

# THE IMPACT OF THE BREEDING POLICY ON THE GENETIC STRUCTURE OF THE SPANISH SPORT HORSE

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## INTRODUCTION

The development of the Spanish equine industry has motivated the creation of a new breed, the Spanish-Sport horse (SSH; Studbook founded in 2002), a composite breed with some genetic influence from other Spanish and foreign breeds. It appeared as the answer to a general demand of animals with a good sport aptitude and performance. Its breeding main goal is "to obtain a horse with good functional conformation, temperament and health, able to attain high performance at either national or international sport events where it participates in".

At the beginning, this Studbook included any individual participating in sports competitions and not registered in any other Studbook. The SSH Studbook was closed in 2004 but is still possible to include individuals of other Spanish breeds as parents of a SSH. Moreover, it is possible to include as parents Sport Horses registered in foreign Studbooks (SSHEx) recognized by the World Breeding Federation for Sport Horses.

**The aim of this research was to assess the genetic structure of the breed and the impact of different mating policies of the SSH regarding to the breeds allowed on the Studbook for the SSH relatives.**

## MATERIAL AND METHODS

Animals registered in this Studbook (from their foundation to December 2009), were used in this study. The total available records were 34017. The reference population included the registered individuals after de Studbook was closed (4289 individuals). Since 2005, the 26.5% of the stallions were Spanish Purebred (SPB), 16.6% were SSH and 9.7% Arab horses (A) and 47.2% were other breeds (foreign and Spanish breeds), regarding mares 43.0% were SSH, 12.9% SSHex and 44.1% were other breeds.

A previous analysis of the genetic variability of the breed was made, in order to attain the possible change in the genetic structure and the effective size of the SSH population, the impact of a new regulation of the Studbook, in which only individuals SSH could act as parents, was considered.

Population and genetic parameters were computed on the reference population using the program ENDOG (v4.5).

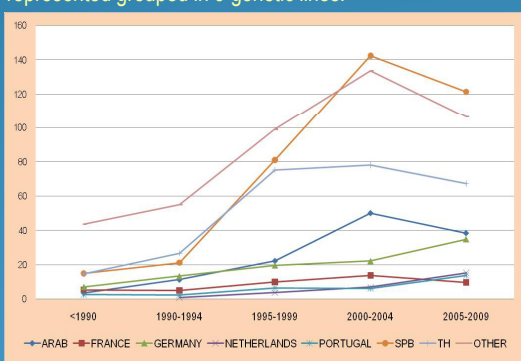


## RESULTS AND DISCUSSION

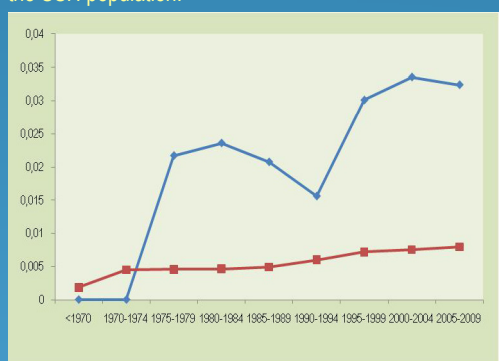
**Figure 1** shows the contribution of ancestors from different breeds. SPB showed the highest contribution in the last generation, followed by Other breeds and TH, increasing considerably their initial contribution.

The mean of equivalent complete generations was 3.8. The inbreeding coefficient (F) and average relatedness (AR) were 0.66% and 0.16%, respectively. Despite of the multiple genetic origins of this breed, the evolution of these parameters (**Figure 2**) showed that the inbreeding is much higher than AR coefficient, pointing out that a subdivision is performing in the population, enhancing a mating policy between relatives.

**Figure 1.** Contribution of the Boichard et al's (1997) ancestors to the reference SSH population. Breeds are represented grouped in 9 genetic lines.

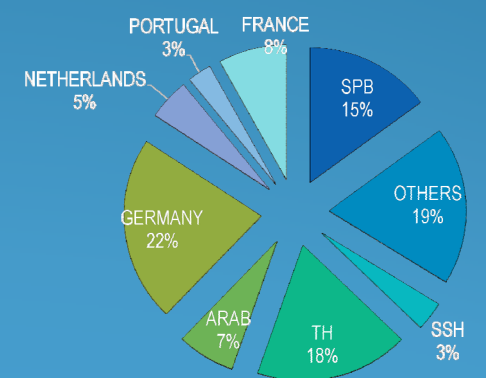


**Figure 2.** Evolution of individual inbreeding coefficient (in blue) and average relatedness coefficient (in red), on the SSH population.



The contributions of the founders belonging to the paternal breeds showed that in origin the TH was the highest contributor (18%) followed by the SPB (15%). Although "Germany" and "Others" genetic lines showed a higher contribution than TH (22% and 19%, respectively), the influence of this last is greater, as those grouped the contribution of several foreign sport breeds (**Figure 3**). Even though SPB stallions were preferred for the animals born in the reference population, aggregated founder contribution from breeds reflects that Thoroughbred genetic background was rather indirectly selected.

**Figure 3.** Contributions (in percentage) of founder genetic lines, to the SSH.



The impact of a new regulation of the Studbook in which only individuals SSH could act as parents was considered (**table below**) in order to attain the possible change in the genetic structure and the effective size. The realized effective size using SSH individuals was 225.8, but if we removed SSH individuals with an external parent from the dataset, the Ne decreased to 51.4.

Probability of gene origin	Reference Population	Both parents SSH	Father SSH	Mother SSH
Number of animals in the population	4289	481	2142	1989
Effective number of Ancestors	407	122	196	288
Effective number of Founders	963	380	535	714
Total number of Ancestors	3230	408	1394	1450
Total number of Founders	6772	1585	3469	3748
Nº of ancestors explaining 50%	248	53	96	132
Effective population (calculated by inbreeding) ± S.E.	225.8 ± 72.4	51.4 ± 16.4	139.8 ± 45.5	139.8 ± 45.5
Effective population (calculated by coancestry) ± S.E.	1046.3 ± 8.2	373.9 ± 6.2	806.0 ± 7.9	806.0 ± 7.9

**The breeding policy carried out shows a subdivision in the population that can be related with the parental lines. Changes in breeding policy of the SSH population, limiting reproduction to SSH animals, would have an impact on its genetic structure.**

CONCLUSION