rising population. Nearly 13% of the total forest area is lying under encroachment and there seems to be hardly any hope of retrieving the situation. Maximum pressure is exerted on the grassland and hence the tiny Pigmy hog may not be able to get back any of its lost territory. The only alternative at the moment seems to be saving the remaining habitat and the populations at any cost. Both Manas and Barnadi have the legal status for the purpose. There have been repeated attempts in the past (last attempt was in 1982) to grab land for cultivation in Manas and Barnadi. But all these attempts have been thwarted. The Government is quite determined to protect these areas, which provides some hope.

Political understanding of the value of the gene pool that is being sought to be protected and the required support for preservation is of utmost importance for the success of the efforts. International concern and help may go a long way to plan and implement the necessary measures.

India



State of Assam

CREATING A PUBLIC UNDERSTANDING OF THE BIOLOGY OF THE BABIRUSA (Babyrousa babyrussa) WITHIN A CARING ZOO ENVIRONMENT

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Abstract: Studies on babirusa, carried out largely in zoos throughout the world and dealing with various biological and veterinary aspects, have yelded data which offer hypotheses which can be examined and tested by the observation of babirusa in the wild. This paper will review the results of these studies and present them within the context of generating interest in and awareness of the biology of the babirusa and the environment within which it lives.

Keywords: Babirusa, *Babyrousa babyrussa,* Suidae, Zoo conservation.

IBEX J.M.E. 3:37-40

1. Introduction

Studies of the anatomy, behaviour, physiology, and veterinary medicine of the babirusa have contributed to our understanding of the biology of the animal. The first part of this paper seeks to illustrate by means of examples how studies of the babirusa are currently being carried out. The second part addresses the topic of reporting the results of research studies. The information generated by research can often be translated into ideas and suggestions for the improvement of zoo practice with respect to enclosure design, nutrition, reproduction and veterinary care. However, it is more important that the next step is also addressed, namely the knowledgeable and interesting display of information to the general public.

But what is a babirusa? It is pig of unusual appearance (Fig. 1), the current opinion with regard to its place within the Suidae having been reviewed within the recently published account of the status survey and conservation action plan for the pigs, peccaries and hippos (Oliver, 1993). Endemic to the Indonesian islands of Sulawesi, Buru and the Sula and Togian groups (Macdonald, 1991; Macdonald, 1993) the subspecies from the northern part of Sulawesi is now represented in 29 zoos world wide. A studbook has been established for the species and active research of its biology has been stimulated (Plasa, 1992). The research activity of recent decades has concentrated largely on material available in museums and zoological collections; only a few studies being carried out in the field (Macdonald, 1991; Macdonald, 1993).

2. Anatomy

Reanalyses of the soft tissue anatomy of the limbs and digestive tract of the babirusa have revealed mistakes of identification in earlier work and the results have reversed the earlier suggestion that the babirusa was constructed in a significantly different way from the pig (*Sus scrofa*); in general the muscular anatomies of the two species are very similar (Macdonald *et al*., 1985; Kneepkens *et al*., 1989) and the stomach of the babirusa does not resemble that of the ruminant (Langer, 1988). Other anatomical studies, of the canine teeth in the skulls of wild-caught adult male babirusa, had led to the conclusion that the upper canines might be used in combat between males (MacKinnon, 1981). One adult was thought to use the curved maxillary canine to hook over one of the lower canines of his opponent, thereby disarming him. It was believed that this would then allow him to use his own lower canine to inflict injury on the throat or face of the disarmed opponent. However, recent X-ray analyses of the male skull demonstrated that the maxillary canine has a relatively shallow socket and would be unable to withstand large leverage forces (Macdonald *et al*., 1993).

3. Behaviour

Studies of the agonistic behaviour of babirusa have so far revealed no evidence that the adult males normally use their teeth during male-male interactions. The boars were seen to go through a series of aggressive behaviours which could be categorised (Macdonald *et al.*, 1993). The ultimate form of agonistic behaviour was described as "boxing", and involved the two males raising themselves off the ground until both were standing on their hind legs facing one another, leaning and paddling against the chest and shoulders of their opponent (Fig. 1A). Their snouts were held as high as possible. Females did not employ the same strategy. Ironically they did use their teeth, in this case their chisel-like incisors to nip at the forelimb or foot of the opponent.

Figure 1A - "Boxing" behaviour demonstrated by two adult male babirusa. Note they are stretching their noses as high as possible and paddling with their forefeet.

Both sexes were able to stand on their hind limbs, however, the female being seen to have the ability to balance on her hind limbs in order to browse the leaves of trees in her enclosure (Fig. 1B). Care of the skin would seem to be implied by the wallowing activity seen often in the heat of the tropics (Fig. 1C); it is an option largely denied that animals in European zoos due to current pen design.

Figure 1B - Adult female balancing on her hind legs while browsing the leaves of a tree.

Figure 1C - Male babirusa bathing in a muddy pond in the late morning tropical heat.

4. Physiology

The reproductive physiology of the babirusa is poorly understood. Observations of animals in zoological collections suggest that the continual presence of the boar within the same enclosure may depress the production of young. By way of contrast, however, the separation of the male and female into adjacent pens, with mixing restricted to during oestrus seems to promote fecundity (Vercammen, 1991). Both the presence of several boars within a single pen of females, or individual boars with sight and scent of one another in adjacent pens of females also appear to stimulate competition and enhanced reproductive activity. The relatively small size of the female reproductive tract is consistent with the small size of the litter which ranges from one to three young after a gestation of about 158 or 159 days (Vercammen, *op. cit.*). However, video recording of the delivery of babirusa piglets has demonstrated that those which are too weak to survive the night are consumed by the mother, and are thus never recorded by the staff when they come on duty. There is an unconfirmed report from the field that the babirusa can produce four fetuses (Patry, 1990).

5. Veterinary

The increased number of babirusa in European and American zoological collections has led to a greater awareness of the need to gather observations related to their husbandry and care. For example the rapid growth of the teeth of the male is such as to require them to be routinely cut in order to prevent them from growing into the forehead. The chronic relatively poor condition of feet has been noted but remains to be investigated. Increasing interest in other parts of the animal's skeletal anatomy has recently drawn attention to the presence of undiagnosed spondylosis and the European coordination of research on the species has revealed the presence of intra-abdominal tumours.

6. Care within zoos

Zoos and their keepers, by their very nature, care for their animals as individuals. For example, attention might be expected to be paid to the structural weakness of the upper canine and its socket with regard to the specific design of fencing. The ability of the animal to stand on its hindlegs inplies that cut branches might be set in holders and on trees above ground level in order to allow the animal to stretch to browse. The ability of the animals to interact in a series of interesting ways without causing one another serious damage suggests that holding them in larger group sizes might be explored.

Increasingly, however, the attention of zoo staff is being called away from the individual to the care of the species as a whole. In a corresponding way, there are changes and an adjustment underway in the role of the zoo, moving it gradually from that of a park exhibiting the range of forms of animal species in the world towards something more akin to an informed teaching and research institution (Macdonald and Leus, 1993). Progressively, the current and prospective status of groups of animals, such as the pigs, are being evaluated and species are being classified as "rare", "vulnerable", "endangered" or "critically endangered" (Oliver, 1993). World-wide the zoo community is being invited to participate in and increasingly concentrate their resources on the captive breeding of species which fall within these categories. Taxon advisory groups (TAGs) are increasingly liaising with workers in the field to help ensure the conservation of species. Effective conservation of the available genetic variability depends upon more thorough collection and dissemination of information about their numbers and distribution in the wild as well as the biology of individual species. Crucially, however, funding and other support of these activities can be expected to rely heavily upon information and the explanation offered to the general public about what is going on within the zoo in this regard and why. Greater effort will be required of the zoos in the future to show and tell the public more of the details of the biology of the babirusa, and to illustrate how and why the animal is being conserved within zoos for its eventual return to a restored natural environment.

7. Acknowledgements

The hospitality shown by the staff in the zoos of Europe and Indonesia during the course of these studies was much valued. We are also grateful to the Commission of the European Community, the Development Trust of the University of Edinburgh and the Balloch Trust for their financial support.

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ANALYSES OF DIETS FED TO BABIRUSA (Babyrousa babyrussa) IN CAPTIVITY WITH RESPECT TO THEIR NUTRITIONAL REQUIREMENTS

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Abstract: Although very little is known about the diet of Babirusa in the wild, they have been successfully kept in captivity in zoos around the world for 200 years. Studies have shown that the anatomy of their digestive tract is quite different from that of the domestic pig and as a consequence their food digestion is also likely to be different. As part of a wider study of the digestion of the Babirusa, the diet fed to animals in 25 zoos worldwide (16 Europe, 7 USA, 2 Indonesia) were analysed for their nutritional content. The results of these analyses will be presented and discussed in the light of the findings of other recent experiments on the food selection, diet digestion and foraging behaviour of Babirusa.

Keywords: Babirusa, *Babyrousa babyrussa,* Suidae, Feeding, Zoo, Diet composition.

IBEX J.M.E. 3:41-44

1. Introduction

Studies have shown that the anatomy of the stomach of the Babirusa is more complex than that of the other pigs (Langer, 1988). As a consequence, the composition of the diet they select and the way in which this is digested can be expected to be different. Information on the composition of the diet of Babirusa in the wild is limited to a few general statements, indicating that they eat leaves, roots and fruits as well as invertebrates, meat and fish (Valentijn, 1726; Whitten *et al.*, 1987; Macdonald, 1991). Despite this lack of information on their food habits in the wild, Babirusa have been successfully kept in captivity for at least 200 years. The first Babirusa kept in Europe were housed in “la Ménagerie du Roi”, Paris, and were fed on a mixture of grass, herbs, roots, fruits and grains as well as occasional animal matter (Geoffroy-St-Hillaire & Cuvier, 1842). In more recent times Babirusa in zoos around the world are still fed on a mixture of roughly the same items. As part of a wider study of the food selection and digestion of the Babirusa, the diets fed to animals in 19 zoos world-wide were analysed for their nutritional contents. A selection of the results of these analyses (dry matter, protein and digestive energy) are presented here and discussed in the light of the findings of other recent experiments on the food selection, diet digestion and foraging behaviour of the Babirusa.

2. Material and methods

From March 1991 until May 1993 all zoos world-wide housing Babirusa (16 zoos in Europe, 7 in the United States and 2 in Indonesia) were sent a questionnaire. It requested information on the constituents of the diet, the way in which the food is offered, the daily amounts fed and the preferences and dislikes of their animals. Additional information was gathered during personal visits to some of the European zoos. Data of a sufficiently detailed nature to allow analyses of the diet’s nutritional contents was received from a total of 19 zoos (13 from Europe and 6 from the United States). Each zoo was allocated a code number and will be referred to by means of this number throughout this paper.

Items fed to the animals were divided into four categories: 1) fruit and vegetables; 2) pellets, grains, bread, nuts and oils; 3) meat, fish and eggs; 4) forage (including grass, hay, alfalfa, hydroponic barley, branches, leaves etc). The amount of dry matter (DM), crude protein and digestible energy (DE) for individual items within these categories was calculated from the data published by Schemmel *et al.* (1969), Jones (1979), ADAS (1986) and Holland *et al* (1991). The nutrient content of commercial pellets was calculated either from the labels sent by the zoos, or in the absence of labels estimated from the information available. The best estimate of DE values for foods fed to the

Babirusa was either derived from values measured in the domestic pig (ADAS, 1986) or calculated from the formula:

$$\mathrm{DE}\ (\mathrm{MJ/kgDM}) = \frac{\begin{array}{c}\text{crude protein(g/kgDM)} \cdot 18 + \text{Ether extract(g/kgDM)} \cdot 31.5 + \\ \text{carbohydrate(g/kgDM)} \cdot 16.3 - \text{Englyst fibre(g/kgDM)} \cdot 14.9\end{array}}{0.96}$$

which was adapted from the Provisional Equation published by the EAAP Working Group (Batterham, 1990).

For this presentation, the daily intake of DM, crude protein and DE by the adult male Babirusa was calculated. Information on the amounts of forage ingested was often too vague to allow even rough analyses of its nutritional composition. The effect of forage on the daily intake of protein and other nutrients will be discussed for those zoos that fed a fixed amount of forage daily and all year round.

3. Results

Results are summarised in figure 1(A-D). For each graph, the amount of food and nutrients offered was plotted in ascending order to illustrate the wide range of amounts fed (total amount of food = 1400 - 4770 g; DM = 355.5 - 2108 g; crude protein = 43.1-398.5 g and DE = 5.49-29.12 MJ). Note therefore that the sequence of the zoo code numbers on the x-axis is different in each of the four graphs. This was to demonstrate that the zoos feeding the highest amounts of food (Fig. 1A) are not necessarily those which also feed the highest amounts of DM, protein and DE (Fig. 1B-D) and vice versa. Zoos feeding the highest amounts of DM (Fig. 1B) tended to be those feeding the highest amounts of protein and DE (Fig. 1C-D).

4. Discussion

The wide range of amounts of total food fed, and the lack of a straight relationship between total food fed and DM can be explained by the differences in the proportions of the various food categories (fruit and vegetable; pellets, grains, bread, nuts and oils and meat, fish and eggs) within the diet. Zoos feeding large amounts of fruit and vegetables may seem to be feeding their pigs a large amount of food. However, a lot of the weight fed to these animals is water. Similarly, when a large proportion of the diet is made up of commercial pellets (water content approximately 13%) the zoos may be perceived to be feeding their animals only a small amount of food. But in fact, the animals are receiving a lot more nutrients than when they would be fed an equal weight of fruit and vegetables. Particular caution should be taken in the feeding of pellets and grains since small amounts of these items can represent a large proportion of the total amount of DM, protein and DE that the animal is receiving.

Four zoos provided data which enabled the exact amount of forage consumed per day to be analysed. For example, zoo number 7 feeds 200 g grass daily which raises the values in figure 1 only slightly (from 3617, 788.91, 55.11 and 7.77 to 3817, 818.90, 60.12 and 8.03 for total amount of food, DM, crude protein and DE respectively). In zoo number 22 the animals receive 1.6 kg of alfalfa hay daily. This raises the values for total amount of food, DM and DE (from 3826, 1827.5 and 23.98 to 5425, 3289.9 and 37.73 respectively), but its impact is most important on the amount of protein in the diet which rises from 398.5 to 647.10. Because it is dried, alfalfa hay contains significantly more dry matter per unit weight than fresh grass. In addition alfalfa hay has a higher protein and DE content than other hays. Therefore, caution should again be taken when feeding alfalfa since small amounts will make large contributions to the total DM, protein and DE intake.

Experience with the feeding of domestic pigs suggests that the range of values for the different nutrients in the Babirusa diets is too wide for all the diets to supply the requirements of the animal. The exact nutritional requirements of the Babirusa remain unknown, but a number of estimates can be made from studies carried out on the domestic pigs. The maintenance DE for a 90 kg Large White pig can be calculated to be 13.5 MJ/day from the equation: ME maintenance $=1.75Pt^{0.75}$, with Pt = protein weight in the body (16% of the body weight for a Large White pig) and DE = ME/0.96 (Whittemore, 1993). Taking into account that the Babirusa has a smaller mature size and is a non-developed pig, its Pt can be expected to be lower than that of a Large White pig. If we estimate the Pt of the Babirusa to be 12% of the body weight, its maintenance DE would be 11.0 MJ/day.

The maintenance requirement for crude pro-

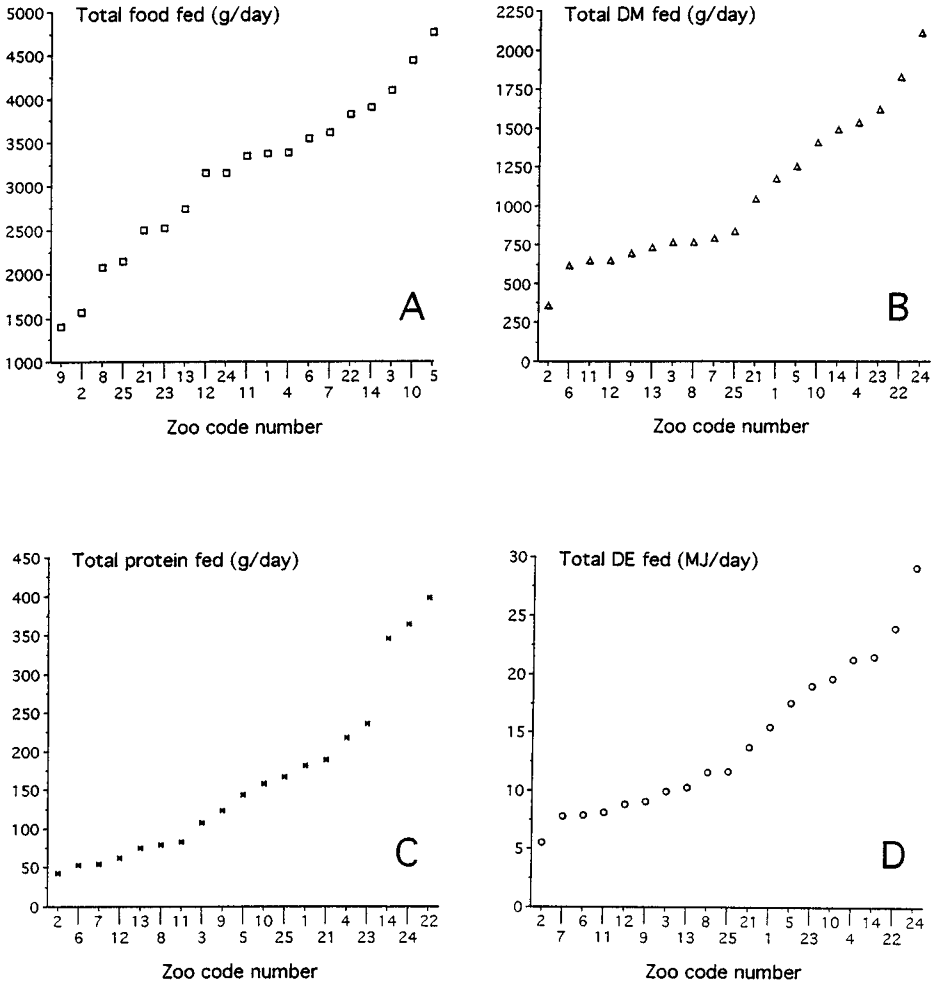

Figure 1 - A: Total amount of food offered daily to an adult male babirusa, not including forage.
B: Total amount of dry matter (DM) offered daily to an adult male babirusa, not including the DM derived from forage.
C: Total amount of crude protein offered daily to an adult male babirusa, not including the crude protein derived from forage.
D: Total amount of digestible energy (DE) offered daily to an adult male babirusa, not including the DE derived from forage.

tein in the diet can be estimated from the formula: Ideal protein maintenance = 0.004 Pt (Whittemore, *op cit.*). Using the same Pt values as above yields 58 g for Large White and 43 g for Babirusa. If we estimate the protein score to be 0.7 and the digestibility 0.75, then the required amount of crude protein in the diet for maintenance of a 90 kg animal is 110 g for Large White and 82 g for Babirusa.

When we apply the estimated values for the Babirusa to figure 1C and 1D, some zoos seem to be feeding their animals up to four times the requirement for protein and up to twice the requirement for DE, which will result in the animals putting on weight. By way of contrast, a number of other zoos seem to be feeding their Babirusa below the maintenance values. These animals should theoretically not be able to survive. This anomaly may be explained either by the feeding of forage (the value of which could not be calculated into the total), the incomplete reporting of information in the questionnaire, or by the extra food given to the animals by the public; peanuts and bread are two of the favourite items fed to the animals in a zoo, both of which are high in energy. For example, 100 g of peanuts contributes 93.7 g DM, 25.6 g crude protein, and 4.42 MJ DE and 100 g bread contributes 60.5 g DM, 8.5 g crude protein, 0.96 MJ DE. Even small amounts of these items fed by the public can therefore make an important impact on the total daily intake.

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PRIORITIES FOR CONSERVATION ACTION AND RESEARCH ON AFROTROPICAL SUIDS

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IBEX J.M.E. 3:45

The research and conservation action priorities for the three genera of Afrotropical Suids (*Phacochoerus*, *Potamochoerus* and *Hylochoerus*) are reviewed and constitute the "Action Plan" of the Pigs and Peccaries Specialists Group of IUCN/SSC for the Afrotropical Region. Although these Suids have large distributions across the continent, incorporating a wide range of natural habitats, our investigations reveal that basic data on their specific distribution, conservation and legal status are lacking. Nonetheless, some of the major gaps in our knowledge have been identified and prioritized for future investigation. The principal threats to the survival of these animals - habitat destruction and over-hunting - vary in importance from country to country, but the Action Plan highlights the main problem areas. Highest priority is given to conservation strategies for the taxa known to be most at risk like *Phacochoerus aethiopicus delamerei*, *Hylochoerus meinertzhageni ivoriensis*, and for local populations of *Hylochoerus meinertzhageni meinertzhageni* and *Hylochoerus meinertzhageni rimator*. More research is needed to assess the taxonomic affinities of *Phacochoerus africanus aeliani* and *H. meinertzhageni* ssp.? of South Ethiopia. Specific field surveys are recommended to determine the status, distribution and management initiatives needed to conserve these remnant populations. Among these, the review of protected areas network, the development of projects promoting sustainable utilisation of natural resources and the role of wild pigs in crop damages and as vectors of diseases are of particular importance. Outside the Muslim countries, all Suids are important sources of protein and constitute a significant part of the bushmeat market. Subsistence and commercial hunting are virtually uncontrolled in most countries and their impact should be assessed in view of regulating the offtake and developing sustainable schemes that can contribute to the local economy. The development of education/awareness programmes in certain countries are identified as a means to focus public attention to the potential importance of conservation. Training of biologists and wildlife managers are recommended to promote adequate research, monitoring and conservation management of Afrotropical Suids. A list of specific future research priorities is appended to the Action Plan; these address the gaps in our knowledge of their systematics and biology which must be tackled in order to develop the most appropriate conservation and management strategies for these species.

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ASSESSMENT OF THE PRESENT DISTRIBUTION OF THE FOREST HOG (Hylochoerus meinertzhageni) IN ETHIOPIA

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Abstract: New data on the present distribution of *Hylochoerus* in Ethiopia are presented and compared with ancient records. The distribution is analysed and discussed. Recommendations for further priority research and conservation action for the species is given.

Keywords: *Hylochoerus*, Suidae, Conservation, Africa.

IBEX J.M.E. 3:46-48

1. Introduction

Once distributed over a wide range of woodlands and Afromontane forests in southern Ethiopia, the Forest hog (*Hylochoerus meinertzhageni*) population is said to have been divided into various isolated sub-populations due to deforestation, hunting and the extension of agricultural lands.

Accounts about the present distribution of the Forest hog in Ethiopia are rare and often very vague; most of the records published in the literature are contained in Ansell (1971) and Yalden *et al.* (1984). These authors enumerate the locations and/or areas where the species was known to occur at the time and list historical records of both field observations and trophies collections. The climatic and tectonic barriers which separate the Ethiopian population of *Hylochoerus* from those of Sudan, Uganda and Kenya have made it to evolve in isolation for a very long period of time. This led several authors (d'Huart, 1978; Yalden *et al.*, *op cit.*) to believe that the Forest hog in Ethiopia might be representing a new subspecies, distinct from the nominate (or "giant") race *Hylochoerus m. meinertzhageni*. Indeed, these ecological barriers are much older than the Dahomey Gap, which separates two distinct subspecies of Forest hog, *H.m. ivoriensis* and *H.m. rimator*. In a recent review of the priorities of conservation actions and research on the Afrotropical Suids (d'Huart & Oliver, 1993) it has been recommended that further investigations on the distribution, conservation and taxonomic status of *Hylochoerus* be made in Ethiopia. The present preliminary assessment has been carried out in that context.

2. Present distribution

On the basis of a review of recent publications (Sierra Club International, 1987; Hillman 1993) and of interviews with various Ethiopian experts, we have been able to draw a preliminary map of the present distribution of *Hylochoerus* in the country (Fig.1). This information is undoubtedly incomplete and further data will be collected in the future.

List of areas/locations where Forest hogs are known or reported to occur:

- Ilubabor/Kefa Province:

1. a vast area extending from the eastern part of Gambela N.P. to the South-East, including Abobo, Gog, Godare, Kaffa Mountains, Guraferda, Bebeka, Tepi, Mizan Teferi and Temenja Yazhi.

- Kefa Province:

2. a limited area between Bonga, Diri Goma and Ameya.
3. between Ameya and Shama.
4. a 30km radius around Jima.
5. between Alga, Atnago, Suntu Genet and Botor Bocho.

- Gamo Gofa Province:

6. the Maze region, between Gesuba, Galecha and Zefine.

- Sidamo Province:

7. a vast area between Finchawa, Agere Maryam, Fiseha Genet, Solemo and Jeri Bule.
8. between Shakiso, Zembaba and Irba Muda.

- Bale Province:

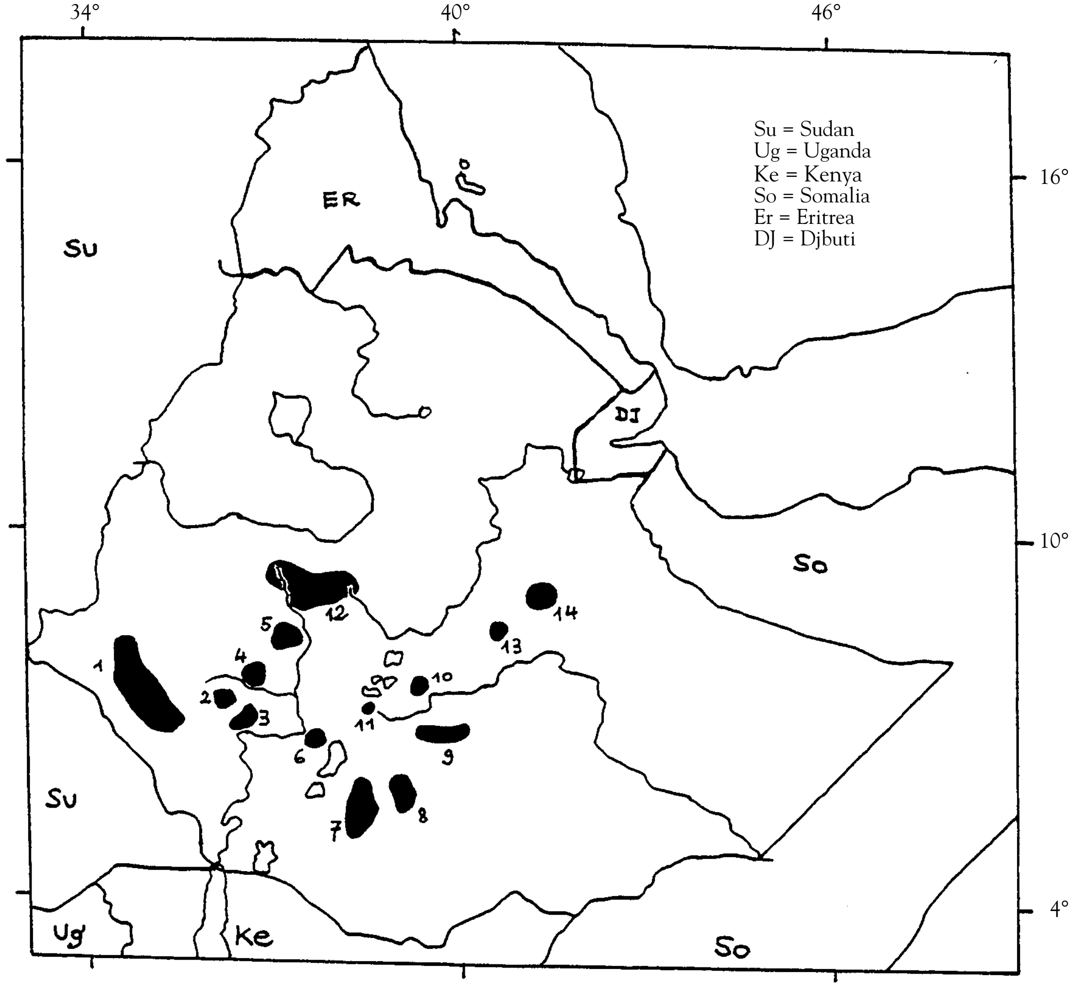

Figure 1 - Distribution of *Hylochoerus* in Ethiopia

9. the vast Harenna Forest, in the Southern part of Bale N.P., North of Mena.

- *Arssi Province:*

10. between Meraro, Gobesa, Ticho, Lemu and Bekoji.

- *Shewa Province:*

11. forested areas surrounding Wondo Genet.
12. a vast area between Adis Alem, Ginchi, Gedo, Bako, Tibe, Seyo, Shenen, Arbi Bila and Boda, including Menagesha Forest Reserve.

- *Harerge Province:*

13. Kuni Muktar Mountain Nyala Sanctuary, between Kuni and Bedesa.
14. Chercher Mountains between Bike, Waybera, Muleta, Kobo and Karamile.

As such, this fragmented distribution does not confirm the records of *Hylochoerus* in the area of Gore (Ilubabor Province) as reported in Yalden *et al.* (*op.cit.*), but it confirms its continued presence in all previously reported areas. In addition, a number of new areas have been added to the known distribution.

3. Discussion

Having superimposed this distribution map of *Hylochoerus* on the vegetation, topographic and conservation areas maps published by

Hillman (*op.cit.*), the following remarks can be made:

- there seem to be two distinct sub-populations of Forest hog separated by the Rift Valley; although this does not represent an impassable obstacle for the species, further investigations should assess the taxonomical homogeneity of the Ethiopian populations.
- *Hylochoerus* still inhabits a wide range of forested habitats: these are principally undifferentiated Ethiopian woodlands, evergreen or semi-evergreen bushlands and thickets and Afromontane forests (*Podocarpus*, *Juniper* or *Hagenia*). It is obvious that both *Acacia/Commiphora* bushland and thickets, as well as tropical altimontane formations are avoided. This can be explained by the Forest hog 's need for very dense cover in some parts of its habitat, but also by the fact that the species tends to avoid extreme variations between diurnal and nocturnal temperatures (d'Huart, *op.cit.*).
- the species is scattered in small isolated populations; it is not clear yet as to what the main causes of these isolations are (deforestation, extension of agricultural lands, overhunting, etc.), and this aspect is worth further investigations. It is possible, however, that the distribution of *Hylochoerus* in Ethiopia is wider than shown in figure 1 and that connecting corridors between the populations of those areas do exist.
- most of the areas shown in figure 1 are above 2,000 m in altitude; this is particularly evident for *Hylochoerus* population living close to the Rift Valley, where human pressure is higher. Therefore, these remnant areas might possibly be seen as isolated refuges.
- *Hylochoerus* lives mainly outside the existing protected areas; Gambela N.P.(1), Bale N.P.(9) and Kuni Muktar Sanctuary (13) seem to be the three single areas allocated to nature protection where the species exists. Some of the other places are comprised within "Controlled Hunting Areas" like Akobo and Mizan Teferi (1), Maze (6), Bale (9), Arssi (10) and Chercher & Abba Guggu Mountain (14). In the absence of precise knowledge on the levels and trends of these populations, this situation does not guarantee a sustainable conservation management of the species. The recent decision (September 1993) by the Ethiopian authorities to temporarily ban all forms of hunting has been taken as a precautionary measure in order to avoid excessive off-take of some fragile species.

4. Conclusion

Although the results of our assessment has revealed new informations about the distribution of the Forest hog in Ethiopia, it has also stressed the many gaps in our knowledge of basic data on this species. As recommended by d'Huart and Oliver (*op cit.*), no appropriate conservation management of *Hylochoerus* in Ethiopia could be implemented unless further research is conducted in the following areas: taxonomical status, geographical distribution, level and trends of the various sub-populations, revision of the protected areas network, revision and adaption of the legislation related to conservation and management of the species.

5. Acknowledgements

The gathering of information about the distribution of *Hylochoerus* in Ethiopia has been possible thanks to the kind cooperation of the following people: Ato Leykun Abunie, Ato Afework Bekole, Dr. J. C. Hillman, Ato Tesfaye Hundessa, Mr. T. Mattanovitch, Dr. M. Nicoll, Ato Goitom Redda, Mr. N. Roussos.

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RELATIVE ABUNDANCES OF PECCARIES IN AREAS OF DIFFERENT HUMAN PRESSURES WITHIN THE BENI BIOSPHERE RESERVE, BOLIVIA

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Abstract: Relative abundances were compared for two species of peccary (*Tayassu pecari* and *T. tajacu*) and four species of diurnal primates (*Ateles paniscus chamek, Cebus apella, Saimiri sciureus boliviensis* and *Alouatta seniculus*) in the Beni Biosphere Reserve, Bolivia. The study area was divided into three zones based on differences in type and intensity of human interference. Patterns of abundance for different species are discussed relative to human uses in the three zones.

Keywords: Peccary, Primates, Human activity, Hunting pressure, Conservation.

IBEX J.M.E. 3:49-52

1. Introduction

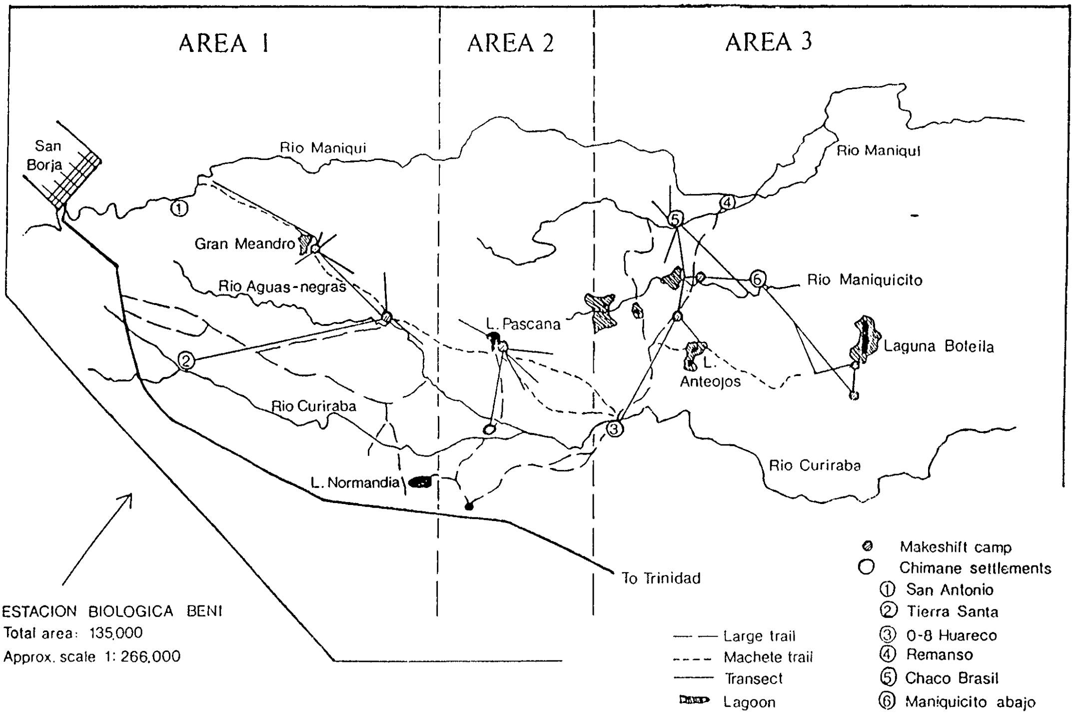
The Beni Biosphere Reserve covers 135,000 hectares within the Beni alluvial plains of Bolivia and comprises an archipelago of subhumid forest surrounded by seasonally inundated savannah. These forests are predominantly low-lying seasonally inundated or gallery forests in which lianas and fast growing species such as *Cecropia* spp., *Ficus* spp., *Scheelea* spp. and *Astrocaryum* spp. predominate (Ribera, 1988).

Both indigenous Chimane and colonists inhabit the reserve and mammal populations are especially affected by this human presence through the direct effects of subsistence hunting. Colonist settlements are found along the banks of the Maniqui river, whereas Chimane settlements are more scattered through the reserve. In 1989 there were approximately 800 Chimane living in the reserve (Chicchón, 1992).

As documented through out Latin America (Redford & Robinson, 1991) peccaries are important prey species for subsistence hunters within the Beni Biosphere Reserve. Chicchón (*op. cit.*) found that peccaries account for almost one fourth of the total number of game animals obtained, followed by rodents and then primates. Peccaries and primates, especially the black spider monkey, *Ateles paniscus chamek*, are highly desired species by the Chimane. Colonists also favour peccary meat but rarely consume primates.

Due to the predominance of concern over deforestation more cryptic but possibly equally destructive effects of "low impact" forest activities may have been overlooked (Redford, 1992). Through the effects of subsistence hunting, large animals may become ecologically extinct despite the apparent integrity of the forest vegetation. Long term ecological effects of defaunation may be considerable because of their important role as seed and seedling predators, seed dispersers or pollinators (Janzen, 1970; Smythe, 1986; Terborgh, 1988). Peccaries are important seed predators that can consume the hard seeds of palms such as *Astrocaryum* spp. and *Socratea* spp. that other terrestrial frugivores are unable to crack (Kiltie & Terborgh, 1983). The white-lipped peccary, *T. pecari*, is also particularly interesting because of its atypical behaviour, for a forest ungulate, of forming large herds. White-lippeds are found in herd of 50-200 individuals and must therefore cover great distances in order to find sufficient food (Kiltie & Terborgh *op. cit.*). Although their wide-ranging behaviour buffers them against local habitat disturbances it renders them more vulnerable to habitat fragmentation.

In the light of these considerations, baseline information on game animal densities was a priority for the reserve administrators. In addition our study sought to provide early indications of any variation of hunting impact by comparing densities across the zones within the reserve.



Map. 1

2. Methods

Research was conducted between July and September 1990. For censusing purposes the reserve was divided into three zones on the basis of perceived differences in the type and intensity of human interference (Map 1). Zone 1 comprised the area closest to San Borja, which is characterized by the greatest number of human settlements, increased encroachment of mestizo agriculturalist and illegal logging. As well as suffering the most habitat disturbance and hunting impact, this area has been settled for at least fifty years. Zone 2 comprised a strip in the centre of the reserve, contains no human settlements and is frequently visited by park guards, tourists or scientists. Thus, human presence is predominantly benign in that hunting pressure and habitat disturbance is minimal. Zone 3 contains a colonist settlement, El Remanso, and the Chimane settlements of Chaco Brasil, Maniquicito and 08 or Maraca. El Remanso was originally established by colonists who were involved in the trade of animal skins and live animals. Today this trade is no longer important, but this area is still affected by subsistence and some commercial hunting.

Transect systems in each of the three study zones comprised a mixture of established and fresh cut trails. Transect length was determined through pacing. For each group of target organisms encountered the position of the group was noted, the number of individuals in the group counted, where possible, and estimated when numbers were too high (frequently for *T. pecari* and *Saimiri sciureus boliviensis*). The perpendicular distance from the transect line to the point where the group was first observed was estimated in the hope of obtaining sufficient sightings for the calculation of absolute densities using line transect methods (Burnham *et. al.*, 1980).

3. Results

A total of 311.6 km was covered in the three zones of the reserve as outward transects. However, not enough encounters with any of the species were obtained for absolute densities to be calculated. Nonetheless, the number of

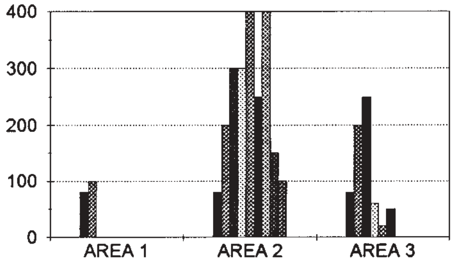
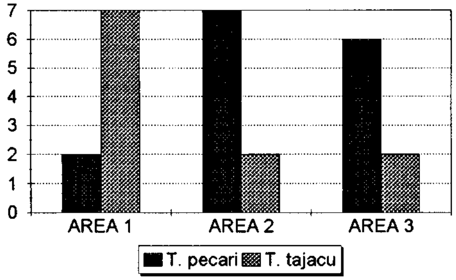


Figure 1. White-lipped peccary (*Tajassu pecari*) group sizes.

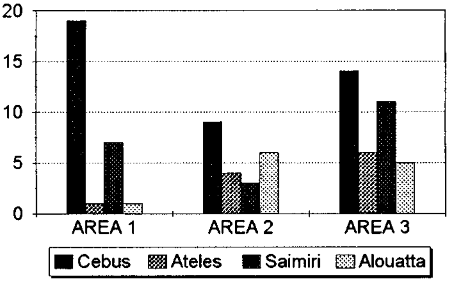
encounters with each species where compared with those expected relative to the number of kilometres walked in each area. Only outward walks along trails were used in the number of encounters, but all encounters were used to calculate mean group sizes.

Group size did not differ significantly between the three areas for any of the species, with great overlaps in the mean group size and their 95% confidence limits. Because of this group encounters were considered an accurate index of relative abundance. The overlap in group sizes of white-lipped peccary between areas is illustrated in figure 1. The numbers of encounters in each area are summarised in figures 2 and 3. In area 1 there were significantly more encounters with *T. tajacu* than areas 2 and 3 but significantly less encounters with *T. pecari*. Encounters with *Cebus apella* were significantly greater in Area 1, whereas *Alouatta seniculus* encounters were significantly reduced. *Saimiri sciureus boliviensis* and *Ateles paniscus chamek* encounters did not differ significantly between the areas.



T. pecari	*T. tajacu*
X2 = 6.8	X2 = 8
d.f = 2	d.f = 2
p<0.05	**p<0.05**

Figure 2. Peccary group encounters.



Cebus apella	*Ateles paniscus*	*Saimiri sciureus*	*Alouatta seniculus*
X2 = 9.46	X2 = 3.3	X2 = 1.13	X2 = 9.9
d.f = 2	d.f = 2	d.f = 2	d.f = 2
p<0.01	**n.s**	**n.s**	**p<0.01**

Figure 3. Primate group encounters.

4. Discussion

The relative abundance of white-lipped peccaries (*T. pecari*) found within the reserve correspond closely to the results we would expect when considering the different pressures from human activity in the separate areas. Collared peccary (*T. tajacu*) relative abundances show some unexpected distribution patterns. The red howler monkey (*Alouatta seniculus*) relative abundances followed the pattern of distribution of white-lipped peccaries. Black spider monkeys (*Ateles paniscus chamek*) are rare through out the reserve and capuchin (*Cebus apella*) and squirrel monkeys (*Saimiri sciureus boliviensis*) seem to mirror patterns of small-sized primate population densities in hunted areas.

Both species of peccaries have similar intrinsic rates of population increase and are highly sought after species by both the Chimane and colonists. However, the proximity of Area 1 to San Borja makes it more prone to visits by commercial hunters. Commercial hunters frequently target white-lipped peccaries in preference of other species because of the facility of harvesting large numbers from one herd. Additionally, collared peccaries are known to inhabit one of the largest ranges of any living ungulate and can therefore adapt to a variety of conditions, whereas white-lippeds are more specialized in their habitat needs (Sowls, 1984). Therefore patterns in habitat disturbance in this area, caused by the increased activity of agriculturalists and the clandestine loggers, could be responsible for the reduced numbers of white-lippeds. It is also possible that collared peccaries are benefitting from the reduced numbers of white-lippeds in this area as both species share a preference for palm nuts, although only the latter can crack the hardest. However, we are unable to test this hypothesis at present.

The red howler monkey has been described as an emergency source of protein for the Chimanes, due to their large size and the ease with which they can be located. It is therefore interesting that its pattern of population density follows that of the white-lipped peccaries. Both the black spider monkey and red howler monkey appeared scarse in the reserve. The spider monkey has become patchily distributed over much of its former range, due to local extinction after excessive hunting pressure (Mittermeier & Coimbra-Filho, 1977).

Capuchin monkeys appear not to have suffered from the activities near San Borja. Both capuchin and squirrel monkeys are sometimes hunted, however their smaller size makes them less attractive. Other studies on hunting of primates have shown a shift to higher densities of smaller species and a reduction in the abundance of larger species (Freese *et. al.*, 1982; Emmons, 1984).

These results are preliminary and regular censusing should be used to corroborate them and monitor wildlife populations in the reserve. However, they do reflect the reduced hunting yields of large species which has been reported in Area 1. Chicchón (*op. cit.*) found that Chimanes in this area concentrate in the hunting of large rodents (Caviomorpha) which frequent their agricultural fallows, due to a reduction in the harvesting rates of larger species.

If the reserve is to ensure species survival and genetic diversity an element of animal population monitoring must be incorporated into its management. Subsistence hunting of vulnerable species should be discouraged and alternatives sought. The simple procedure outlined above could easily be carried out by parkguards as part of their regular routine patrols. Additionally at present the Beni Biosphere Reserve is an isolated conservation unit for large mammals because of the prevalence of hunting in the surrounding logging concessions. Species such as the white-lipped peccaries, with large area requirements will benefit the greatest from the inclusion of wildlife conservation into the mandate of logging concessions. The legal ban on hunting by loggers must be enforced.

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NOTE ON THE TAXONOMY OF PLEISTOCENE HIPPOPOTAMUSES

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Abstract: Although there are several recent works about systematics of genus *Hippopotamus* during Pleistocene, great confusion still remains. In Author's opinion *Hippopotamus incognitus* (referred to *H. amphibius*) and *Hippopotamus tiberinus* (referred to *H. antiquus*) are not valid species.

Keywords: Hippopotamidae, *Hippopotamus antiquus*, *Hippopotamus amphibius*, Paleontology, Phylogeny, Africa, Europe.

IBEX J.M.E. 3:53-55

Problems concerning the origin, the systematics and the stratigraphical distribution of the genus *Hippopotamus* have been discussed in the last years by several authors: Coryndon & Coppens, 1973; Coryndon, 1978; Pickford, 1983, 1989; Faure, 1984; Faure & Méon, 1984; Petronio, 1986; Mazza, 1991; Di Stefano *et al*, in progress.

At present the writer is involved in the morphometric study of some cranial remains, preserved at the Museum of Natural History of Paris, which were collected in several African deposits: Ternifine (Algeria), Omo Valley (Ethiopia) and Ain Hanech (Algeria). According to a preliminary study of these remains and taking into account some considerations about the phylogeny of the European hippopotamuses (Petronio, 1986; Di Stefano *et al,* in press), the following conclusions can be proposed in this note, which will be better justified and explained in a next and more descriptive paper.

1. Among all the hypotheses on the origin of the Hippopotamidae, the writer retains valid those of Pickford (1983, 1989), who assumes that Hippopotamidae originated from the Doliochoerinae and, more precisely, from the genus *Xenohyus* Ginsburg, a Tayassuidae of great size from the Early and Middle Miocene of Europe. The dental pattern of *Xenohyus* is similar to that of *Kenyapotamus* Pickford from the Middle and Late Miocene of Africa (Pickford, 1983) (16-8 Ma), which represents the more ancient genus of the family Hippopotamidae. Therefore, it is probable that the hippopotamuses originated from the Tayassuidae and that the genus *Kenyapotamus* gave origin to the genus *Hippopotamus*. The more archaic forms of this latter genus migrated towards Europe about 7-5 Ma ago (*Hippopotamus siculus* Hooijer and *Hippopotamus pantanelli* Joleaud in Italy, *Hippopotamus crusafonti* Aguirre in Spain and France). About 4 Ma ago, in the Kaiso Basin (Uganda) the presence of *Hippopotamus kaisensis*, the probable ancestral form of the lineage of the living *Hippopotamus amphibius* is signaled.

Hippopotamus protamphibius, the direct ancestor of this latter species is very abundant in the Omo Basin (Ethiopia) in the Shungura Formation, particularly in the levels C-H, dated between 2.5 and 1.5 Ma.

2. *H. amphibius* itself appears for the first time in the same basin in the Omo Valley in the levels G of the Shungura Formation, dated about 2 Ma ago, with more specialized forms than *H. protamphibius*.

3. In the Olduvai section (Tanzania) (Hay, 1976), about 1.8 and 0.4 Ma, hippopotamuses more adapted to an aquatical way of life have been collected from level 1 to level 4. Particularly, in the level 1 (about 1.9-1.8 Ma) some specimens referable to *H. amphibius* have been found (short and high skull, rather low orbits, long and only slightly inclined postorbital region, reduced or absent P2-P3 diastema; high mandible with convex lower border of the horizontal ramus).

From the level 2 (about 1.7-1.6 Ma) a hippopotamus species, already more specialised for an aquatical habitat than the level 1 species, was collected, with more elongated muzzle, higher orbits, more inclined parietals, more elongated mandible with straight or concave lower border of the horizontal ramus. This form was named by Dietrich (1928) as *Hippopotamus gorgops*, a new species separated both from the african *H. amphibius* Linnaeus and from the European species *H. antiquus* Desmarest. Mazza (1991) considers *H. antiquus* from Valdarno morphologically near to *H. gorgops* of the level 2 of Olduvai.

Finally, from level 4 (about 0.7 Ma) (the level 3, according to Geraads, 1982, did not yield fossil remains) several remains of *H. gorgops* were collected with a more advanced degree of specialisation towards the aquatical environment (even more elongated skull, shortened and high neurocranium, high orbits and presence of P2-P3 diastema). According to Mazza (*op. cit.*) these remains show morphological similarities with the new European species *H. tiberinus* Mazza.

4. From the study of some cranial remains from Ternifine (Algeria) (in progress), referable to the Middle Pleistocene, it is possible to stress that the cranial structure typical of the European *Hippopotamus antiquus* is present also in the African gisements; moreover, the strict morphological similarity between the bone structures of *H. antiquus* and *H. gorgops*, leads to assign those two forms to the same species; in this case *Hippopotamus antiquus* Desmarest has the priority.

5. Besides, the writer had the opportunity to observe some skulls preserved in the Natural History Museum of Paris, coming from Ain Anech (Algeria), some of those collected and illustrated by Arambourg (1979), other still undescribed; among this material, some skulls show the cranial morphology typical of *H. antiquus*, while a hippopotamine neurocranium perfectly fits the diagnosis of *H. tiberinus* given by Mazza (*op. cit.*).

6. The gisement of Ain Hanech is correlatable (Arambourg, *op. cit.*; Geraads, *op.cit.*) with the level 1 of Olduvai and corresponds approximately to the age of the Olivola faunas or, at least, to the Tasso faunas from Valdarno (Late Villafranchian).

7.What has been previously illustrated implies those more specialized forms of *H. antiquus* (the European forms of which are referred by Mazza (*op. cit.*) to the species *H. tiberinus* and, on the contrary, are considered by the writer (Petronio, in progress) inside the intraspecific variability of *H. antiquus*) are present also in Africa in the same locality and maybe in the same levels as the archaic form of *H. antiquus*.

8. According to the writer's opinion, in Africa during the Middle Pliocene and Pleistocene, in a temporal succession to be verified, four tetraprotodont hippopotamuses species exist: *H. kaisensis* (about 4 Ma), *H. protamphibius* (about 2.5 Ma), *H. amphibius* (about 2 Ma) and *H. antiquus* (about 1.8 Ma) the derived species better adapted to the aquatical environment.

It was thought (Petronio, 1986) that, apart the insular endemic species as the Cretan *Hippopotamus creutzburgi creutzburgi* and *H. creutzburgi parvus* and the siculo-maltese *Hippopotamus amphibius pentlandi* and *Hippopotamus melitensis*, the European Pleistocene was characterized by the presence of two different species: *Hippopotamus antiquus* (Late Villafranchian-Galerian) and *Hippopotamus amphibius*, nowadays living in Africa, but present in Europe during the time interval Galerian-Late Pleistocene.

Faure (*op. cit.*) and Mazza (*op. cit.*) have recently described two new species: *Hippopotamus incognitus* Faure and *Hippopotamus tiberinus* Mazza.

The holotype of *Hippopotamus incognitus* is represented by a skull from Barrington (Cambridge, England) preserved in the Sedwich Museum of the Cambridge University. This species differs from *H. antiquus* in having a shorter muzzle and in the morphology of the postorbital and occipital region, but, according to the writer's opinion, these features fit in the intraspecific variability of the living species *Hippopotamus amphibius*. In fact, the same skull and mandible characters observed in the Barrington skull are also showed both in a complete Middle Pleistocene skull from Tor di Quinto (Rome) and in the living hippopotamus. Thus, as stressed in a previous work (Petronio *op. cit.*), *H. incognitus* is not to be considered a valid species, and the hippopotamus from Barrington must be referred to the living species *Hippopotamus amphibius*.

The holotype of *Hippopotamus tiberinus* is represented by an incomplete skull collected in a middle Galerian deposit from Maglianella (Rome), preserved in the Museum of Natural

History of the Certosa di Calci (Pisa). Mazza (*op. cit.*) choosed as paratype the rather complete skeleton from S. Oreste (Rome) (previously considered as *H. antiquus* by Caloi *et al*, 1980), which he refers to *H. tiberinus*. According to the same Author, other specimens which must be referred to that species are the Middle-Late Pleistocene of Rhine Valley (Germany) ones.

H. tiberinus is considered a more derived form than *H. antiquus*, showing similarities, as already mentioned, with the evolution of the African *H. gorgops* lineage from Olduvai Gorge (Tanzania).

Mazza (*op. cit.*) considers that *H. tiberinus* differs from *H. antiquus* mainly in having very short post-orbital region, elevated orbits, occiput slightly inclined forward and occipital condyles strongly protruding.

The writer, considering the wide variability which characterizes the present hippopotamuses species (Arambourg, *op. cit.*; Petronio, *op. cit.*), does not consider valid the species *H. tiberinus*, because the morphological differences with its ancestral form listed by the Author seem to represent a continuum not easily separable.

Moreover, the holotype is represented only by a portion of skull on which it is impossible to observe several other morphological characters which are recognized as diagnostic by Caloi *et al.* (*op. cit.*) and Petronio (*op. cit.*) for the definition of the species *H. antiquus*. Mazza himself (*op. cit.*), describing the paratype skull of S. Oreste (Rome), lists other peculiar characters of *H. tiberinus* that can not be recognized in the holotype skull, and ignores that the S. Oreste skull is compressed and many parts of it have been reconstructed. Besides, no importance is given to the mandible characters, which instead are considered by Caloi *et al.* (*op. cit.*) as diagnostic for the specific attribution to *H. antiquus*. Nevertheless, whether if *H. tiberinus* is maintained as a valid species or, more likely, the characters of that species may be fitted those of *H. antiquus*, it is to be noted that hippopotamuses forms with specialized characters from other localities of different ages extend the vertical distribution of the species *H. antiquus* up to the Late Pleistocene.

In conclusion, it is possible to assert that in the European Pleistocene only two hippopotamuses species are present: *H. amphibius*, from the Middle Pleistocene (not better specified) to the Late Pleistocene (isotopic Stage 4 of the oceanic paleotemperature curve) and *H. antiquus* from the Late Villafranchian to the Late Pleistocene (Rhino terraces, Mazza, *op. cit.*).

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