

Pedigree Analysis of Holstein Dairy Cattle Populations

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Summary

A pedigree analysis on the Holstein populations of France, Germany, Italy, and The Netherlands was performed. Generation interval, number of founders and Country-Gene origin contribution to populations were calculated from the complete pedigree of each population. Generation intervals averaged 6 years in all populations. Founders are mostly indigenous but a proportion of 60% to 80% of gene contribution to the living populations comes from USA founder population, while 10% from Canadian one.

Introduction

Project PROTEJE aims to develop an international evaluation system for bulls and cows (Canavesi, 2001). Four countries participate to the project: France, Germany, Italy and The Netherlands. Each partner of the group has specific tasks to address. One of the Italian group goals is to define the structure of the Phantom groups.

Because global market of bull semen, gene migration has been active in the four populations for years. Gene migration occurs especially from USA and Canada, but some exchange occurs also across the UE populations.

In a study on Italian Haflinger horse Gandini *et al.* (1997) showed the proportionate gene contribution of founder breeds, due to migration, to herd book recorded population.

Aim of this work is to perform a preliminary analysis on the complete pedigrees of the four countries in order to understand the dynamics of genes migration.

Material and Methods

Complete pedigree data base from France, Germany, Italy and The Netherlands were available for the analysis. Consistencies of the four populations are reported in Table 1.

Table 1. Pedigree size.

Country	N° of individuals
FRA	9,602,174
DEU	5,693,176
ITA	2,841,979
NLD	3,338,103

For each pedigree the following descriptive statistics were calculated: i) population size across years (calculated as number of recorded animals per year); ii) generation interval, calculated for each of the four selection pathways using part of the Pedig software package (Boichard, 1997); iii) number of founders per origin, calculated per year assuming as founder each individual with unknown parents.

Eight different founder populations (gene origins) were defined: Italy, France, Germany, The Netherlands, USA, Canada, Europe (including, Austria, Belgium, Czech Republic, Denmark, Spain, UK, Israel, Sweden, Slovakia, Hungary, Ireland, Norway, Portugal), and Other. For each pedigree the genetic contribution of founder breeds to each population was calculated. A founder population origin (gene origin) was assigned to each founder individual according to its Country of birthplace. For individuals with only one known parent, the origin of the unknown parent was assumed as the Country of birthplace of the animal itself. Gene origin contribution of each parent animal was then halved in each generation and tracked along the pedigree. Founder populations contributions were successively averaged by birth year and sex.

Results and Discussion

Figures 1 and 2 show the population size by year of the four males and females populations respectively. All the populations show an increase in size since 1975 and until 1990, when each population reach a plateau in the number of recorded individuals. The situation is similar for all four male and female populations.

Figures 3 to 6 show generation intervals by 5-years periods in the four populations for the four pathways of selection: sires of bull (SB), sires of cow (SC), dams of bull (DB), dams of cow (DC). In this figures is also reported the average generation interval per year.

Figure 1. Size of female population per year.

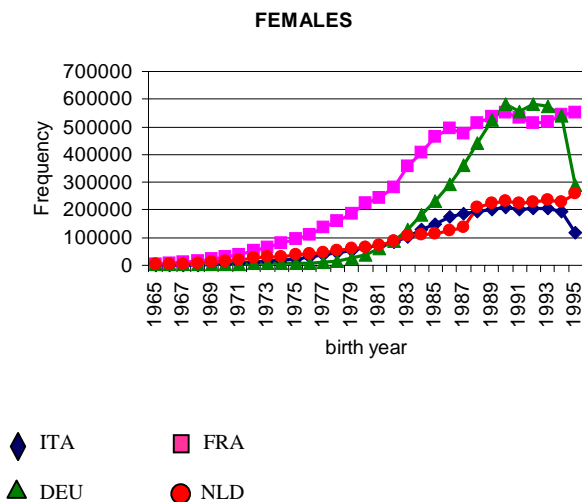
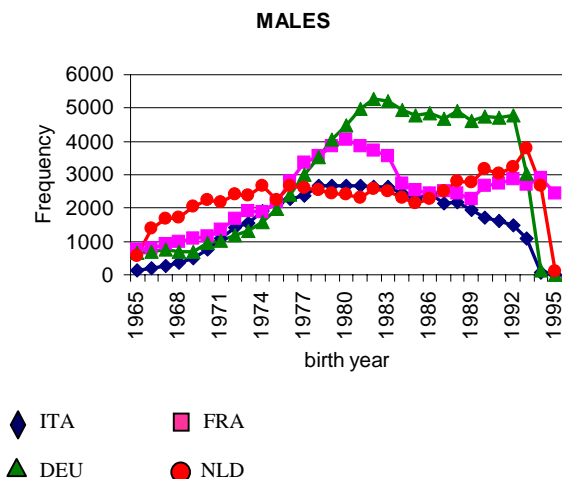


Figure 2. Size of male populations per year.



Generation intervals are similar in all the populations. Italian population shows a larger generation interval for SB during the period from 1970 to 1980 which is related to the fact that before 1986 no genetic improvement programs were in place in the Holstein population. The average generation interval is close to 6 years for all the populations. The reduced generation interval in age '60-'70 in Figure 4 (German pedigree) is due to missing information of animals birth year.

Figure 3. Generation Interval for France.

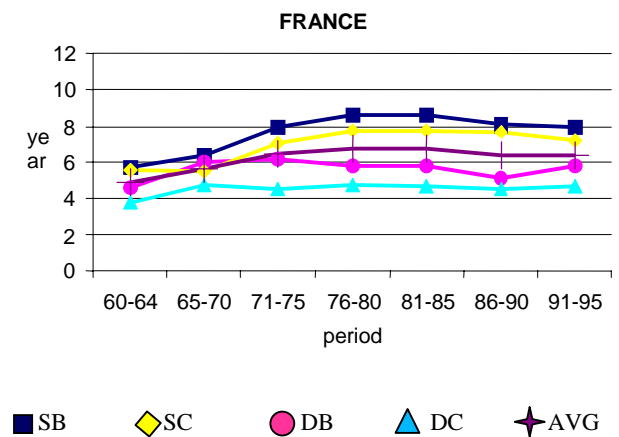


Figure 4. Generation Interval for Italy.

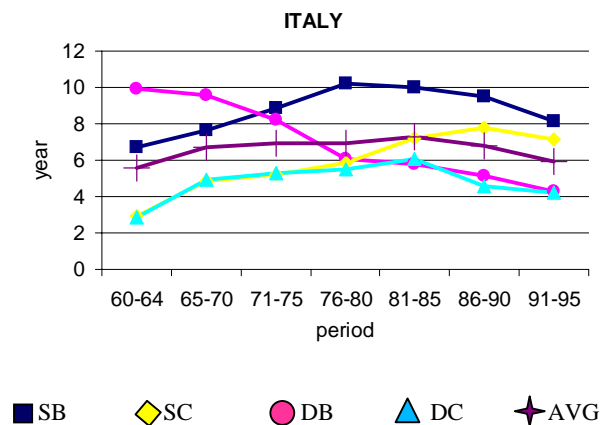


Figure 5. Generation interval for Germany.

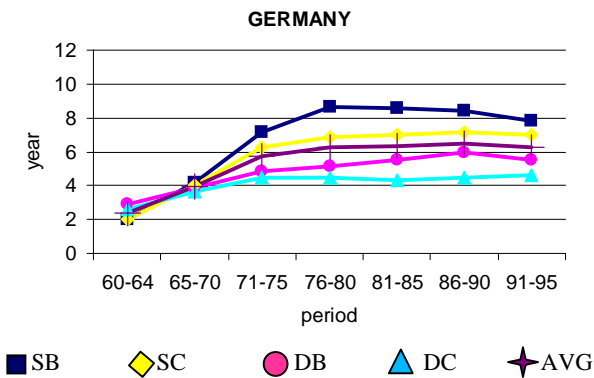


Figure 6. Generation Interval for The Netherlands.

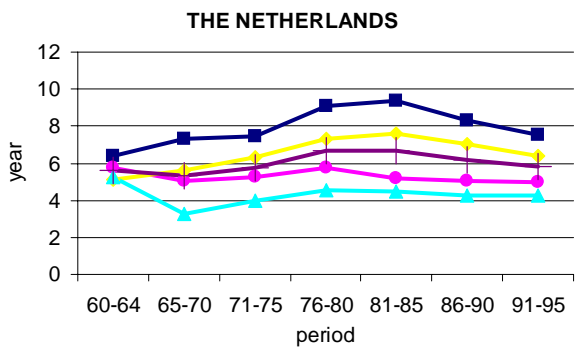


Figure 7 and 8 show the percentage of founders by origin in the four male and female populations respectively. The Italian male population shows a large founder contribution from foreign countries, especially from USA. The other populations show to have the largest proportion of genes from indigenous founders and, regarding foreign founder animals, a prevalence of USA and Canadian ones.

Figure 7. Male population - Percentage of founders by origin.

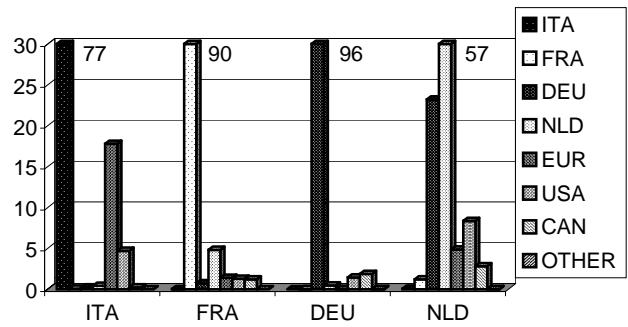
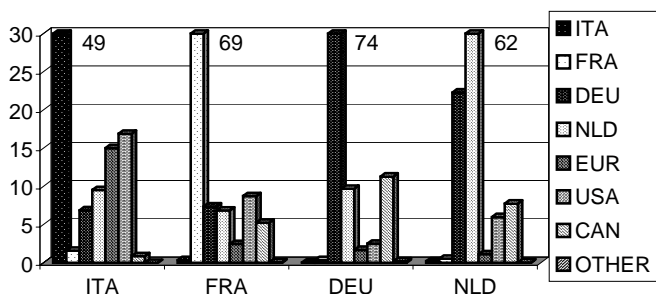


Figure 8. Female population – Percentage of founders by origin.

Figures 9 and 10 show the proportion of founders on recorded population by birth year for the four male and female populations respectively. In the male populations a large proportion of founders is shown in the older recorded individuals, while in recent registered animals the percentage of founders comes close to zero. The Italian female population shows a different trend with respect to other females populations: the proportion of founder individuals on recorded population vary from 60% to 80% until age '80. This is due to the openness of Italian genealogical herd book where cows are registered on a herd basis. In the Dutch population the percentage of females founders is always close to zero. This is probably due to the fact that recorded animals have at least one known parent.

Figure 9. Males populations – Proportion of founders by birth year.

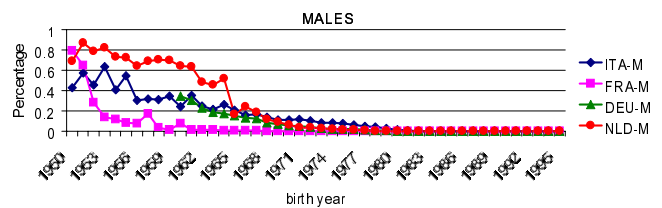
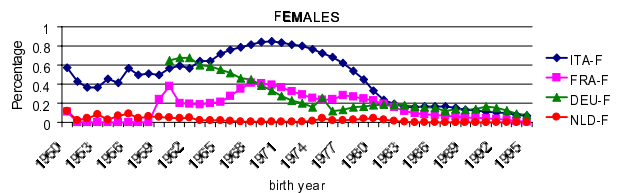


Figure 10. Female populations – Proportion of founders by birth year.



Figures 11 to 18 show the contribution by year, of each of the eight founder populations (gene origin) to the composition of the four male and female populations. All the graphics show a similar trend. While animals recorded in older periods (1950 to 1970) own a large native population gene contribution, individuals of the living population (1995 to present) exhibit a large proportion of genes from foreign populations. Because of gene migration, the native population contributions were gradually substituted by USA genes and, at a smaller rate, by Canadian ones. Animals of the four populations born in the most recent years own a percentage of USA genes that vary from 70% up to 80% in the male populations and from 60% up to 80% in the female populations. Canadian genes are present in a proportion close to 10% in all populations. There is some evidence of a larger European gene migration across France Germany and the Netherlands respect to Italy even if the proportion of genes coming from the four EU populations is very small.

Conclusions

Italian and German populations seems to maintain a larger proportion of native genes in living female populations. In all populations the largest contribution comes from USA population and, in smaller proportion, from Canada.

The high proportion of USA genes and Canadian ones does not imply that same genes were equally sampled and bred in the four different populations. Different selection criteria and different selection objectives produced different crosses across populations and this result in the different characteristics that the living male and female populations do maintain across countries.

References

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- Gandini, G.C., Samorè, A.B. & Pagnacco, G. 1997. Genetic contribution of the Arabian to the Italian Haflinger horse. *J. Anim. Breed. Genet.* 114, 457-464.

Acknowledgements

The partners of PROTEJE project are gratefully acknowledged for providing the pedigree data and for the useful comments.

Figure 11. Proportion of gene origin in France male population.

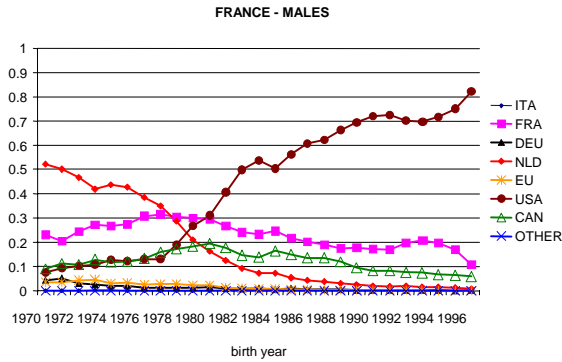


Figure 12. Proportion of gene origin in France female population.

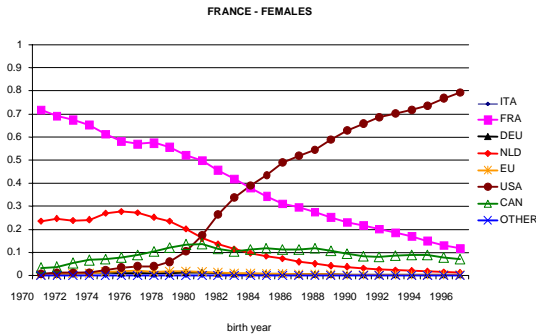


Figure 13. Proportion of gene origin in German male population.

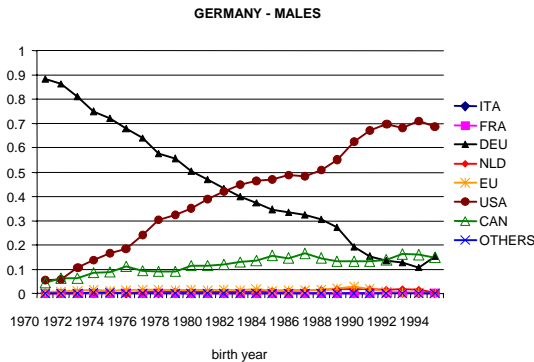


Figure 14. Proportion of gene origin in German female population.

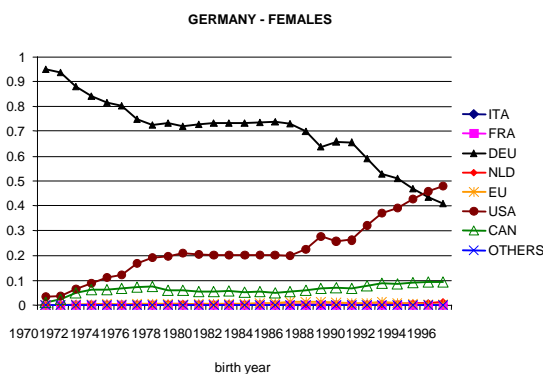


Figure 15. Proportion of gene origin in Italian male population.

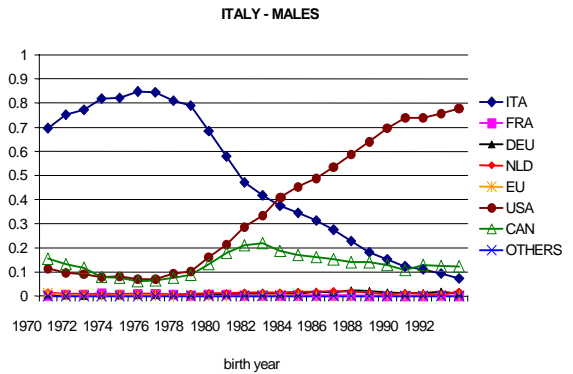


Figure 16. Proportion of gene origin in Italian female population.

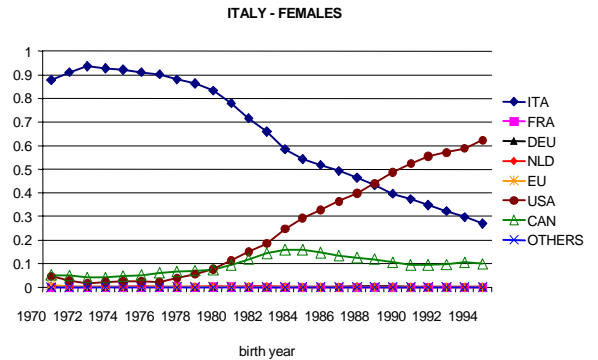


Figure 17. Proportion of gene origin in Dutch male population.

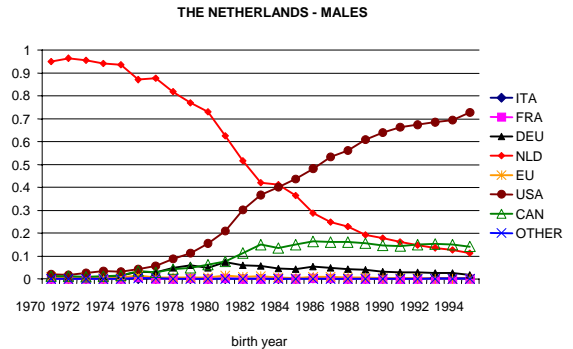


Figure 18. Proportion of gene origin in Dutch female population.

