

Evaluation of connectedness in the registered population of the Sardinian dairy sheep breed

Sotero Salaris¹, Pancrazio Fresi², Sara Casu¹

¹Settore Genetica e Biotecnologie - DIRPA, AGRIS-Sardegna, Olmedo, Italy

²Associazione Nazionale della Pastorizia (ASSONAPA), Roma, Italy

Corresponding author: Sotero Salaris. Settore Genetica e Biotecnologie - DIRPA, AGRIS-Sardegna. Loc. Bonassai SS291 km 18.6, 07040 Olmedo (SS), Italy – Tel. +39 079 3750361 – Fax: +39 079 389450 – Email: salsalaris@agrisricerca.it

ABSTRACT - Connectedness across flocks of the registered population of the Sardinian dairy sheep breed was evaluated. Used **criteria were: number of sires used in the same contemporary group;** number of direct links and the average within and between contemporary group relationship coefficients. Dataset including yearlings' first lactation records of 1990 and 2008 were compared to evaluate the effect of coupling artificial insemination with controlled natural mating on connectedness. An increase of number of sires and direct links were registered between 1990 and 2008. **These results confirm that the across years prolonged use of well planned moderate rates of artificial insemination** had a strong effect on the overall statistical connectedness across flocks so permitting more accurate estimations of the management and genetic effects. **As a whole, the decreasing of the average relationship within flock coupled to a marked enhance of the average relationship between contemporary groups,** indicates that the genetic connectedness of the Sardinian registered population presents a clearly increasing trend. This fact assures that current genetic evaluations are reliable across flocks.

Key words: Direct link, Relationship coefficient.

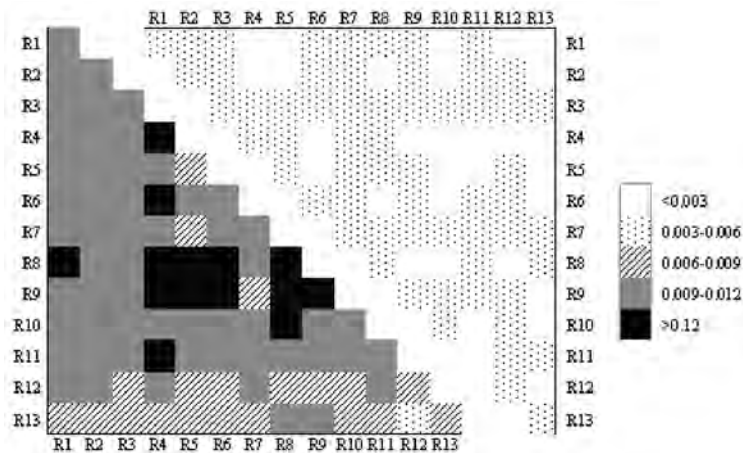
Introduction - The selection scheme of the Sardinian dairy sheep breed is based on a pyramidal management of the purebred population with at the top the registered flocks where selection tools are applied to generate genetic progress. Genetic evaluation by BLUP method, applied since 1992, allows taking into account for management effects and therefore to compare estimated breeding values (EBV) across flocks. Then the accuracy of genetic evaluation and the selection of elite sires can be influenced by the connectedness across flocks. Statistical connectedness is created through either unrelated sires used in the same management group or management groups sharing at least one sire. Both effects avoid confounding between management and genetic effects. Genetic connectedness relates to blood relationships between management groups. The genetic connectedness is essential to provide the most likely ranking of animals at whole population level by influencing the accuracy of all pairwise contrasts of EBV. Different criteria, based on prediction error variance of EBV, were suggested to measure connectedness in genetic evaluation under an animal model (Foulley *et al.*, 1992; Kennedy and Trus, 1993; Khuen *et al.*, 2007; Fouilloux *et al.*, 2008). These criteria are often hardly feasible on large datasets in which a great number of management units have to be handled. In the Sardinian registered population the genetic links between flocks are created by moderate rates of AI (on average 8% of annual replacement) and, at a lesser extent, by controlled natural mating (NM) i.e., grouping ewes with a single ram during the reproduction period (Salaris *et al.*, 2008). Where AI is not widespread used, as in case of most selection schemes of dairy sheep, the prevailing use of NM sires can lead to different genetic subpopulations relatively isolated from each other. The objective of this study was evaluating the effect of coupling AI to NM on the connectedness of the registered population of the Sardinian dairy sheep breed.

Material and methods – Yearlings' first lactation records from the database of the National Association of Breeders (ASSONAPA) used for the 2008 genetic evaluation were analysed. Contemporary groups (CG) included yearlings' first lactation records performed in the same flock-year of production. Connectedness criteria were calculated using as reference the production years 1990 (16,048 yearlings from 1,015 sires in 710 flocks) and 2008 (35,216 yearlings from 1,404 sires in 923 flocks). The choice of comparing these two years was because until 1990 artificial insemination (AI) had been only sporadically applied (0.4% of lactating ewes with known parents was from AI) whereas on 2008 AI has been realised for 15 years on large scale (on average 13,000 AI per year in the last 5 years). The first criterion was the number of sires (NS) used in the same CG. Secondly, per each CG with at least 5 ewes with known sire, the number of direct links (DL) i.e., the number of other CG in the same or previous production years with at least one common sire was calculated. The additive relationship coefficients (r_a) between all pairs of sires were calculated by PEDIG software (Boichard, 2002). Considering that the main source of genetic connectedness derives from shared sires, the additive relationship coefficients between ewes (r_{be}) were estimated as $\frac{1}{4}$ of r_a of their sires so neglecting the blood relationships deriving from the dams. Finally, **genetic connectedness was evaluated** through: i) the average within CG relationship coefficient (r_{wCG}) i.e., the average of $(n^*(n-1)/2) r_{be}$ where n was the number of ewes; ii) the average between CG relationship coefficient (r_{bcg}) i.e., the average of $(n_i^*n_{i+1}) r_{be}$ where n_i and n_{i+1} were the number of ewes in CG i and $i+1$ respectively. To evaluate the degree of shared blood between geographical subpopulations, CG of 2008 were grouped in 13 areas: twelve in Sardinia (R1-R12) and one including all flocks sited in the mainland (R13). The average additive relationship coefficient within areas (r_{wr}) was calculated as the average of $(n^*(n-1)/2) r_{bcg}$ within CG where n is the number of flocks. The average additive relationship coefficient between areas (r_{br}) was calculated as the average of $(n_i^*n_{i+1}) r_{bcg}$ where n was the number of flocks in area i and $i+1$ respectively.

Results and conclusions - The total number of CG with at least 5 ewes with known sires increased from 1990 (527) to 2008 (601). Also the percentage of CG with all ewes from unknown parents increased (from 11 to 18%) due to higher turnover of the registered flocks in the last years. This fact limits the depth of the relationship matrix and the effective size of the selected population. The average NS per CG was 2.1 ± 2.1 in 1990 (50% of CG with only one sire) and 3.6 ± 3.7 in 2008 (33% of CG with only one sire). The number of CG directly linked to other CG was similar (57% and 54% in 1990 and 2008, respectively). On the other hand, the average DL strongly increased from 8 in 1990 (with 65% of CG with less than 5 DL) to 42 in 2008 (with 60% of CG with more than 20 DL). These results confirm that the prolonged use of well planned moderate rates of AI across years had a strong effect on the overall statistical connectedness across flocks so permitting more accurate estimates of the management and genetic effects. Indeed, before the introduction of the AI program, links between flocks were created exclusively by the exchange of NM rams mainly between neighbouring flocks. The average r_{wCG} was higher in 1990 than in 2008: 0.173 ± 0.062 vs. 0.144 ± 0.083 . This trend was mainly due to the increase of the average NS per CG as reported above. The average r_{bcg} was 0.003 (range: 0-0.375 with 53% of 0) in 1990 and 0.01 (range: 0-0.372 with 3% of 0) in 2008. As an example, r_{bcg} of 0.003 corresponds to a situation where one shared sire between two CG produces 11% of ewes of both CG. In the case of r_{bcg} of 0.01 as in 2008, the reported percentage corresponds to 22% of ewes. As a whole, the decreasing average relationship within CG coupled to a marked enhance of the average relationship between CG, indicates that the genetic connectedness of the Sardinian registered population presents a clear increasing trend. This fact assures that current genetic evaluations are reliable across flocks. This is further confirmed by the observation of the trend of relationship between geographical areas (Figure 1). In 1990 r_{br} ranged from 0.002 to 0.005 (mean=0.003), whereas in 2008 it ranged from 0.006 to 0.017 (mean=0.010). The same trend can be observed also for r_{wr} ranging from 0.003 to 0.015 (mean=0.005) in 1990 and from 0.008 to 0.018 (mean=0.011) in 2008. However, it is still evident a certain aptitude to preferentially ex-

change sires between flocks of the same area. In 2008, Campidano di Oristano and Marmilla (R8) and Sarcidano and Trexenta (R9), which are located in the central-west part of Sardinia, showed the highest values of r_{wr} and r_{br} . In fact, these two areas, and in particular R9, represented the historical regions where selection of the Sardinian breed started. Breeders of these regions usually raise own homebred rams and are the main rams sellers among the registered flocks. However, in some Sardinian areas, such as Sulcis and Cixerri (R12) in the south-west part of Sardinia, the use of external rams by NM or AI is still to enhance. The mainland (R13) showed a preferential exchange of animals with R8 and R9 ($r_{br} = 0.011$) respect to a general low relationship with the other Sardinian areas.

Figure 1. Average relationship coefficient of 1990 (above) and 2008 (below): within area (r_{wr}) in diagonals, between areas (r_{br}) out of diagonals.



Results of this study showed that the effect of combining controlled natural mating, as main reproductive technique, with well planned moderate rates of AI in the registered population allowed to obtain reliable EBV across flocks. Only few flocks with known parents still show low connectedness to the rest of the population. In the future, it would be useful coupling the rams EBV with an index of their connectedness in order to limit the use of completely disconnected sires.

This work was funded by the research program "APQ per la ricerca scientifica e l'innovazione tecnologica, progetto P5a - Attivazione del Centro di biodiversità animale per la valorizzazione del patrimonio animale con riferimento alla produzione e alla ricerca al servizio dell'allevamento" of the Regional Government of Sardinia.

References - Boichard, D., 2002. Pedig: a fortran package for pedigree analysis suited to large populations. 7th World Congr. Genet. App. Livest. Prod., Montpellier, 19-23 August, n. 28-13. Fouilloux, M.N., Clément, V., Laloë, D., 2008. Measuring connectedness among herds in mixed linear models: From theory to practice in large-sized genetic evaluations. Genet. Sel. Evol. 40:145-159. Foulley, J.L., Hanocq, E., Boichard, D., 1992. A criterion for measuring the degree of connectedness in linear models of genetic evaluation. Genet. Sel. Evol. 24:315-330. Kennedy, B.W., Trus., D., 1993. Considerations on genetic connectedness between management units under an animal model. J. Anim. Sci. 71:2341-2352. Kuehn, L.A., Lewis, R.M., Notter, D., 2007. Managing the risk of comparing estimated breeding values across flocks or herds through connectedness: a review and application. Genet. Sel. Evol. 39:225-247. Salaris, S., Casu, Sara, Fresi, P., Carta, A., 2008. Effect of combining controlled natural mating with artificial insemination on the genetic structure of the flock book of Sardinian breed sheep. 36th ICAR Session, Niagara Falls, 16-20 June.