

EVALUATION OF MOLAR SIZE AS A BASIS FOR DISTINGUISHING WILD BOAR FROM DOMESTIC SWINE: EMPLOYING THE PRESENT TO DECIPHER THE PAST

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Introduction

The domestication of swine (*Sus scrofa* L.) and other animal species was a keystone cultural achievement of early human populations, and identifying the time(s) and place(s) of its occurrence has been an important goal of archaeological investigations. The ability to accurately identify wild ancestors from truly domestic forms in associated faunal remains is often based on the presence of derived or altered morphological characters in comparison to the wild ancestor (Bökönyi 1969; Zeuner 1963). Skull characteristics, which have been widely recognized by taxonomists as one of the best means of classifying vertebrates (Lowe and Gardiner 1976), have been among the most important traits used to document the domestication process (Bökönyi 1969; Clutton-Brock 1981; Zeuner 1963). Unfortunately, cranial and mandibular material recovered from archaeological sites is often insufficient to allow either quantitative or qualitative comparisons.

Unlike the skull, teeth are frequently preserved intact in prehistoric sites due to their compact and dense structure. Since dentition is almost invariably affected by proportional size changes in the skull, measurement of tooth size has long represented an alternative technique for identifying cranial size changes resulting from domestication (Bökönyi 1974; Zeuner 1963).

Domestic swine are all descended from a single species, the Eurasian wild boar. Domestication of *S. scrofa* has been reported as having occurred indepen-

dently in a number of sites ranging from Europe to the Far East (Clutton-Brock 1981; Epstein 1971; Flannery 1961; Keller 1902; Kowalski 1976; Kuşatman 1992; Pira 1909; Staffe 1922; Zeuner 1963). Thus, a number of different subspecies of Eurasian wild boar (Fig. 1) would have been collectively ancestral to modern-day domestic swine. The earliest known domestication of this species is estimated to have taken place in the region encompassing the Middle East and eastern Europe between 6,000 and 8,000 B.C. (Clutton-Brock 1981; Epstein 1971; Herre and Rohrs 1990; Kuşatman 1992; Zeuner 1963).

As in several other species, the transition from ancestral wild boar to derived domestic forms of swine entails a shortening of the rostral region of the cranium and associated changes in the mandible (Bökönyi 1974; Clutton-Brock 1981; Epstein 1971; Kelm 1938; Kowalski 1976; Mayer and Brisbin 1991; Pira 1909; Rutimeyer 1862; Stampfli 1983; Zeuner 1963). Such brachycephalic alterations have also resulted in the subsequent shortening of the molariform dentition (Flannery 1961; Stampfli 1983). Because teeth preserve well, the lengths of the second and third molars have received a fair amount of attention in distinguishing wild vs. domestic swine. This widely recognized difference has led to the use of crown length in these molars for identifying the time course for domestication in swine, with greater molar lengths being considered to represent wild forms (Amschler 1939; Bökönyi 1974; Flannery 1961, 1983; Higham 1968; Lawrence

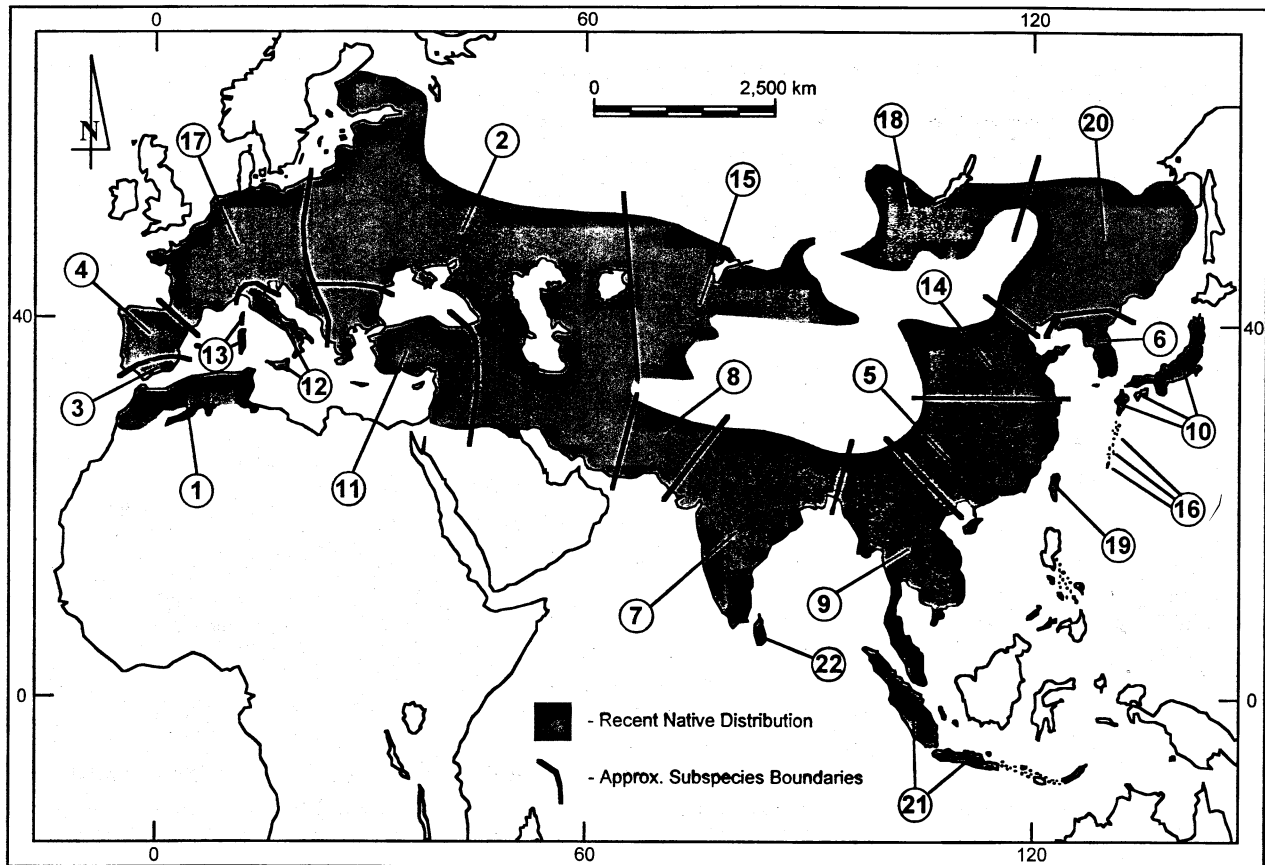


Fig. 1. Present-day distribution (shaded area) of Eurasian wild boar (*Sus scrofa* spp.) with approximate subspecies boundaries. The subspecies are as follows: (1) *S. s. algira*; (2) *S. s. attila*; (3) *S. s. baeticus*; (4) *S. s. castilianus*; (5) *S. s. chirodontus*; (6) *S. s. coreanus*; (7) *S. s. cristatus*; (8) *S. s. davidi*; (9) *S. s. jubatus*; (10) *S. s. leucomystax*; (11) *S. s. lybicus*; (12) *S. s. majori*; (13) *S. s. meridionalis*; (14) *S. s. moupinensis*; (15) *S. s. nigripes*; (16) *S. s. riukiuanus*; (17) *S. s. scrofa*; (18) *S. s. sibiricus*; (19) *S. s. taiwanus*; (20) *S. s. ussuricus*; (21) *S. s. vittatus*; and (22) *S. s. zeylonensis*. Data modified from Mayer and Brisbin 1991 and Oliver, Brisbin, and Takahashi 1993.

1980; Reed 1969; Stampfli 1983; Stein 1989). In spite of the widespread use of this technique, the size variation of these teeth within and between the various types of *S. scrofa* has not been sufficiently studied to validate its continued application.

The purpose of this paper is to evaluate the use of second and third molar length and width as a diagnostic basis for identifying archaeological specimens of domestic swine. This study compares variation observed in recent *S. scrofa* material and uses it to identify and evaluate analogous changes in the morphological transition from the wild ancestor to derived domestic forms of swine. To further examine the man-made progression from wild ancestor to derived domestic, a known cross-bred form between these two types was used to determine if very early derived morphological types (i.e., transitional forms) could also be distinguished from the wild ancestor. Within and among these three types, the

variations attributable to sex and age were analyzed as potentially confounding parameters. In addition to univariate differences in molar size, the relationship of molar allometry (i.e., width vs. length) was also analyzed to determine if significant differences exist among the three types of swine. Finally, if molar size differences are found between wild and domestic swine, these data could be used to develop a more statistically sound method for distinguishing between types.

Assessment Approach

The typical approach taken by researchers in applying the aforementioned technique is to use specimens of regionally indigenous Eurasian wild boar to determine a minimum size for the second and third molars (Flannery 1961, 1983; Higham 1968; Stampfli 1983). These size limits are then used to establish a wild-domestic size threshold.

This commonly used approach is based on the assumption that there has been no translocation of non-native wild individuals or stocks of different sizes into the regions being studied. The potential for such translocation events is a potentially confounding possibility which raises questions about the use of only indigenous specimens to establish a wild-domestic molar size threshold. The sudden appearance of physically smaller swine might not necessarily always be the result of the importation or development of derived domestic forms. The importation of a smaller captive or tamed Eurasian wild boar cannot be totally discounted. Similar sudden size changes among domestic stocks, for example, have previously been attributed to just such introductions of outside sources (Zeuner 1963). In general, the size variation among the subspecies of Eurasian wild boar is gradual. However, abrupt size differences between adjacent subspecies do exist. A few immediately adjacent mainland subspecies exhibit marked size differences (e.g., between *S. s. scrofa* and *S. s. attila*, and between *S. s. castilianus* and *S. s. baeticus*) (Groves 1981; Kuşatman 1992; Mayer and Brisbin 1991). Size contrasts between mainland and nearby island subspecies can also be significant. Potential translocations of smaller adjacent subspecies would throw doubt on the exclusive use of a larger indigenous subspecies in the determination of a wild vs. domestic threshold based upon molar size.

It should be noted that at this time we are not aware of any case where such translocations of non-native subspecies have occurred or impacted any conclusions in the analysis of a local archaeological site. However, since the long-distance transportation of early domestic swine is widely thought to have taken place (Clutton-Brock 1981; Zeuner 1963), would it not also have been possible for immature or juvenile captive wild boars to have been carried or transported along ancient trade routes to be sold in distant lands? It therefore may be prudent to employ a broader representation of the variation seen among the different subspecies of *S. scrofa*.

In addition to potential effects of translocation events, sexual dimorphism in size exhibited by Eurasian wild boar creates a further confounding aspect in determining a valid wild-domestic threshold. Size dimorphism between male and female Eurasian wild boars has been well documented (e.g., Briedermann 1970; Harrison 1968; Hell and Paule 1983; Heptner, Nasimovic, and Bannikov 1966; Koslo 1975; Mayer and Brisbin 1991, 1993; Payne and Bull 1988; Romic 1975) and is significant in adults (Hell and Paule 1983; Mayer and Brisbin 1991). The possibility thus exists for the larger males to be identified as Eurasian wild boars and the smaller females as domestic swine on the basis of molar size alone. A similar size difference between the sexes

has been a complicating factor in distinguishing wild from domestic cattle (Grigson 1969, 1982a, 1982b).

Finally, teeth appearing during the intermediate stages of the dental eruption pattern within swine have the potential to decrease in crown length due to abrasion from adjacent teeth (Payne and Bull 1988). Such age-related factors would have the potential to affect the crown length of the second molar in going from immature to adult specimens and could compromise the validity of any wild-domestic size threshold.

These aforementioned factors (i.e., geographic, sexual dimorphism, and age-related variability) require a broader look at the crown length and width variation exhibited by the molars of the different types of swine. If sufficient molar size differentiation indicative of wild vs. domestic status were still found to exist, a method that would be more robust to these factors could be produced. On the other hand, if the overlap of size between wild vs. domestic forms is large relative to these factors, this would seriously question the use of molar size as a basis for distinguishing wild from domestic swine.

In the present study, data from known extant forms are used to define the variability found in these teeth and then to evaluate the validity of using the second and third molar mensural size and width allometry as the basis for identifying wild from domestic swine. Recent specimens of known Eurasian wild boars are currently available for morphological analysis. However, the molar size and shape of either very early domestic swine or of the transitional forms between the wild ancestor and prehistoric domestic forms of swine are not well documented.

Due to the paucity of intact and readily identifiable specimens, the morphological appearance of an early domestic swine phenotype is difficult to determine with certainty. Recent/modern-day domestics (i.e., from the late 1880s through the present day), although admittedly distinct from Eurasian wild boars, are also almost certainly different from prehistoric domestic swine. In comparison to the four recent major types of *S. scrofa* (i.e., Eurasian wild boar, recent/modern domestic swine, feral swine, and wild boar x feral swine hybrids), archaeological cranial material of domestic swine (e.g., as illustrated in Bökönyi 1974; Keller 1902; and Pira 1909) qualitatively most closely resembles feral swine. Feral swine are defined as wild *S. scrofa* whose ancestry is solely from domestic swine (Mayer and Brisbin 1991). In canonical variates analyses of crania, specimens of prehistoric domestic swine fell within the recent feral swine target group (Fig. 2). Many feral swine populations have been wild-living for three to five centuries, and a few for more than 1000 years (Mayer and Brisbin 1995). Feral swine populations on

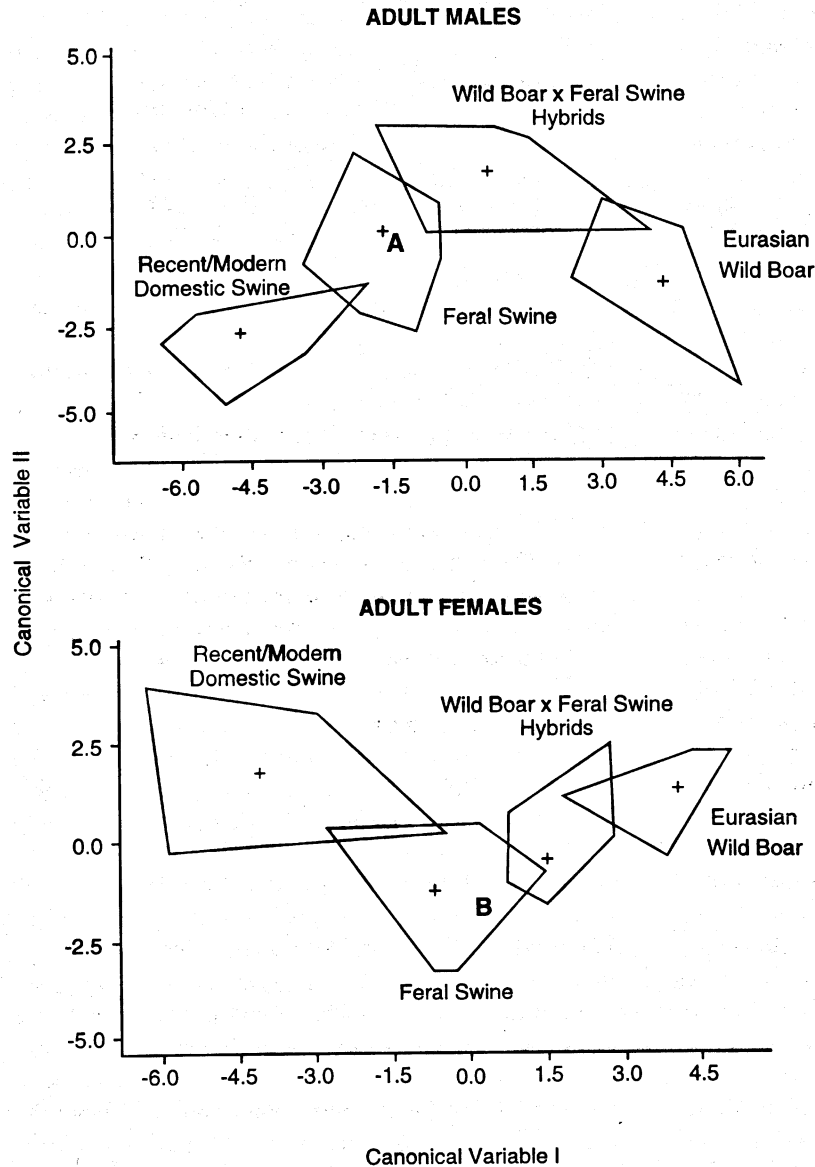


Fig. 2. First two canonical variables for adult male (top) and female (bottom) crania of *Sus scrofa* comparing the four general types with two domestic specimens (male = A; female = B) from an archaeological site in Uppsala, Sweden, dating back to the Middle Ages (measurements taken from Pira 1909). Canonical variable plots based on Mayer and Brisbin 1991.

We further propose that present-day wild boar x feral swine hybrids are the most appropriate surrogate for the transitional stage between Eurasian wild boar and early domestic swine. This type of *S. scrofa* represents a morphological middle ground between the two extremes of ancestral wild boar and derived feral/domestic stock. Hybrids, possessing a mixture of both wild boar and feral/domestic characters, would also resemble a potential evolutionary middle ground occupied by the transitional stage described above.

This study will use the phenotypic variation of recent individuals of wild boar, hybrids, and feral swine as sequential stages in a surrogate model to characterize the morphological transition from wild to early domestic individuals respectively (Fig. 3). In this model, the feral swine and hybrid specimens would be used as morphological surrogates for the early domestic swine and the wild/domestic transitional form, respectively.

Ossabaw Island off the southeastern coast of the United States and on the Andaman Islands in the Bay of Bengal are two such examples (Brisbin 1989, 1990; Mayer and Brisbin 1995; Oliver and Brisbin 1993). Some of these feral populations have in fact been found to resemble early or former domestic breeds which no longer exist under husbandry conditions. A few such feral populations have even been found to represent the last remnants of long-gone domestic breeds (Mayer and Brisbin 1995; Van Vuren and Hedrick 1989). Therefore, because of the close morphological resemblance of the skull, we propose that recent or modern-day feral swine are probably the best present-day analog or surrogate for early prehistoric domestic swine.

Materials and Methods

A total of 937 recent specimens (198 Eurasian wild boars, 212 wild boar x feral swine hybrids, and 527 feral swine) were examined during this study. The sample of Eurasian wild boars consisted of recent museum specimens collected from various locations throughout the native distribution of the wild species in Europe, North Africa, and Asia. These specimens included representatives of 21 of the 22 normally recognized geographic subspecies of Eurasian wild boar (Fig. 1). The one subspecies not represented in this sample was *S. s. riukiuanus*. The feral swine and wild boar x feral swine

hybrid samples included both museum specimens and animals recently collected in the field. Most of the feral specimens came from mainland and island populations in the United States; however, museum specimens representing feral populations from the Andaman Islands, Australia, Belize, Costa Rica, Galapagos Islands, Gardener Island, Mariana Islands, Mexico, Nicobar Islands, New Zealand, and Pemba Island were also included. Despite their varied origins and scattered distributions, the general phenotype of the feral swine skull is consistently uniform and identifiable as such in comparison to that of the other recent major types of *S. scrofa* (Mayer and Brisbin 1991, 1993). All of the wild boar x feral swine hybrid samples came from populations in the United States. Specimens within each of the three groups consisted of varying combinations of crania and mandibles. In addition to the aforementioned samples, 79 recent/modern-day domestic swine were included for comparative purposes with the Eurasian wild boar and the two morphological surrogate samples. A listing of the specimens obtained from existing collections is provided in Mayer and Brisbin 1991. Those specimens not contained in that reference were recently collected in the

field, and are currently contained in the senior author's personal holdings.

Based either on the known past history of the source population or analysis of the individual specimen's cranial morphology (Mayer and Brisbin 1991, 1993), each of these specimens was categorized into one of the three types of swine as follows: Eurasian wild boar, wild boar x feral swine hybrids, and feral swine. They were also identified as to both sex and age class. Sex was determined by the data provided on the museum specimen tag, examination of fresh specimens collected in the field, or the morphology of the canines for museum/pick-up specimens of unknown sex (Mayer and Brisbin 1988). Age class categories included yearling, subadult, and adult, and were based on erupted dental patterns as described in Mayer and Brisbin 1991. Lacking either of the molars being studied, animals younger than the yearling age class were not included.

Linear measurements were taken from both the upper and lower second and third molars present in the specimens, with teeth measured on the right side of the specimen where possible. Measurements were made with 150-mm dial calipers to the nearest 0.1 mm. Ten

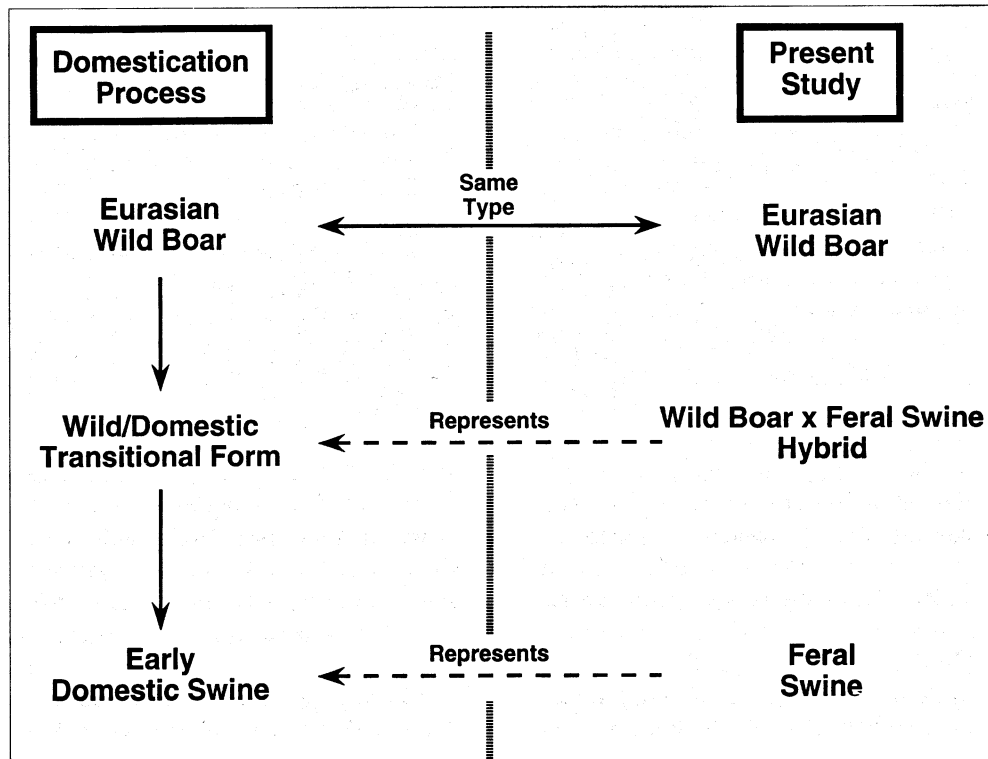


Fig. 3. Schematic representation of the approach used in the present study to classify groups of present-day *Sus scrofa* as morphological surrogates for earlier stages in the initial domestication of the species. The recent Eurasian wild boar sample is considered to be equivalent to the archaeological representatives of this same type of *Sus scrofa*.

Table 1. Sizes (in mm) of second and third molars of the three types of *Sus scrofa*. Sex and age class data were combined within each type

Type of Swine	Molar	Measurement	N	Mean	Observed Range	SE
Eurasian Wild Boar	Upper 2nd	Length	190	22.6	17.5–28.8	0.13
		Width	190	19.2	13.7–26.5	0.10
	Upper 3rd	Length	156	35.2	24.0–50.0	0.27
		1st Width	168	21.6	15.0–30.0	0.14
		2nd Width	160	18.9	12.6–27.0	0.13
	Lower 2nd	Length	191	21.8	16.0–27.9	0.13
		Width	191	16.0	11.9–20.3	0.09
	Lower 3rd	Length	154	39.0	27.0–53.0	0.32
		1st Width	170	18.0	13.0–24.5	0.12
		2nd Width	166	17.4	13.2–22.5	0.11
Wild Boar x Feral Swine Hybrid	Upper 2nd	Length	182	21.2	15.4–25.9	0.13
		Width	182	16.8	14.4–19.8	0.10
	Upper 3rd	Length	78	31.5	25.2–40.0	0.38
		1st Width	109	19.2	12.8–23.5	0.17
		2nd Width	86	16.3	13.9–19.3	0.17
	Lower 2nd	Length	154	20.7	17.2–24.1	0.15
		Width	154	14.2	11.6–19.2	0.10
	Lower 3rd	Length	60	33.5	24.6–41.4	0.51
		1st Width	93	16.0	13.3–18.7	0.16
		2nd Width	85	15.5	12.6–17.4	0.15
Feral Swine	Upper 2nd	Length	361	20.3	15.5–24.5	0.09
		Width	361	16.5	13.2–20.5	0.07
	Upper 3rd	Length	177	30.0	23.5–38.0	0.25
		1st Width	231	18.5	15.0–22.0	0.12
		2nd Width	201	16.1	12.8–19.0	0.11
	Lower 2nd	Length	475	19.8	12.3–27.7	0.08
		Width	475	13.8	11.2–18.8	0.06
	Lower 3rd	Length	198	32.0	24.2–40.3	0.28
		1st Width	299	15.3	12.2–20.2	0.09
		2nd Width	272	15.2	11.3–19.2	0.08

measurements (five on the upper and five on the lower tooth rows) were taken as follows: second molar length—the greatest length of the crown of the second molar; second molar width—the greatest width of the crown across the posterior cusp row of the second molar; third molar length—the greatest length of the crown of the third molar; width of first cusp row of third molar—the greatest width of the crown across the first cusp row of the third molar; and, width of the second cusp row of third molar—the greatest width of the crown across the second cusp row of the third molar. These measurements were taken consistent with the methods described in Driesch 1976 and Mayer and Brisbin 1991.

All statistical analyses were performed using the Statistical Analysis System (SAS) version 6.12 (SAS Institute Inc. 1989). All variables were analyzed for conformation to a normal distribution using a Shapiro Wilk test in Proc Univariate and normal probability plots. Analyses of variance were performed using the SAS Mixed procedure which allows both fixed and random effects in the models. All effects in these models were considered fixed, but the procedure provides statistics useful for model selection to allow discrimination of models with different terms and different numbers of terms. Analyses of covariance models were first fit with all relevant interaction terms of covariates (heterogeneity of

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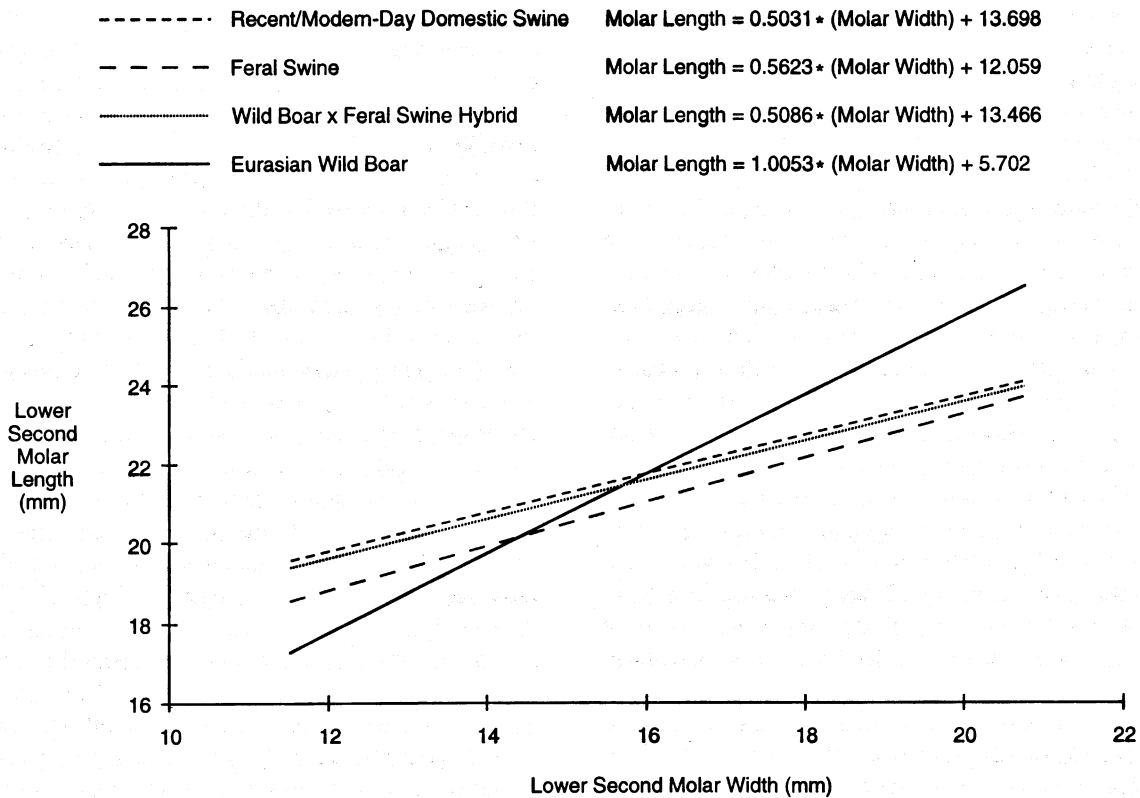


Fig. 4. Linear plots of lower second molar length and width (in mm) among the three types of swine used in the present study. Recent or modern-day domestic swine are included for comparison with the three types.

variance models). If the interactions were not significant, then the models were fit with only the main effects of the covariates included. Statistical significance was accepted at $P < 0.05$, with acceptance criteria modified for multiple tests using a sequential Bonferroni procedure as required.

The wild-domestic thresholds for the various measurements were developed using the lower limits of the 95% confidence intervals for Eurasian wild boar, and the upper limits of the 95% confidence intervals for hybrids and feral swine. The use of this metric instead of the minimum and maximum limits of the observed range (e.g., Flannery 1961, 1983; Higham 1968; Stampfli 1983) provides a more statistically sound threshold. The use of range limits (i.e., minimum and maximum values) as identification thresholds entails the application of extreme observations to define differences between sample groups. The range overlap created by such extremes can obscure the valid separation of a measurement exhibited by the majority of specimens being analyzed.

Results

Summaries of the ten molar measurements for the three types of swine are presented in Table 1. The uni-

variate differences among the three types (i.e., with sex and age classes combined) were significant for all of the molar lengths and widths. In each measurement, the wild boars were the largest, decreasing in size to the hybrids, and then followed by feral swine as the smallest. Therefore, the surrogate model was consistent within the molar size gradient among the three types of swine. In light of these significant differences, it should also be noted that range overlap by extreme observations did occur among the three types for all of the parameters measured (Table 1).

The overall differences in molar size between the sexes with the types combined were significant for all ten measurements. Males were consistently larger in all of these intersex size comparisons. However, within each type, although males averaged and ranged larger than females, the differences between the sexes were not found to be significant ($F = 0.57$, $d.f. = 714$, $p = 0.56$). Thus, size differences due to sexual dimorphism would not represent a significant confounding aspect in determining the wild-domestic threshold.

Because of the initial absence and then eruption and presence of the third molar immediately posterior to the

second molar (in going from yearling to subadult and then adult), one would expect that interproximal abrasion of the posterior face of the second molar crown would result in a decrease in crown length along this age class gradient. Second molar crown lengths were found to follow this expected pattern of decreasing size in successively older age classes within each type except for the Eurasian wild boar sample. This latter pattern was due to a seeming increase in second molar crown length in the subadult Eurasian wild boar sample. However, upon investigation, only the larger wild boar subspecies (e.g., *S. s. attila*) were represented among the specimens comprising this subadult sample. Thus, this apparent increase was likely an artifact of this particular data set. In general, however, like sexually dimorphic differences, age-related differences in molar size were not sufficient to obscure the overall difference between the types.

The allometric relationship of all molar widths and lengths was found to be significant among the three types of swine. The length-width relationships were consistent among the three types for each of the molars except in the lower second molar ($F=11.77$, $d.d.f.=814$, $p=0.0001$). The Analysis of Covariance of that tooth showed that the allometric relationship did not differ between the feral swine and hybrids, but that both of those were significantly different from the Eurasian wild boar (Fig. 4). This

would indicate that molar allometry as well as size of the second lower molar could be used to distinguish wild ancestral vs. prehistoric domestic swine.

Based on the 95% confidence intervals, the wild and domestic thresholds for the various molar measurements are provided in Table 2. The upper prehistoric domestic threshold was defined as the upper limit of the 95% confidence interval for the hybrids. Although close in some parameters (e.g., lower second molar length), no overlap occurred in any of the measurements between the upper limit of the domestic and the lower limit of the wild boar 95% confidence intervals. Overall, the third molar length had the broadest gap between thresholds, and the second molar length the narrowest. For both of the third molars, the gap breadth was greatest for the crown length, followed by the second cusp row width, and then by the first cusp row width. A reverse pattern was observed in the second molars, with the cusp row widths having the broadest gaps, followed by the crown lengths.

The combined percentage of specimens incorrectly classified using the 95% confidence interval limits were also calculated for the three samples of known swine. The lowest percentage of incorrect identifications was for the upper second molar width (only 4.4%), followed by the second cusp row width of the upper third molar (5.6%). In spite of the fact that it had the broadest threshold gap, the lower third molar length had the next lowest percentage (7.3%) of incorrect identifications. The highest percentage of incorrect assignments of specimens was for the lower second molar length (22.8%), with upper second molar length (15.7%) as the next highest. The percentage of unknowns (i.e., specimens falling within the threshold between wild and domestic) was highest for the second cusp row width of the upper third molar (32.4%) and lowest for the lower second molar length (7.0%). Overall, if a measurement had a low percentage incorrectly classified, it tended to have a high percentage of unknowns among the three types of swine.

Discussion

The present study confirms the value of second and third molar size as a basis for differentiating wild boar from early domestic swine. However, the determination of valid thresholds for these molar lengths and widths needs to be predicated on the knowledge of the variation in these dental measurements exhibited in both wild ancestral and derived domestic forms of *S. scrofa*. Based on the results of the present study, the few critics of the validity of

Table 2. Listing of the maximum domestic and minimum wild size thresholds for each length and width measurement (in mm) of the upper and lower second and third molars of *Sus scrofa*

Molar	Crown Measurement	Maximum ^a Domestic Swine Threshold	Minimum ^b Wild Boar Threshold
Upper Second	Length	21.4	22.4
	Width	17.1	19.0
Upper Third	Length	32.2	34.6
	1st Width	19.6	21.4
	2nd Width	16.6	18.7
Lower Second	Length	21.0	21.5
	Width	14.4	15.8
Lower Third	Length	34.5	38.3
	1st Width	16.3	17.7
	2nd Width	15.7	17.2

^a Based on the upper limit of the 95% confidence interval for hybrids

^b Based on the lower limit of the 95% confidence interval for wild boar

these size differences in wild vs. domestic swine (e.g., Bolomey 1973; Chaplin 1969; Teichert 1969) would not appear to be completely justified.

Within the comparisons undertaken in the present study, Eurasian wild boar are a known morphological entity which can be carefully examined and defined on the basis of extant free-living populations worldwide. The current distribution of Eurasian wild boars ranges from the Iberian Peninsula to the Maritime Territory of Siberia. The observed size variation among the different subspecies of Eurasian wild boar is notable (Groves 1981; Kuşatman 1992; Mayer and Brisbin 1991). In fact, this size variation has been widely used to describe and distinguish the various geographic races of this species. A loose clinal situation appears to exist, with the physical body size (e.g., head-body length, shoulder height, snout length, hind foot length, etc.) of wild boar increasing somewhat to the north, and more significantly to the east.

The largest described subspecies include *S. s. attila* and *S. s. ussuricus*. The smaller subspecies are mostly represented by insular forms, including *S. s. meridionalis*, *S. s. taivanus*, *S. s. riukiuanus*, and specific Southeast Asian island populations of *S. s. vittatus*. This observation is consistent with the phenomenon of insular dwarfing documented in a number of other ungulate species occupying both mainland areas and islands (Case 1978; Foster 1964). It should also be noted, however, that at least some of the insular subspecies of wild boar (i.e., *S. s. leucomystax* and *S. s. zeylonensis*) do not seem to exhibit dwarfing effects in restricted insular habitats. Conversely, some continental or mainland subspecies are of relatively small size. These would include *S. s. baeticus* and *S. s. majori*. Several theories have been advanced to explain the species-wide variation in body size of Eurasian wild boar. The most common hypotheses center around a post-glacial intermixing of previously isolated larger northern and smaller southern forms (Ammon 1938). Habitat also appears to be a factor, with animals found in mesic habitats being larger than those found in xeric areas (Epstein 1971; Spitz, Valet, and Brisbin 1998). A similar size differentiation reportedly also occurs between populations found in mountains vs. plains habitats (Epstein 1971). Using a representation of most of the variation seen among the different subspecies, the present study provides thresholds which would have a broader application regionally than any of the previous studies that used molar size differences based mostly upon local subspecies.

With the size variation found in Eurasian wild boar, there would be some instances in which using the threshold values provided in Table 2 would be inappropriate for identifying domestic swine. Such circum-

stances include studies which encompass areas inhabited by those subspecies or populations of wild boar occupying the lower end of the physical size spectrum. Examples of this include *S. s. baeticus*, *S. s. meridionalis*, *S. s. taivanus*, *S. s. riukiuanus*, and specific island populations of *S. s. vittatus* (Fig. 1). The second and third molars of these wild boar are equivalent to or smaller than the 95% confidence intervals of both surrogates used in this study and samples of known prehistoric domestics. Thus, molar size could not be used validly to identify the presence of prehistoric domestic swine in lands inhabited by these wild boar subspecies.

Analysis of size variation in Eurasian wild boar skeletal or dental material from an archaeological setting is further complicated by the larger size of prehistoric specimens as compared to recent specimens from the same locations. The physical size of wild boar was determined to have decreased during the postglacial periods (Ammon 1938; Bökönyi 1974; Epstein 1971; Herre 1949; Kurten 1968; Kuşatman 1992; Stampfli 1983). Moreover, this decline in size has been noted to continue into present times, with series of specimens from the same locations generally appearing to become smaller from the 1800s through the 1900s (Heptner, Nasimovic, and Bannikov 1966; Herre 1949). Given the thresholds for the second and third molars determined in this study, these larger prehistoric specimens would still be classified as wild boar. Granted the existence of this complicating premise, however, transitional specimens originating from this larger wild ancestral phenotype could also possibly be identified as wild boar.

The morphological surrogate for the wild-domestic transitional form used in the present study (wild boar x feral swine hybrids) may not be a truly intermediate form. Although positioned correctly in the transitional size sequence (i.e., being smaller than the Eurasian wild boar, but larger than the prehistoric domestic morphological surrogate), the molar lengths and widths were closer to those of the domestic surrogate and were not truly intermediate in size. This is perhaps a result of the hybrid populations used in this study being predominantly feral swine in ancestry (Mayer and Brisbin 1991). The reduced contribution of the wild boar founding stock has produced a population which is morphologically more like the feral end of the hybrid spectrum in terms of molar morphology.

In some instances, a specific archaeological investigation may necessitate the identification of "culturally domesticated" (i.e., tamed/captive) wild ancestors versus truly domestic individuals. Unfortunately, the data suggest that nothing more than little to no distinguishable morphological changes would occur for many years following the first efforts at domestication of wild

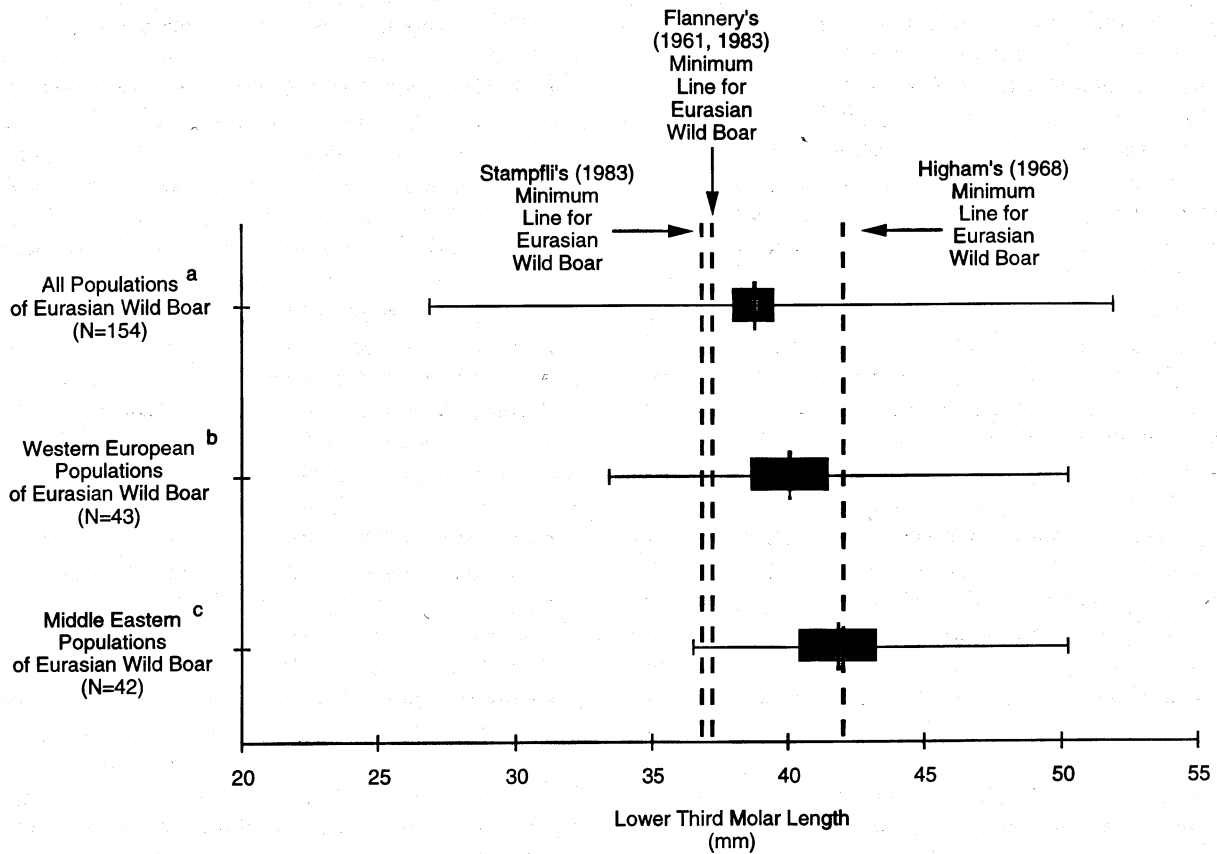


Fig. 5. Comparisons of lower third molar lengths between samples of all populations, western European populations, and Middle Eastern populations of Eurasian wild boar versus the minimum lines for Eurasian wild boar as given by Stampfli (1983), Higham (1968), and Flannery (1983). The bold vertical line, shaded box, and smaller vertical lines at the ends of the horizontal line represent the mean, 95% confidence interval, and observed range, respectively. The samples depicted were all measured in the present study and consisted of the following: (a) specimens of all Eurasian wild boar; (b) specimens of *Sus scrofa attila*, *S. s. majori*, and *S. s. scrofa*; and (c) specimens of *S. s. attila*, *S. s. davidi*, *S. s. lybicus*, and *S. s. nigripes*.

individuals. Within samples of recent captive wild boar, morphological analyses indicate that no significant quantifiable differences occur even after a number of generations. Based on specimens of zoo wild boar, the cranial morphology continues to be uniform, with such specimens still being classified in canonical variates analyses as Eurasian wild boar (Mayer and Brisbin 1991). Therefore, recently domesticated or tame wild boar living in the confined situation of an agricultural society may not be morphologically discernible from truly wild individuals being harvested solely under a strict hunting regime. Because of this fact and the lack of definitive archaeological evidence, the actual time period between initial domestication and a resultant response in the form of an observable morphological change in molar characteristics remains unknown.

Molar size alone cannot be used as the sole criterion for establishing the practice of an agrarian rearing (with

selective breeding) of domestic swine for a given archaeological site or prehistoric society. The establishment of feral swine populations around some ancient settlements could have conceivably occurred given the early use of free-ranging husbandry practices for this species in some areas (Clutton-Brock 1981; Zeuner 1963). Jarman (1971) discussed the impossibility of detecting early feral individuals and the misleading interpretations that may result when using wild vs. domestic characters to distinguish between hunter-gatherer vs. agrarian-production societies. For example, even if such prehistoric societies had been provided with derived domestic swine through trade, it is possible that these animals could have been released to forage on their own until individual animals were harvested as needed by the human owners. The actual rearing practices used in such a scenario could have been minimal, and not comparable to other more strict agrarian-based social systems during the same his-

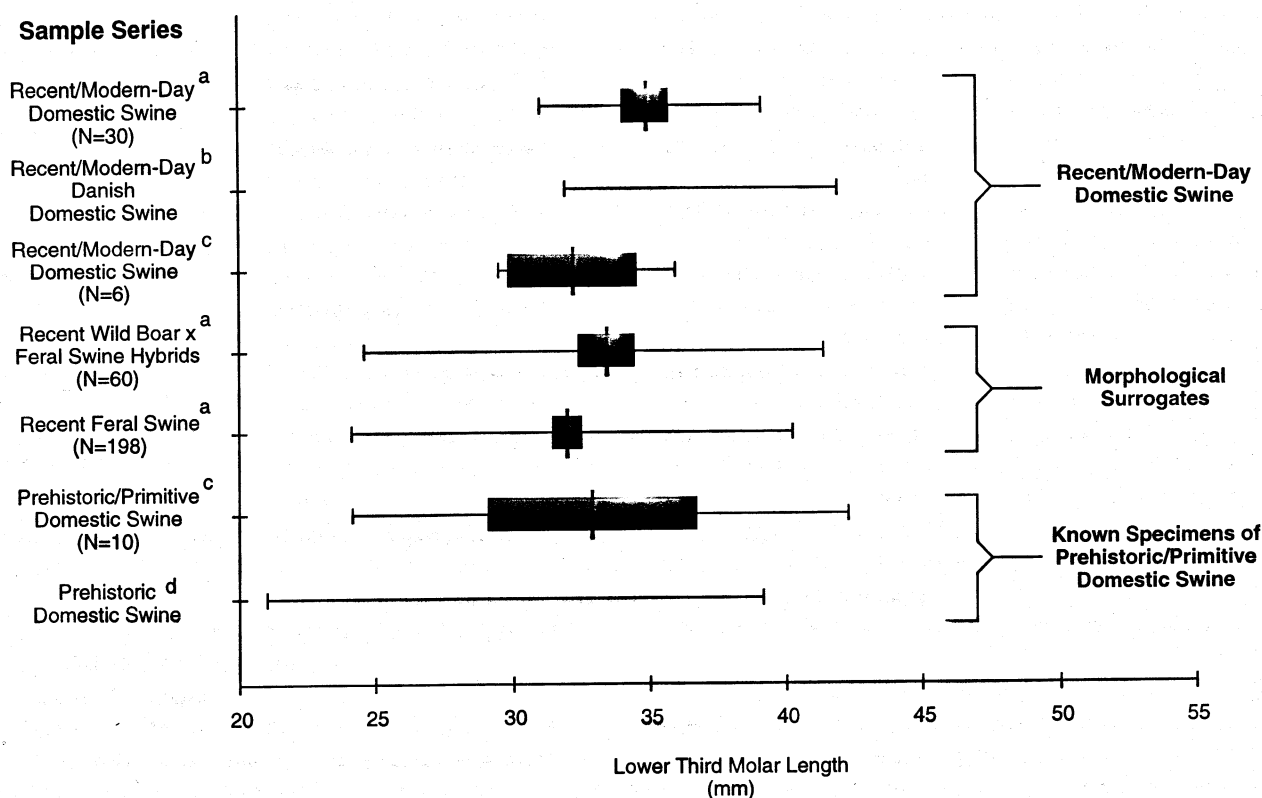


Fig. 6. Comparisons of lower third molar lengths among various samples of recent/modern-day domestic swine, the two morphological surrogates used in this study, and known specimens of prehistoric/primitive domestic swine. The sample conventions follow those defined for Figure 5. The sources of the sample series were as follows: (a) the present study; (b) taken from Higham (1968), sample size, mean, and standard deviation unknown; (c) taken from Pira (1909); and (d) taken from Nanninga (cited in Stampfli 1983), sample size, mean, and standard deviation unknown.

torical period. Further, the potential for free-ranging domesticates to hybridize with local wild boar could serve to further mask the presence of derived domestic swine and decrease the value of molar size as a parameter for identifying domesticates (Bogucki 1989; see also discussion in Redding and Rosenberg, this volume).

The most accurate (i.e., with the lowest percentage of incorrect classifications) measurement determined in the present study was upper second molar width, followed by the second cusp row width of the upper third molar. The best of the remaining measurements had incorrect percentages of only slightly less than twice that of the upper second molar length. Both Payne and Bull (1988) and Kuşatman (1992) pointed out the value of molar widths over lengths in looking for separations between wild and domestic populations of swine. This is attributed to the low overall variation, low sexual dimorphism, and low age-related variation exhibited by the molar widths (Kuşatman 1992; Payne and Bull 1988).

Comparisons with existing wild-domestic thresholds of third molar crown length reveal that some are reason-

able (e.g., Flannery 1961, 1983; Stampfli 1983), while others (e.g., Higham 1968) are overly conservative (Fig. 5). Higham's (1968) minimum line for wild boar was greater than the mean of all of the subspecies found in and around the geographic areas where his study sites in Europe were located (i.e., *S. s. attila*, *S. s. majori* and *S. s. scrofa*). In fact, his minimum line is above even the upper limit of the collective 95% confidence interval for these subspecies.

Higham's and Flannery's methods provide a single threshold value above which an individual would be classified as a wild boar and below which a domestic *S. scrofa*. Stampfli's (1983) method uses a revised wild boar minimum observation (largely based on the same specimens used by Flannery [1961, 1983]), and combines that with a maximum observation taken from Nanninga (cited in Stampfli 1983). Stampfli's (1983) wild boar minimum value is less than the maximum domestic value, thereby creating a zone of overlap within which a specimen could be either type of *S. scrofa*. Our study has two threshold values similar to Stampfli's;

however, the wild and domestic threshold values do not overlap for any of the molar measurements studied. The specimens which fall between the two values would remain as unknowns, due to the inability to accurately identify these as either wild or domestic in origin.

Similar to the subspecific refinements made to the wild-domestic thresholds as depicted in Figure 5, it would also be important to set specific thresholds which consider only the molar sizes of the particular subspecies endemic to the area of the archaeological site in question, as well as those found in adjacent regions. Broader size variation would result if it is considered that subspecies found in such adjacent sites could have been translocated to the region of the archaeological site. For example, the area of the Fertile Crescent is located within the range of the subspecies *S. s. attila*. However, if one were also to consider the adjacent subspecies (*S. s. davidi*, *S. s. lybicus*, and *S. s. nigripes*), then a greater size variation would be expected as a result of possible translocations. In fact, both Flannery (1961, 1983) and Stampfli (1983) used specimens of *S. s. attila* and *S. s. lybicus* in their respective studies.

Comparisons between the two morphological surrogates and other samples of prehistoric and modern-day domestic swine provided mixed results. Stampfli's use of Nanninga's maximum for the lower third molar length of prehistoric domestic swine (cited in Stampfli 1983) compares favorably to the various samples of primitive and modern domestic swine and the two morphological surrogates used in the present study (Fig. 6). Again, a few extreme observations were above the threshold line; however, most would be correctly identified as domestics. At the same time, a few of Nanninga's (Stampfli 1983) specimens were smaller than any of the other data sets illustrated in the present study or in other studies of prehistoric domestic swine (e.g., Higham 1968). It should also be noted that none of the calculated upper limits of the 95% confidence intervals were equal to or exceeded the lower limit of the wild boar 95% confidence interval as determined in our study.

The potential of accidental incorporation of modern-day domestic swine into archaeological sites raises the question of how this recent material compares to Eurasian wild boar and the two surrogates investigated in the present study. In comparing modern-day domestic swine molars with these three types, the upper limits of the 95% confidence intervals of the recent domestics were above those of surrogates and below those of wild boar for all of the molar measurements. These upper limits for each measurement (in mm) within the modern-day domestic sample were as follows:

upper second molar: 21.8

upper second molar width: 17.2

upper third molar length: 33.6

width of first cusp row of upper third molar: 19.9

width of second cusp row of upper third molar: 17.5

lower second molar length: 21.5

lower second molar width: 15.1

lower third molar length: 35.7

width of first cusp row of lower third molar: 17.3

width of second cusp row of lower third molar: 16.9.

Thus, any modern-day domestic swine material becoming accidentally incorporated into an archaeological deposit is not likely to be identified as a wild ancestor, but at worst as an unknown. Based on the modern-day domestic specimens used in the present study, less than 4% of the recent domestic material would be above the minimum wild threshold.

In choosing the use of minimum/maximum observations vs. the upper/lower limits of 95% confidence intervals, one must decide upon the type of information desired as an outcome of the analysis to be applied to archaeological material under study. In comparing the results of the methods of Flannery (1983) and Stampfli (1983) with the present study, the percentage of known wild boar specimens that were incorrectly identified as domestic swine was more than two to almost three times higher using Stampfli's and Flannery's methods, respectively, than using the wild-domestic thresholds developed in the present study. However, the overall percentage of specimens which could not be identified as one type or the other was higher in the present study. Therefore, if one needed to be able to identify every specimen as either wild boar or domestic swine, the present method would not accomplish that goal. On the other hand, if one needed to more accurately determine whether or not the population sample from a given archaeological site represented wild boar vs. domestic swine, then the thresholds described in the present study would be a more reliable and statistically sound method.

The differences in width allometry of the lower second molar are an aspect of the dental variation among the types of *S. scrofa* that has not been previously noted by archaeozoologists. The primary practical difficulty of this method is that it requires a series of these molars from an archaeological site. Minimum sample sizes would be determined by the ability to produce a significant regression of molar width and length. Individual or small numbers of these teeth would not be a sufficient sample size to enable a wild-domestic identification. However, for locations producing large series of pig molars, this method could be used in conjunction with the ten 95% confidence interval thresholds for the second and third molars to determine what type of *S. scrofa* was present at those locations.

Conclusions

Comparisons of the molar size differences shown by recent specimens of *S. scrofa* have generally validated the use of molar size criteria to distinguish Eurasian wild boars from smaller primitive domestics. The effects of sex and age on the molars were not found to be substantial enough to obscure the differences between wild vs. domestic forms. This further substantiates the robust nature of the wild-domestic thresholds determined for use in this identification technique. Of the ten measurements included in the present study, upper second molar width was found to provide the lowest percentage of incorrect classifications and therefore the best potential for identifying wild vs. domestic forms accurately. On the same basis, the least useful measurement was lower second molar length. For the upper third molar, second cusp row width was a better discriminator than crown length, with the reverse relationship being found for the lower third molar. In both second molars, cusp row width was a more accurate discriminator than crown length. Analysis of Covariance indicated that the allometric relationship of lower second molar width differed between wild boar and the morphological surrogates. Given a sufficient sample size of *S. scrofa* lower second molars from an archaeological site, this would provide additional information that could increase the usefulness of this tooth for differentiation of individuals into wild boar or domestic swine morphotypes.

Based on 95% confidence intervals, the application of the thresholds developed during the present study would result in fewer incorrect identifications of pure Eurasian wild boar as early domestic swine. The primary shortfall of these thresholds would be the potential for a higher percentage of specimens to be identified as unknowns.

In spite of the conclusion from the present study validating the use of molar length and width to distinguish wild vs. domestic swine, the application of methods based on this size relationship should be undertaken with care. Tooth size alone is minimal evidence at best in trying to distinguish between hunting versus agrarian prehistoric societies or in determining wild-living vs. captive-reared specimens of swine. Molar size is an important small part of the domestication puzzle, but it is far from being either the complete picture or an infallible basis for identifying wild ancestors from truly domestic forms of swine.

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