Somatic variability in wild boar (Sus scrofa L.) in different areas of Central Italy

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Abstract

A survey of wild boar shot during two consecutive years (hunting seasons 2002-2004) was carried out in order to evaluate which somatic measurements are most significant in identifying and discriminating among different morphotypes in central Italy. Biometric data from 688 wild boars was collected in three different areas of central Italy, two in Viterbo and one in the Province of Rieti. The following somatic measurements were individually recorded for each specimen: head-body length, height at withers, hind-foot length, ear length, ear-snout distance and ear-shoulder distance. Body weight was registered, and age was estimated from tooth eruption and wear. The animals were divided into three age classes; young (aged less than 12 months), sub-adults (aged between 12 and 36 months), and adults (36 months and older). After a preliminary ANOVA procedure, which did not give satisfactory results, a statistical analysis was performed using a canonical discriminant procedure, given an a priori classification (geographical area) and several quantitative variables (somatic measurements and weight). The separation between areas was estimated calculating the squared distance of Mahalanobis. The data referring to all 688 specimens was subjected to factor analysis. The results of the canonical discriminant analysis highlight the existence of two distinct groups within all three age classes. There is a statistically significant difference between the southern Maremmana (SM) vs the Apennine (A) and sub-Apennine (SA) areas, for young (P<0.0001), sub-adults (P<0.001) and adults (P<0.001). The difference between the A and SA areas was significant only for sub-adults (P<0.05). The first canonical variable account for 92.5, 92.7 and 89.9% of the total variance for the three age classes respectively, but this is unequally correlated with the original variables suggesting that the separation between the two areas is due to differences in conformation rather than in body size. On the basis of the discriminant analysis large part of the animals were correctly categorised in the sampling areas. As regards the factor analysis results for the adult group, the first three common factors are able to explain 78, 92, and 64% of the covariance for the data of the SM, A and SA groups respectively. These results suggest that, for the SM group, a differentiation among morphotypes may be possible on the basis of a few somatic measurements. These results confirm the need for biochemical and genetic studies to identify if the different morphotypes refer to the autochthonous wild boar strain.

Introduction

Wild boar numbers in Europe underwent a severe decrease from the Middle Ages to the Second World War. In contrast, in the post-war period a massive expansion took place both in Europe and in Italy (De Beaux and Festa, 1927; Boitani et al., 1995a; Danilkin, 2001) due to many cofactors difficult to isolate, including land cover changes, feed availability and land management (Schley and Roper, 2003; Bieber and Ruf, 2005; Geisser and Reyer, 2005). The current increase in wild boar numbers and their expansion, into unusual habitats (Cocca et al., 2007) as well as throughout Italy (Amici et al., 2008), have important management implications concerning crop damage (Geisser and Reyer, 2004) and vehicle collision (Primi et al., 2009). The spread of wild boar was due to the massive restocking which was done using animals from central and eastern Europe (Saez-Royuela and Telleria, 1986; Apollonio et al., 1988) and spontaneous colonisation from France. The reproductive potential of animals from central Europe (Nahlk and Sandor, 2003) is of major importance. They show a higher prolificacy in comparison to autochthonous Italian wild boar (Perco, 1987) and this plays an important role in population increase (Massai and Toso, 1993).

According to Randi (1995), Italian and European wild boar can be distinguished into different genotypes on the basis of mitochondrial DNA analyses. Nevertheless, the systematics of wild boar is controversial and recent studies have shown a limited impact of the massive restocking on mitochondrial DNA translocations (Vernesi et al., 2003).

Firstly, it should be underlined that the wild boar populations of central Italy have undergone a massive increase, greater than in other European countries. Secondly, it is interesting to note that this expansion has (probably) helped to maintain pre-glacial diversity (Scandura et al., 2008). In fact, as reported by Scandura et al. (2008), restocking with non-autochthonous animals has not produced a strong impact on genetic variation, thus only 7% of the individuals studied was characterized by having a significant proportion of their genome related to central European wild boar. These considerations support the adoption of species management policies aimed at avoiding both accidental escapes from wild boar breeding farms and hybridisation with free-range domestic pigs (Scandura et al., 2008). This also confirms a great interest for local group conservation since genetic differences are evident among wild boar populations in Italy (Vernesi et al., 2003).

In recent decades, several studies on wild boar morphology have been performed with the aim of distinguishing between autochthonous and introduced genotypes (Genov et al., 1995; Tinelli et al., 1999), studying growth patterns (Gallo Orsi et al., 1995; Pedone et al., 1995) and obtaining a morphological characterisation (Massai and Genov, 1993). A large part of these studies was based on craniometrical measures only (Genov et al., 1991; Gallo Orsi et al., 1995; Genov, 2004) even if this type of measurement is one of the most adequate systematic techniques, it has two main limitations. First, it requires very accurate measurements, implying the use of appropriate equipment. Secondly, such measurements are difficult to perform in field conditions, and the specimens should be transferred to a laboratory. Moreover, in the case of wild boar, hunters tend to hand over females heads only, and the resulting of the discriminant analysis large part of the animals were correctly categorised in the sampling areas. As regards the factor analysis results for the adult group, the first three common factors are able to explain 78, 92, and 64% of the covariance for the data of the SM, A and SA groups respectively. These results suggest that, for the SM group, a differentiation among morphotypes may be possible on the basis of a few somatic measurements. These results confirm the need for biochemical and genetic studies to identify if the different morphotypes refer to the autochthonous wild boar strain.
Materials and methods

Biometric data from 688 wild boars (319 males, 379 females) were collected in three different areas of central Italy (Figure 1), during two consecutive years (2002-2003 and 2003-2004, the hunting period lasting from November throughout January). The first of the three areas is a flat zone of the southern-Maremma (SM) in the Province of Viterbo, the second is a hilly sub-Apennine (SA) area (Province of Viterbo) near the borders with Tuscany and Umbria. The third, in the province of Rieti, is a mountainous zone of the Apennines (A) near the Abruzzo border. The first two are divided by a wide urban area and intensively cultivated lands. All three zones match wild boar habitat preferences (Abagiar et al., 1994; Fonseca, 2008).

The data were collected after shooting and before slaughtering. All the animals legally shot in the area during the hunting seasons were included in the data set. Nine animals were excluded from the statistical analysis on the basis of signs of cross-breeding with domestic pigs (Andersson-Eklund et al., 1998; Randi, 2005). As no selective hunting is practised in the three areas, the animals were shot with the technique of dog drive hunting (Massi et al., 1993).

On the basis of the literature available (Mayer and Brisbin, 1991; Moretti, 1995; Tinelli et al., 1999) selected morphological traits were measured, using a flexible meter with a mm scale (Figure 2), and recorded in an appropriately designed format. The following somatic measurements were individually recorded for all the specimens: head-body length; height at withers, from the distal extreme of the fore leg to the upper part of the wither; hind-foot length, from the calcaneum process to the distal part of the nail; ear length, from the base to the tip; ear-snout distance, from the base of the ear to the snout; ear-shoulder distance, from the basis of the ear to scapula-humerus joint. Body weight was measured by a dynamometer (CAMI S.r.l., DIN 1, Accuracy: ± 0.5%), and age was estimated from tooth eruption and wear (Iff, 1978; Dzieciołowski et al., 1989; Boitani and Mattei, 1992).

The animals were divided into three age classes; young (12 months or less), sub-adults (between 12 and 36 months), and adults (36 months and older). This was performed with reference to the results obtained in previous studies (Amici et al., 2003; Amici et al., 2005).

All the data, separated on the basis of the age class, have been preliminarily analysed with an ANOVA (GLM procedure) including year, sex, area and the interactions area ¥ year, sex ¥ area and sex ¥ area as fixed factors. Since the analysis showed no significant differences between sex and years and contrasting results concerning the areas, the data were merged and a different statistical approach was adopted. The statistical analysis was then performed using a canonical discriminant procedure (SPSS, 2007) that, given an a priori classification (geographical area) and several quantitative variables (somatic measures and weight), derives linear uncorrelated combinations of the original variables. In the space defined by the first two canonical variables, the separation among areas was estimated by the squared distance of Mahalanobis that is non affected by linear transformations and accounts for the correlations among the original variables. Discriminant analysis also allowed to categorise the animals in the areas. It should be underlined that the result could be biased, since the same data that has been classified is also used to derive the discriminant function. As a second step the data underwent factor analysis (SPSS, 2007). This procedure is based on the assumption that so called common factors (unobservable latent variables) are able to explain the variance – covariance structure of the original variables. On the basis of the comparison between simple (each pair of variables) and partial (each pair of variables controlling for all other variables) Pearson correlation coefficients, it is possible to calculate the Kaiser measure of sampling adequacy (MSA) indicating the suitability of the data structure for factor analysis.

Since males heads are in demand for trophies (Randi et al., 1987). On the basis of the results reported in a large part of the studies performed in Italy in order to discriminate the Sus scrofa majori, it is possible to hypothesise that a limited number of somatic measurements match the differences among the phenotypes (Amici et al., 2003, 2005; Adriani et al., 2005). The aim of the present study was i) to determine which somatic measurements allow different morphotypes to be distinguished; ii) to select the somatic measurements to be registered after drive hunting sessions for the purpose of monitoring wild boar population morphotypes; and iii) to point out the different morphotypes for further genetic analysis.
Results and discussion

The results refer to 688 animals, 253 from the SA area (119 males, 134 females), 301 from the SM area (139 males, 162 females), and 135 from the A area (62 males, 73 females). The sex ratio is similar to that observed in field surveys by Perco (1987) and Boitani et al. (1995b). Raw means of the somatic measurements are reported in Table 1, according to specimen age class. The analysis of variance showed no significant effect of the year and sex (unreported results). With reference to the sampling areas (Table 1) the results of the statistical analysis put in evidence that some variables were significantly different (ear-shoulder distance, height at withers, hind-foot length), but these differences were not homogenous for all the age classes and were unable to highlight differences among the areas.

These mean values are comparable to those observed in other Italian populations (Randi et al., 1987; Massei and Genov, 1993; Tinelli et al., 1999). However, it should be considered that a large part of the studies reported by various authors, both in Italy (Randi et al., 1987; Apollonio et al., 1988; Genov et al., 1995; Martinoli et al., 1997; Tinelli et al., 1999) and in other countries (Brishin et al., 1977; Mayer and Brisbin, 1991), refer to variables not directly comparable with those of the present study.

Concerning total length of young animals, Moretti (1995) registered higher values in the

Table 1. Mean ± SD of somatic measurements of wild boar, and F probability of the difference among the areas.

| Area | SA | A | SM |
|------|----|---|----|
| Young | | | |
| Number | 32 | 14 | 36 |
| Body weight | 27.1±7.2 | 25.3±6.9 | 29.0±10.8 |
| Head-body length | 95.8±8.1 | 96.1±8.6 | 113.3±13.9 |
| Height at withers | 48.0±6.1 | 51.2±5.2 | 59.1±4.6 |
| Hind-foot length | 22.1±1.6 | 22.7±2.2 | 22.1±2.6 |
| Ear length | 10.6±1.8 | 10.9±1.1 | 12.8±0.8 |
| Ear-snout distance | 26.2±2.9 | 25.0±3.3 | 25.5±3.1 |
| Ear-shoulder distance | 14.6±2.9 | 15.2±2.2 | 17.9±3.1 |

| Sub-adults | | | |
| Number | 53 | 59 | 32 |
| Body weight | 54.7±11.2 | 60.1±10.9 | 52.3±15.3 |
| Head-body length | 126.1±8.6 | 124.1±8.2 | 127.0±11.4 |
| Height at withers | 63.4±4.9 | 64.9±4.8 | 68.8±6.9 |
| Hind-foot length | 26.2±1.6 | 27.5±1.9 | 26.4±1.9 |
| Ear length | 15.3±1.1 | 14.1±1.2 | 14.1±1.7 |
| Ear-snout distance | 33.8±2.3 | 31.8±2.0 | 33.7±3.1 |
| Ear-shoulder distance | 18.6±3.9 | 17.6±5.1 | 18.6±3.2 |

| Adults | | | |
| Number | 34 | 42 | 24 |
| Body weight | 77.8±16.1 | 81.2±14.3 | 75.6±16.0 |
| Head-body length | 138.6±8.6 | 140.0±10.1 | 134.2±8.3 |
| Height at withers | 73.7±8.9 | 71.0±6.9 | 74.7±8.9 |
| Hind-foot length | 28.7±1.9 | 27.2±1.8 | 26.6±2.3 |
| Ear length | 14.9±1.2 | 14.1±1.1 | 14.4±1.2 |
| Ear-snout distance | 36.9±2.5 | 34.9±2.4 | 34.8±3.2 |
| Ear-shoulder distance | 21.1±3.2 | 19.7±3.5 | 21.7±4.2 |

Table 2. Mahalanobis quadratic distance between the three areas.

| Age groups | Young | Sub-adults | Adults |
|------------|-------|------------|--------|
| | A | SA | A | SA | A | SA |
| SA | 0.85ns | - | 1.19* | - | 1.23ns | - |
| SM | 3.11*** | 2.74*** | 2.95** | 2.41** | 3.18** | 2.48** |

* P<0.05, ** P<0.01, *** P<0.001, *ns non significant.

Table 3. Correlations between canonical and original variables.

| Age groups | Canonical variable | Young | Sub-adults | Adults |
|------------|--------------------|-------|------------|--------|
| | 1st | 2nd | 1st | 2nd | 1st | 2nd |
| Original variable | | | | | | |
| Body weight | 0.274 | -0.233 | -0.267 | 0.257 | -0.532 | 0.489 |
| Head-body length | 0.305 | -0.146 | 0.039 | 0.130 | -0.099 | -0.008 |
| Height at withers | 0.742 | 0.053 | 0.282 | 0.380 | 0.313 | -0.101 |
| Hind foot length | 0.211 | -0.040 | -0.447 | 0.310 | -0.409 | 0.204 |
| Ear length | 0.239 | -0.002 | -0.195 | 0.144 | 0.234 | 0.044 |
| Ear-snout distance | -0.081 | 0.639 | -0.334 | 0.568 | -0.116 | 0.001 |
| Ear-shoulder distance | 0.721 | 0.391 | 0.466 | 0.774 | 0.560 | 0.688 |

Variance explained, % 92.5 7.5 92.7 7.3 89.8 10.2
Ticino area (Switzerland), compared with the present study (males 107.9 vs 100.1; females: 112.5-99.0). A similar trend for adults was registered by Perco (1987), compared with the present study (males 155.0-137.4; females 135.0-132.8). Live weight showed wide differences comparing different studies, and a wide individual variability (Gallo Orsi et al., 1995; Moretti, 1995; Pedone et al., 1995). In addition differences in live weight between sexes can be put in evidence only after two years of age, and do not show statistic significance (Boitani et al., 1995a).

The canonical discriminant analysis reveals the existence of two different area groups within the three age classes, as shown by the quadratic Mahalanobis distance (Table 2). Specifically, there are statistically significant differences among the SM and the A and SA areas, for young, sub-adults and adults. A difference between A and SA is clearly evident only for the sub-adults (P<0.05).

The first canonical variable accounts for the young and sub-adults, shows the highest correlations with height at withers and ear-shoulder distance. For adults, height at withers and ear-shoulder distance but also hind-foot length and body weight (negative correlations) are relevant. In Table 4 the simple and partial correlation coefficients for all the variables are reported. The differences indicate that unobservable factors, able to control the dependence structure of the observed variables, exist. This is also confirmed by Kaiser’s Measure of Sampling Adequacy (MSA), which is considered acceptable with values over 0.8 (Cerny and Kaiser, 1977). In fact, the MSA was 0.810, 0.829 and 0.816 for young, sub-adults and adults respectively. Table 5 shows the results of the discriminant analysis in the correct classification of the data in the groups. It is useful to underline that a large part of SM animals are correctly classified and a higher percentage of misclassification can be observed for A and SA groups. This result is not easily explainable but the effect of artificial restocking for hunting purposes can be supposed.

Concerning the factor analysis results, only the data concerning the adults (Figure 3) are reported. For this age class, the first three common factors are able to explain 78, 92, and 64% of the covariance for the data of SM, A and SA respectively. The first common factor (Figure 3A) is clearly associated with body weight, head-body length, height at withers and hind-foot length, which expresses the largest portion of communality. The percent-age of covariance explained by the first common factor was 75, 72 and 68% for A and SA and SM respectively, of the total explained variance. The second common factor (Figure 3B) accounts for a limited part of communality.
Conclusions

These results confirm that different morphotypes of wild boar are detectable in some different areas of Central Italy. These morphotypes are differentiated on the basis of height and length measurements (head-body length, height at withers and hind-foot length) and body weight can be relevant only for animals over three years of age.

The above mentioned somatic measurements allow different morphotypes to be distinguished and are easily registered after drive hunting sessions, implying that a wide number of field data can be collected. This study highlights the need to perform biochemical and genetic studies to identify the autochthonous wild boar strain presently populating Central Italy. These studies should be done taking into consideration the results of a field survey on population morphology.

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