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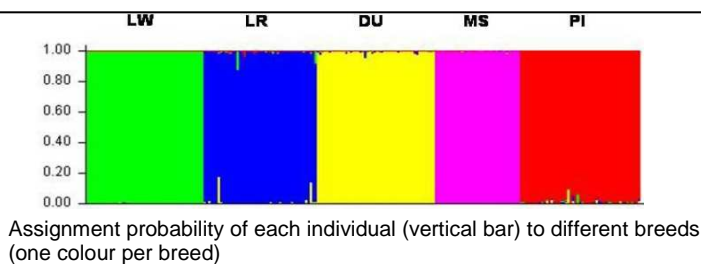
Effective population sizes and historical divergence of Western pig breeds estimated from microsatellite data.

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Introduction

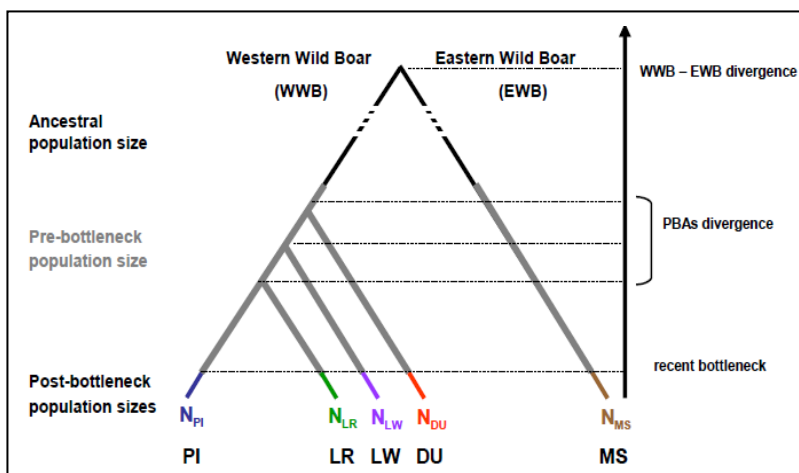
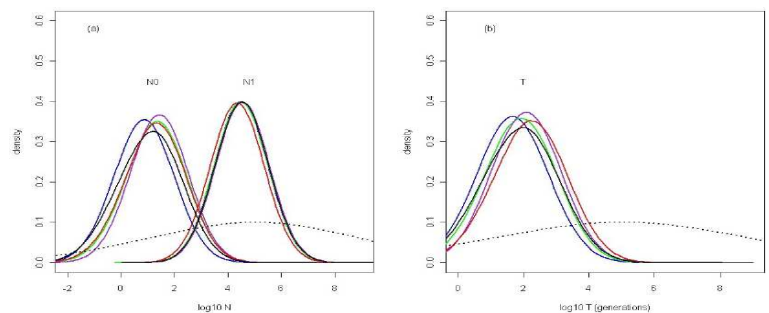
Domesticated farm animal species are the result of complex ancient history and modern intensive breeding programs. However, the evolutionary history of these species is generally poorly detailed. For instance, little is known regarding the historical divergence of major Western pig breeds from their wild ancestor, the European wild boar, and the impact of recent breeding programs on their effective population sizes. Nevertheless, the evolutionary and demographic status of pig breeds turns out to be a source of decision for sustainable breeding programs and conservation management. In this study, we **infer some aspects of the demographic history of four major Western pig breeds (Large White, LW; Landrace, LR; Piétrain, PI; Duroc, DU) and one Eastern pig breed (the Chinese Meishan, MS)**, using samples of 36 to 51 animals genotyped at 50 microsatellite markers (PigBioDiv project, SanCristobal et al. 2006).



Population structure was assessed using F -statistics and a Bayesian clustering method implemented in the software STRUCTURE (Pritchard et al. 2000). **Genetic differentiation among breeds was strong** ($0.15 < F_{st} < 0.40$). All individuals were unambiguously assigned to their respective breed of origin, showing a clear genetic distinction between breeds and a high genetic homogeneity within each breed.

Population size change was estimated using a full-likelihood MCMC method that allows simultaneous estimation of the present (N_0) and past (N_1) population size and the time of population size change (T), under an exponential increase/decrease demographic model (Storz and Beaumont 2001).

A strong signature of **population size decrease** was found, which was simultaneous across breeds less than 250 generations ago. This decrease was grossly contemporary to the first breeding efforts initiated by pig farmers in the late 18th century.



Breed divergence scenarios were investigated using an Approximate Bayesian Computation (ABC) method (Cornuet et al. 2008). **Topology analysis suggests a sequential divergence scheme** that began well before the recent bottleneck of population size, perhaps during a phase of postglacial expansion, as suggested by Scandura et al. (2008). The Western (mostly European) pig breed ancestor (PBA) of the current Duroc breed (formerly developed in North America) was the most deeply divergent. Further analyses are needed to allow admixtures and introgressions in the model, as pig breeds have probably undergone such events in the past.

Conclusion

This work is a first attempt to infer the complex history of main Western pig breeds. Our results indicate that **different Western pig breed ancestors, or wild boar subpopulations, could have been differentiated sequentially from the ancestral wild boar during a phase of postglacial demographic expansion. The genetic diversity within and between breeds accumulated during this expansion, which may have contributed to phenotypic diversification, was recently affected by intensive breeding programs that have drastically reduced the effective population size of pig breeds ($N_e < 100$ for all breeds).**

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