

Searching for genes of interest in Sheep

Carole R. Moreno^{1†}, Jean-Michel Elsen¹, Andrès Legarra¹, Rachel Rupp¹, J. Bouix¹, François Barillet¹, Isabelle Palhiere¹, Hélène Larroque¹, Daniel Allain¹, Dominique Francois¹, Christele Robert¹, Gwenola Tosser-Klopp², Loys Bodin¹ and Philippe Mulsant²

¹INRA, UR631, Station d'Amélioration Génétique des Animaux, F-31320 Castanet-Tolosan, France; ²UMR 444 INRA-ENVT– Génétique cellulaire, F-31320 Castanet-Tolosan, France

In the past, several studies have been performed to look for genes affecting traits of interest using microsatellite markers in sheep. Even if numerous chromosomal regions have been detected, few genes and causal mutations have been identified. The recent availability of high density SNP chips in sheep is a technological revolution for genomic research and breeding selection.

Firstly, genomic research in small ruminants will be boosted towards the identification of causative mutations underlying large genetic effects on sustainability traits, or the identification of very closely linked genetic markers that allow selecting genes in sheep. Even if this strategy needs a large investment to detect causal mutation, the gene selection allows to select trait (1) without phenotyping which is particularly suitable for traits difficult to measure such as disease resistance, (2) whatever the population size (at the farm or the breed level) (3) without expensive genotyping. Because of these three advantages, when mutations are available, the gene selection is really adapted to selection in developing countries. However, be careful to select only one gene, mainly for disease resistance which is a real important trait in tropical areas. In fact, the breakdown of resistance by the pathogen could be observed in such conditions. To escape this problem, the selection of a major gene could be associated to chemical treatment or, in the best way, to the selection of other genes affecting the same trait.

Secondly, such new molecular tools allow considering a new type of selection: the genomic selection. The principle of this selection is to use marker effects (without any information about the underlying genes) estimated within a part of the population which is phenotyped and genotyped (called the training population) and applying these effects to the rest of the genotyped population. However, the genomic selection might not always be a profitable strategy in sheep, particularly in developing countries. In fact, it is necessary to produce several thousands of individuals in the training population in order to estimate correctly the marker effects. Moreover, this population has to be generally selected within breed except when the commercial population is a mixture of several close breeds in terms of evolution. So the production of the training population is really difficult to produce particularly in small breeds.

† E-mail: carole.moreno@toulouse.inra.fr

Characterization and importance of pig breeds in the pork industry of the Bobo-Dioulasso zone (Burkina Faso, West Africa)

Timbilfou Kiendrebeogo^{1†}, Y. Mopate Logtene², S. R. Kondombo¹ and C. Y. Kabore-Zoungana³

¹Institut de l'Environnement et de recherches Agricoles (INERA), Département Productions Animales (PA)/Programme Monogastrique, Station de Kambouinsé, BP. 476 Ouagadougou, Burkina Faso; ²Laboratoire de Recherches Vétérinaires et Zootechnique de Djaména, BP 433, N'Djaména, Tchad. Chercheur associé au LERNSE de l'Université Polytechnique de Bobo-Dioulasso; ³Laboratoire d'Etudes et de recherches sur les Ressources Naturelles et les Sciences de l'Environnement (LERNSE), Université polytechnique de Bobo-dioulasso (UPB), 01B.P.1091 Bobo-Dioulasso 01 Burkina Faso

Porcine breeding is dominant in Burkina Faso in comparison with pig number (1886 234 pigs) (MED/MRA, 2004), with an increase of 20.6%/year. But its contribution to the meat supply of the population is weak (approximately 10% between 1993 and 2003). The Haut-Bassins whose main city is Bobo-Dioulasso is classified 4th/13 regions with approximately 12% of porcine pig number. To characterize and evaluate the importance of pig breeds in the pork industry of this zone, the data from an investigation diagnosis of breeding systems (2003) and from an investigation into the supply pig meat of the town of Bobo-Dioulasso (2005) were analyzed. Three main pig breeds (Korhogo, local breed

† E-mail: timbilfou@gmail.com

and Large White) and of the Mongrel breed were inventoried and characterized according to the data from the literature. The local breed (61% of pig number) is more present in the breeding zone, followed by the Korhogo breed (34%), the Mongrel race (4%) and Large White (0.48%). According to the breeding systems, the Korhogo breed is exclusively reared in the intensive system, the Korhogo breed followed by the local breed in the semi intensive and the local breed followed by the Korhogo breed in the traditional system. The Korogho breed was the more implicated in the exchanges of boars in the various systems than the other breeds (local breeds and mongrel). Pig meat transformers and distributors in Bobo-Dioulasso globally prefer the local breed (51.41%) more than improved breeds (40%). Butchers and Pork butchers prefer the local breed (50%) as well as improved breeds (50%), (Korhogo breed, Large White breed and Mongrel breed). Cookers with a furnace prefer the local breed (53.33%) more than improved breeds (40). Restorer (1/1) and a part of Cookers with the furnace (6.67%) do not choose a breed. In conclusion, the presence and importance of the local breed or improved breed are characteristic of pig breeding systems. The uncontrolled exchanges and hazardous crossing between pig breeds constitute risks of absorption of the local breed, consanguinity and threat on genetic diversity. It is necessary to carry out a genotypic characterization of these breeds in order to better organize a more productive and durable management of pig breeds and breeding in the zone of Bobo-Dioulasso.

doi:10.1017/S2040470010000336

Is there room for selection in a small local pig breed? – a simulation study

Jean-Luc Gourdine^{1†}, A. C. Sørensen² and L. Rydhmer³

¹Institut National de la Recherche Agronomique, UR143, Unité de Recherches Zootechniques, 97170 Petit Bourg, Guadeloupe, France; ²University of Aarhus, Faculty of Agricultural Sciences, Department of Genetics and Biotechnology, P.O. Box 50, DK-8830 Tjele, Denmark; ³Animal Sciences Group of Wageningen UR, PO Box 65, 8200 AB Lelystad The Netherlands; Swedish University of Agricultural Sciences, Department of Animal Breeding and Genetics, PO Box 7023, SE-75007 Uppsala, Sweden

Introduction

Local breeds are defined as breeds that occur only in one country (FAO, 2007). It is important that the pig biodiversity be maintained by keeping and using a sufficient numbers of breeds, in order to secure the availability of important genes for future needs (Fimland, 2007). Furthermore, “loss of local breeds will cause cultural erosion and diminish the ability of communities to maintain their cultures and livelihoods” (FAO, 2007). There are few examples of well defined breeding programs with selection for genetic improvement of local pig breeds. Focus is on management of genetic diversity in small populations. However, in the presence of pedigree information, optimal contribution selection (OCS) can be applied to control inbreeding rate and simultaneously avoid low performance in valuable traits (Meuwissen, 1997). Strategies for moving from conservation to utilisation include defining the breeding goal and marketing the products to secure profitability (Gandini and Oldenbroek, 2007). If the products are marketed as “high quality”, it could be wise to select for the weakest meat quality trait of the breed. The main objective of the present paper was to examine, using stochastic simulation (Pedersen *et al.*, 2009), the possibility to design a breeding program to improve a key trait in a small local breed population without increasing inbreeding above the recommended rate.

Materials and Methods

A pig population with the characteristics of a small local breed population in an extensive system was simulated. The population consisted of 860 male and female reproducers in 35 herds or 2002 male and female reproducers in 77 herds. The production system was a commercial production of high quality products for a niche market. Each sow weaned 3 female and 3 male piglets and produced 2 litters per year with a maximum of 6 litters. Of the male piglets, 2 were castrated and one was kept intact in each litter. Castration was performed within the first week of birth. Two types of matings were simulated: natural service (NS) and artificial insemination (AI). Litter identity was recorded on the farm at castration and the selection trait was recorded at slaughter. The breeding goal consisted of one meat quality trait (MQT), recorded at the slaughterhouse on relatives of selected boar and gilt candidates. A breeding scheme with optimal contribution selection (OCS) was compared to a breeding scheme with BLUP selection (BLUP) and to a scheme with no selection (NoS). OCS was performed using EBV based on information from relatives (BLUP-EBV selection). Thus, selection was based on information from relatives. The infinitesimal model was used to estimate BLUP EBV, with the fixed effect of herd year season and the random additive genetic effect, the random maternal environmental effect and the residual. The additive genetic variance was set to 1, so that the estimated genetic change is directly expressed in genetic standard deviations. This study used the stochastic simulation program ADAM (Pedersen *et al.*, 2009) to calculate the genetic progress and the rate of inbreeding per generation in each breeding scheme. Simulations were performed by applying ADAM to 20 scenarios, different with regards to number of herds (35 vs. 77); type of mating (AI vs. NS); selection rules (NoS, BLUP or OCS) and heritability of MQT ($h^2 = 0.2$ vs. 0.4). All scenarios were replicated 50 times. Statistical tests of differences between scenarios in rates of genetic gain and inbreeding were performed (proc GLM, SAS[®]), with the fixed effects of time.

[†] E-mail: Jean-Luc.Gourdine@antilles.inra.fr