

Characterisation of several Connemara Pony populations

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Introduction

The Connemara Pony is one of Ireland's few indigenous equine breeds. The Department of Agriculture and Food in Ireland have classified the breed as endangered. In the 1940s an extensive export market developed for the breed and Connemara Ponies were exported worldwide.

The results generated from a characterisation of the population in Ireland indicate that past breeding practices have caused a substantial loss in the breeds' genetic diversity (Feely, 2004). As a consequence of this project a study is currently being undertaken to characterise and compare the genetic diversity of Connemara Pony populations outside Ireland. The study is also aimed at identifying sources of genetic variability that could be used to widen the gene pool of the Irish Connemara Pony population.

Materials and Methods

A total of 47,515 pedigree records were used in the analysis. These records consisted of all registered Connemara Ponies from the various countries under study. A reference population for each country was defined as all purebred foals born between 1998 and 2001 inclusive (Table 1).

Data cleaning and the calculation of inbreeding and relationship coefficients were conducted using SAS[®] software (SAS[®] Language and Procedures, 1989). Parameters derived from the probabilities of gene origin and pedigree completeness levels were estimated using the software *Pedig* (Boichard, 2002).

Table 1 The number of records in the dataset and reference population of each country.

Country	No of records	
	Dataset	Reference Population
Ireland	20,032	2,844
UK	5,368	611
N.America	3,288	340
France	11,304	2,240
Sweden	4,552	431
Denmark	2,547	209
Finland	424	54

Results

The complete generation equivalent (CGE), average inbreeding coefficient (F), average relationship coefficient (AR), number of founders (f), effective number of founders (f_e), effective number of ancestors (f_a) and the f_e/f_a ratio for the individuals in all of the reference populations are shown in Table 2.

The parameters derived from the probabilities of gene origin (f, f_e, f_a) indicate that the genetic diversity of all of the reference populations have been adversely affected by unequal founder and ancestor contributions.

Table 2. The CGE, average F , AR , f , f_e , f_a and f_e/f_a ratio for the individuals in the reference populations.

	Ire	UK	NA	Fra	Swe	Den	Fin
CGE	6.59	6.36	6.38	6.48	6.66	6.97	6.75
Ave F (%)	4.65	4.44	4.04	4.17	4.72	4.18	4.97
AR (%)	10.66	9.29	8.57	8.91	11.53	12.84	19.64
f	351	353	331	346	184	137	127
f_e	35.8	36.5	37.7	40	37.4	41.9	35.2
f_a	18	18.9	23.6	20.25	18.2	18.08	8.35
f_e/f_a	1.99	1.93	1.6	1.98	2.05	2.31	4.22

Table 3 shows the AR between the sires of the various reference populations and the sires and dams of the Irish reference population. North America had the lowest average relationship to the Irish sires and dams. They also had the sire with the lowest relationship to the dams of the Irish reference population.

Table 3 The AR between the sires of the reference populations to the sires and dams of the Irish reference population and the minimum AR to the Irish dams.

Country	AR to Irish sires (%)	AR to Irish dams (%)	Min AR to Irish dams (%)
Ireland	10.64	10.15	5.41
UK	8.62	9.03	4.18
N.America	6.64	6.64	1.09
France	8.36	8.20	4.99
Sweden	8.40	8.51	5.88
Denmark	7.98	8.03	5.57
Finland	7.66	7.89	5.18

Conclusions

It is apparent that, to varying degrees, the level of genetic diversity in the different Connemara Pony populations is in need of observation. It may be necessary to manage the level of genetic variability, in some populations, in order to avoid high levels of inbreeding in future generations.

It may be possible to widen the gene pool of the Irish Connemara Pony population by utilising the genetic resources of Connemara Ponies in other countries.

Acknowledgements

This work was funded by the Department of Agriculture. The authors wish to thank all of the Connemara Pony Breeder Societies for their assistance.

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