

## Genetic determination of cervid antlers in relation to their significance in social interactions

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Antler traits (length of the main beam, circumference of the main beam, coronet circumference, and the number of antler points) in roe deer *Capreolus capreolus* (Linnaeus, 1758) from a population in Casentino (Northern Tuscany) were examined for associations with genotypes at loci coding for enzymes. Significant associations were found only in yearlings. Individuals homozygous for the allele *Mpi*<sup>120</sup> had significantly larger antlers than carriers of other genotypes at *Mpi*. Individuals homozygous for *Pep-2*<sup>100</sup> had significantly smaller antlers than carriers of other genotypes at *Pep-2*. In adults the results were essentially the same, but only as a statistically insignificant trend. The data were interpreted in terms of one or more genetic components having a major influence on antler development only in yearlings. This corresponds with behavioural data suggesting that in adults antler size is not related to reproductive success, but in yearlings it is correlated with sexual maturity and the rate of being expelled from the home range of their mothers by territory holders. The situation in the roe deer was compared with previous results on the genetics of antler development in the red deer, where males are social rather than solitary, yearlings do not participate in reproduction, and some antler characteristics are related to reproductive success of adult stags.

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### Introduction

Antlers are the most obvious secondary sexual traits in most male cervids. Their significance in social interactions has been found to be chiefly related to inter-male competition for females (cf Clutton-Brock *et al.* 1980, Clutton-Brock 1982). On the one hand, antler size may be positively correlated with reproductive success of a male (eg Clutton-Brock *et al.* 1988). On the other hand, depending on the species, the annual rebuilding of antlers may require a considerable expenditure of energy. Taking into account the potential benefit of relatively large antlers in terms of increased reproductive success and their potential cost in terms

of increased metabolic effort, it would not be surprising to find some genetic mechanism responsible for balancing these components under variable environmental conditions. The genetic basis of antler development can be expected to differ from species to species, depending on the actual importance of male antlers for social interactions and ultimately for reproductive success, and may be elucidated by using molecular markers (eg Scribner and Smith 1990, Hartl *et al.* 1991a, 1995).

In the present study relationships between allozyme variation and antler development are examined in various age classes of roe deer *Capreolus capreolus* (Linnaeus, 1758) and compared with data on red deer *Cervus elaphus* Linnaeus, 1758 published by Hartl *et al.* (1991a, 1995). These two species show remarkable differences in social organization and male antler development. Thus, different patterns as to relationships between allozymes and antler traits may be expected.

### Material and methods

Liver and kidney samples of 46 male and 72 female roe deer came from the Province of Arezzo in Northern Tuscany. This population is probably autochthonous and stems from the remaining nucleus of the Foreste Casentinensi (Lorenzini *et al.* 1993). All animals were shot during the hunting season of 1993. A total of 12 loci found polymorphic in European roe deer in previous investigations were examined for electrophoretic variation (cf Hartl *et al.* 1991b). Age determination was performed on the basis of dentition. Body weights of eviscerated specimens were measured immediately after shooting using a spring-balance. Mandible length served as an indicator of body size. As far as available, antler dimensions (number of antler points – NAP, length of the main beam – LMB, circumference of the main beam measured 1 cm above the coronet – CMB, and coronet circumference – CC) in the males studied electrophoretically were measured on skulls collected for trophy records.

Alleles were designated according to the relative mobility of the corresponding allozymes. All alleles found in the present study had been already defined by Hartl and Reimoser (1988) and Hartl *et al.* (1991b). Genotypic proportions were tested for agreement with Hardy-Weinberg expectations using the BIOSYS-1 programme package of Swofford and Selander (1989; release 1.7). Heterozygosity classes in yearlings and adults of both sexes were formed by grouping the specimens according to the number of heterozygous loci per individual). Standard statistical analyses were performed using SPSS for Windows (release 5.0).

Separately for yearlings and adults in each sex, differences in body weight and mandible length among heterozygosity classes were examined by the Kruskal-Wallis test. The same statistical procedure was used for examining antler traits in yearlings and adults (NAP, LMB, CMB, CC – measurements of both beams added) as to differences among heterozygosity classes. Antler traits were checked visually for differences among genotypic classes at *Pep-2* and *Mpi* using boxplots. Apparent differences were tested for statistical significance by *t*-test and Kruskal-Wallis test, respectively.

### Results

Electrophoretic polymorphism was detected at *Dia-2*, *Ak-1*, *Pgm-1*, *Pgm-2*, *Acp-1*, *Pep-2*, *Mpi*, and *Gpi-1*. Allelic frequencies, observed ( $h_o$ ) and expected ( $h_e$ ) heterozygosities are given in Table 1. At none of the polymorphic loci genotypes were sex or age dependent (cross-tabs and chi square test). Both in males and in

Table 1. Allelic frequencies and heterozygosity at 8 polymorphic loci in male and female roe deer from Casentino.  $n$  – sample size,  $h_o(h_e)$  – observed (expected) heterozygosity. Allelic frequencies were not significantly different between sexes ( $\chi^2$ -test of Workman and Niswander).

| Locus        | Allele | Males | $n$ | $h_o(h_e)$   | Females | $n$ | $h_o(h_e)$   |
|--------------|--------|-------|-----|--------------|---------|-----|--------------|
| <i>Dia-2</i> | 100    | 0.924 | 46  | 0.065(0.141) | 0.924   | 72  | 0.125(0.141) |
|              | 118    | 0.076 |     |              | 0.076   |     |              |
| <i>Ak-1</i>  | 100    | 0.054 | 46  | 0.109(0.103) | 0.042   | 72  | 0.056(0.080) |
|              | 250    | 0.946 |     |              | 0.958   |     |              |
| <i>Pgm-1</i> | 100    | 1.0   | 46  | 0.0(0.0)     | 0.993   | 72  | 0.014(0.014) |
|              | -16    | 0.0   |     |              | 0.007   |     |              |
| <i>Pgm-2</i> | 100    | 0.913 | 46  | 0.130(0.159) | 0.887   | 71  | 0.169(0.200) |
|              | 70     | 0.087 |     |              | 0.113   |     |              |
| <i>Acp-1</i> | 100    | 0.989 | 46  | 0.022(0.022) | 0.993   | 72  | 0.014(0.014) |
|              | 200    | 0.011 |     |              | 0.007   |     |              |
| <i>Pep-2</i> | 100    | 0.656 | 45  | 0.467(0.509) | 0.529   | 69  | 0.377(0.609) |
|              | 115    | 0.200 |     |              | 0.254   |     |              |
|              | 107    | 0.144 |     |              | 0.217   |     |              |
| <i>Mpi</i>   | 100    | 0.685 | 46  | 0.239(0.432) | 0.771   | 72  | 0.208(0.353) |
|              | 120    | 0.315 |     |              | 0.229   |     |              |
| <i>Gpi-1</i> | 100    | 1.0   | 46  | 0.0(0.0)     | 0.993   | 72  | 0.014(0.014) |
|              | 500    | 0.0   |     |              | 0.007   |     |              |

Table 2. Observed and expected genotypes at *Pep-2* and *Mpi* in male and female roe deer from Casentino.  $p$ -values in parentheses are from  $\chi^2$ -tests with pooling of heterozygous genotypes and of homozygous genotypes, respectively, for rare alleles (cf Swofford and Selander 1989).

| Locus        | Geno-<br>type | Males                 |                       |          |    |                  | Females               |                       |          |    |                   |
|--------------|---------------|-----------------------|-----------------------|----------|----|------------------|-----------------------|-----------------------|----------|----|-------------------|
|              |               | Observed<br>frequency | Expected<br>frequency | $\chi^2$ | df | $p$              | Observed<br>frequency | Expected<br>frequency | $\chi^2$ | df | $p$               |
| <i>Pep-2</i> | 100/100       | 19                    | 19.225                |          |    |                  | 25                    | 19.182                |          |    |                   |
|              | 100/115       | 14                    | 11.933                |          |    |                  | 14                    | 18.650                |          |    |                   |
|              | 100/107       | 7                     | 8.618                 |          |    |                  | 9                     | 15.985                |          |    |                   |
|              | 115/115       | 2                     | 1.719                 |          |    |                  | 9                     | 4.343                 |          |    |                   |
|              | 107/115       | 0                     | 2.629                 |          |    |                  | 3                     | 7.664                 |          |    |                   |
|              | 107/107       | 3                     | 0.876                 |          |    |                  | 9                     | 3.175                 |          |    |                   |
|              |               |                       |                       | 8.485    | 3  | 0.037<br>(0.022) |                       |                       | 24.494   | 3  | <0.001<br>(0.005) |
| <i>Mpi</i>   | 100/100       | 26                    | 21.462                |          |    |                  | 48                    | 42.692                |          |    |                   |
|              | 100/120       | 11                    | 20.077                |          |    |                  | 15                    | 25.615                |          |    |                   |
|              | 120/120       | 9                     | 4.462                 |          |    |                  | 9                     | 3.692                 |          |    |                   |
|              |               |                       |                       | 9.680    | 1  | 0.002            |                       |                       | 12.689   | 1  | <0.001            |

females, genotypic proportions at the loci *Pep-2* and *Mpi* deviated significantly from Hardy-Weinberg expectations (Table 2).

Table 3. Differences in antler dimensions (LMB – length of the main beam, CMB – circumference of the main beam, CC – coronet circumference) in carriers of different genotypes at *Mpi*. *n* – sample size, ns – statistically not significant.

|     | Yearlings                        |                               |                   | Adults                           |                               |                   |
|-----|----------------------------------|-------------------------------|-------------------|----------------------------------|-------------------------------|-------------------|
|     | <i>Mpi</i> <sup>non120/120</sup> | <i>Mpi</i> <sup>120/120</sup> | <i>p</i> (t-test) | <i>Mpi</i> <sup>non120/120</sup> | <i>Mpi</i> <sup>120/120</sup> | <i>p</i> (t-test) |
| LMB | 15.9 ( <i>n</i> =13)             | 30.3 ( <i>n</i> =2)           | 0.001             | 43.6 ( <i>n</i> =13)             | 46.8 ( <i>n</i> =4)           | ns                |
| CMB | 8.8 ( <i>n</i> =13)              | 11.7 ( <i>n</i> =2)           | 0.077             | 14.2 ( <i>n</i> =11)             | 14.9 ( <i>n</i> =4)           | ns                |
| CC  | 10.8 ( <i>n</i> =13)             | 17.0 ( <i>n</i> =2)           | 0.000             | 24.0 ( <i>n</i> =11)             | 26.9 ( <i>n</i> =4)           | ns                |

Antler traits (NAP, LMB, CMB, CC) were highly correlated in yearlings ( $r = 0.67-0.98$ ,  $p = 0.007-0.000$ ,  $n = 15$ ), and somewhat less so in adults ( $r = 0.40-0.80$ ,  $p = \text{ns}-0.000$ ,  $n = 15$ ). Mandible length was significantly correlated with body weight in yearlings ( $r = 0.67$ ,  $p = 0.034$ ,  $n = 10$ ) but not in adults. In both age classes, antler traits were not correlated with either body weight or mandible length. In both sexes and age classes, body weight and mandible length were not related to individual heterozygosity. The same was the case for antler traits in males. Both for *Pep-2* and *Mpi* associations between genotypes and the development of antler traits became apparent. In yearlings, homozygous carriers of *Mpi*<sup>120</sup> had significantly larger antlers than homo- or heterozygous carriers of *Mpi*<sup>100</sup>. In adults, there was a statistically insignificant trend in the same direction (Table 3). Based on the same grouping of genotypes (*Mpi*<sup>non120/120</sup> vs *Mpi*<sup>120/120</sup>), a two-way ANOVA revealed a significant influence of both age ( $p < 0.001$  in all cases) and *Mpi* genotypes ( $p_{\text{LMB}} = 0.05$ ,  $p_{\text{CC}} = 0.031$ ) on antler dimensions. In yearlings, homozygous carriers of *Pep-2*<sup>100</sup> had significantly smaller antlers than carriers of any other genotype. There was the same trend in adults, but except for CMB, again statistically insignificant (Table 4). Based on the same grouping of genotypes (*Pep-2*<sup>non100/100</sup> vs *Pep-2*<sup>100/100</sup>), a two-way ANOVA revealed a significant influence of both age ( $p < 0.001$  in all cases) and *Pep-2* genotypes ( $p_{\text{LMB}} = 0.015$ ,  $p_{\text{CMB}} = 0.001$ ,  $p_{\text{CC}} = 0.031$ ) on antler dimensions.

Table 4. Differences in antler dimensions (NAP – number of antler points, LMB – length of the main beam, CMB – circumference of the main beam, CC – coronet circumference) in carriers of different genotypes at *Pep-2*. *n* – sample size, ns – statistically not significant.

|     | Yearlings                          |                                 |                   | Adults                             |                                 |                   |
|-----|------------------------------------|---------------------------------|-------------------|------------------------------------|---------------------------------|-------------------|
|     | <i>Pep-2</i> <sup>non100/100</sup> | <i>Pep-2</i> <sup>100/100</sup> | <i>p</i> (t-test) | <i>Pep-2</i> <sup>non100/100</sup> | <i>Pep-2</i> <sup>100/100</sup> | <i>p</i> (t-test) |
| NAP | 2.9 ( <i>n</i> =9)                 | 2.0 ( <i>n</i> =6)              | 0.021             | 6.0 ( <i>n</i> =10)                | 5.4 ( <i>n</i> =7)              | ns                |
| LMB | 23.4 ( <i>n</i> =9)                | 9.5 ( <i>n</i> =6)              | 0.027             | 45.0 ( <i>n</i> =10)               | 43.3 ( <i>n</i> =7)             | ns                |
| CMB | 10.4 ( <i>n</i> =9)                | 7.4 ( <i>n</i> =6)              | 0.015             | 15.1 ( <i>n</i> =9)                | 13.4 ( <i>n</i> =6)             | 0.019             |
| CC  | 13.7 ( <i>n</i> =9)                | 8.5 ( <i>n</i> =6)              | 0.022             | 26.1 ( <i>n</i> =9)                | 22.8 ( <i>n</i> =6)             | ns                |

### Discussion

There are substantial differences between roe and red deer as to their respective social organization and reproductive behaviour. Roe deer males are generally solitary and often territorial from March to September (Kurt 1991). They do not form bachelor groups and yearlings may participate in reproduction. In mature males, access to females is a function of possessing a territory rather than of antler size and physical strength (Kurt 1991). Caused by the aggression of territory holders against possible competitors in reproduction, the dispersal of young males from the home ranges of their mothers may take place in their first year of life (Strandgaard 1972, Ellenberg 1978). It is the large-antlered yearlings, which are most frequently attacked and most likely to disperse (Wahlström, in press). Indeed antler size in yearlings was found to be positively correlated with the development of testes (Wahlström, in press), suggesting a relationship with sexual maturity (Møller 1989).

On the contrary, red deer males are generally social, and are often associated in bachelor groups outside the rutting period. Their reproductive success may be correlated with the dominance rank they held in social groups in the previous winter (Appleby 1982). Yearlings are excluded from reproduction. The dispersal of young males from the home ranges of their mothers takes place in the second or third year of life and is not due to the aggression of older males. General antler characteristics of adult males may not be directly correlated with dominance or reproductive success, however, antler size, antler weight, and the number of antler points sometimes are. Moreover, these traits reflect general body condition and are often correlated with body weight, which is strongly linked to dominance and reproductive success (Clutton-Brock *et al.* 1979, Gibson and Guinness 1980, Appleby 1982, Clutton-Brock 1982).

In both species, these considerations are reflected by the data on relationships between allozymes and antler development. In roe deer, one or more marked genetic components seem to be responsible for differences in antler dimensions only among yearlings, and are chromosomally or functionally linked to *Mpi* and *Pep-2*. In contrast to many other allozyme polymorphisms in roe deer, those at *Mpi* and *Pep-2* are present for the same major alleles in virtually all populations examined so far (cf Hartl *et al.* 1991b, Lorenzini *et al.* 1993). Given the considerable human impact on population structure of large game animals, which may cause dramatic losses of allelic variation by genetic drift (cf Hartl and Pucek 1994, and references therein), the ubiquitous presence of particular alleles at an enzyme locus provides a strong argument in favour of their maintenance through balancing or countervailing selection. The deficiency of heterozygotes at *Mpi* in both sexes may be related to an increased dispersal of large-antlered yearlings. In an expanding population like Casentino (Lorenzini *et al.* 1993), many of these yearlings may have had the opportunity to establish new territories at the margins of its range. In roe deer territories females usually form stable mother clans which,

due to non-random mating, ultimately leads to some genetic substructuring of a population (Kurt *et al.* 1993). Thus, in some parts of the population, animals homozygous for *Mpi*<sup>120</sup> (the otherwise rare allele) may have accumulated with time, and the non-random distribution of genotypes in the population may have become apparent as a Wahlund effect in the random sample of roe deer drawn for our study. At *Pep-2* there was a significant excess of homozygotes as well, but generally the large number of genotypes requires larger sample sizes of individuals to be investigated as to their detailed relationship with antler traits in the presence of different *Mpi* genotypes. At any rate, all of the large-antlered yearlings with *Mpi*<sup>120/120</sup> had a *Pep-2* genotype other than *Pep-2*<sup>100/100</sup>.

In red deer at least two different components responsible for antler development could be identified (Hartl *et al.* 1991a, 1995). One of them was associated with *Idh-2*, where homozygous carriers of the allele *Idh-2*<sup>125</sup> had a significantly higher number of antler points from the second year of life on. However, the average difference from carriers of all other *Idh-2* genotypes was highest between 2 and 6 years of age, suggesting a more rapid antler development in the respective stags. The second genetic component was associated with *Acp-2*, where, from seven years on, homozygous carriers of *Acp-2*<sup>100</sup> had generally significantly larger antlers (NAP, LMB, CMB, CC) than carriers of the other *Acp-2* genotypes. Interestingly, homozygous carriers of *Acp-2*<sup>100</sup> had smaller antlers than average between 2 and 6 years of age, suggesting that the respective stags are slow in antler development during their first period of life, whereas they grow exceptionally large antlers once they are older. The presence of only three genotypes at each locus allowed us to check the combined effect of the component associated with *Idh-2* and that associated with *Acp-2* on antler development, and we found that both components can compensate or reinforce each other at the various stages of lifetime antler growth. In fact, by playing a role in balancing benefits and costs of male reproductive success, they may be part of a mechanism enabling the rapid adaptation of a population to various environmental and demographic conditions (Hartl *et al.* 1995).

Altogether, the data of the present study as well as those of Hartl *et al.* (1991a, 1995) suggest that the genetic control of antler development in cervids is clearly related to the respective significance of antlers in social interactions.

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