

Molecular biogeography and genetic structure of the Irish Draught breed: a comparison to other domestic horse populations

McGahern, A., Hill, E.W., MacHugh, D.E., Brophy, P.
Department of Animal Science, Faculty of Agri-Food and the Environment, UCD

Introduction

The Irish Draught (ID) horse is considered an endangered breed by the Department of Agriculture, Food and Rural Developments classifications, derived from rules as applied by the EU under FAO criteria. Recent demographic and pedigree genetic analysis suggests that the ID horse population is at risk of further loss of genetic diversity (O'Toole *et al.*, 2001). Studies of molecular genetic diversity have been shown to contribute valuable intrinsic information about population histories and are becoming widely used in decision making for the conservation and management of wild animal populations. In particular, mitochondrial DNA (mtDNA) is a useful tool to understand female population history and has been widely used in studies of human genetic diversity.

The objectives of this project were to estimate the genetic diversity in the modern ID population and to make inferences about its history. To achieve a global context, a comparative analysis of the variation in mtDNA was performed with the ID and other horse breeds from Europe, Near East and Far East.

Materials and Methods

Founder ID females were identified through pedigree analysis of the Irish Horse Register. One DNA sample representing one of each of 59 founder females was collected. DNA sequencing was performed for an 851base pair (bp) segment of the hypervariable mtDNA D-loop segment. The sequences were aligned with 108 novel sequences from six Russian breeds, and 806 sequences from 64 geographically disparate horse breeds taken from the GenBank database.

The ID founder population was reconstructed in an unrooted median joining evolutionary network, using Network (version 4.1.0.8). A neighbour joining phylogeny was created in ClustalX and viewed in Treeview (see Figure 1). Diversity statistics were calculated in Arlequin (version 2.0). The probability of identity (PI) was calculated as in Hill *et al.*, 2002.

Results and Discussion

In 59 ID families, 63 polymorphic sites in an 851bp mtDNA D-loop fragment defined 31 sequences. Sequence sharing, measured by probability of identity (PI) values, among the ID founders was lower than observed in the Russian breeds: Yakutian (YH), Vyatskaya (VH), Mesenskay (MH), Akahltekin (AH), Orlov (OH) and Mongolian (MnH) (Table 1) and is similar to estimates of the Arab horse (0.05) and three times less than that found in the thoroughbred (0.15). This suggests that present day ID mtDNA sequences derive from a diverse foundation stock.

Table 1 PI values observed for ID and Russian breeds

Breed	ID	YH	VH	MH	AH	OH	MnH
PI value	0.06	0.1	0.13	0.14	0.15	0.18	0.21

Visual examination of horse population diversity revealed a star like branching structure (Figure 1) similar to that found by Vila *et al* (2001) and Jansen *et al* (2002).

In general there was a lack of phylogenetic sorting of sequences into geographic groups unlike the pattern for other large domesticates. The ID sequences were found throughout the tree with the exception of branches F and G, which were mostly represented by Far East and Middle East sequences. Branch D contained 48% of the ID sequences but only 15% of Far East sequences.

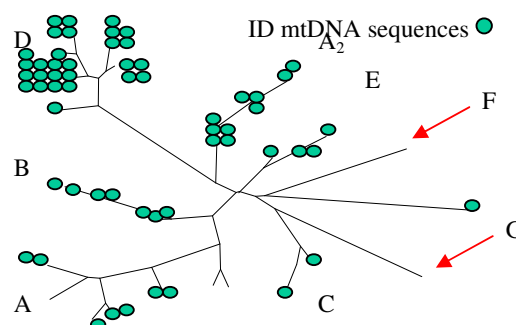


Figure 1 A simplified neighbour joining phylogenetic tree relating ID founder mtDNA.

Conclusion

Mitochondrial DNA sequence sharing among Irish Draught founders is lower than observed in other horse breeds suggesting significant genetic diversity. The most common global horse sequence, found in branch D, is also the most common ID sequence. The genetic origins of the ID *per se* cannot be determined from mtDNA data because of the extent of sequence sharing among breeds of horse. The high mobility of the horse, enabled by the nature of its domestic roles will have led to an obscuring of genetic structure within the species through post domestic migration. There is some indication however that the Far Eastern sequences may demonstrate some geographic clustering to the exclusion of western breeds, which may be a consequence of their geographic isolation and their origins at the centre of horse domestication.

References

- O'Toole, H., Brophy, P., Kelleher, D., Aldridge, L., Quinn, K. 2001.
- Vila, C., Leonard JA, Gotherstrom A, Marklund S, Sandberg K, Liden K, Wayne RK, Ellegren H. 2001.
- Jansen, T., Forster, P., Levine, M., Oelke, H., Hurles, M., Renfrew, C., Weber, J., and Olek, K. 2002.
- Hill, E.W., Bradley, D.G., Al-Barody, M., Ertugrul, O., Splan, R.K., Zakharov, I., and Cunningham, E.P. 2002.