

GENETIC DIVERSITY AND TRENDS OF AUSTRALIAN JAPANESE BLACK CATTLE

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SUMMARY

Japanese Black is the predominant strain of Australian Wagyu cattle. Due to limited importation of cattle from Japan into Australia, there are concerns of declining genetic diversity and increasing inbreeding. This study investigated inbreeding status and genetic diversity in Australian Japanese Black cattle. Average generation interval was 6.4 years. Inbreeding coefficients increased from 4.2% in 2000 to 7.2% in 2019. The average effective population size was 43.4. Estimated F-statistics suggested that subpopulations were not evident in Australia Japanese Black cattle. It is advisable for Australia Japanese Black breeders to continue monitoring inbreeding levels and to develop breeding strategies to balance genetic gain and increased rates of inbreeding.

INTRODUCTION

Australian Wagyu cattle production started in the 1990s and was initiated from semen, frozen embryos and live animals imported from Japanese Black cattle in Japan via the United States of America. Wagyu cattle have increasingly become popular due to their high intramuscular fat deposition. This breed has developed from a small source of genetics and there are concerns that declining genetic diversity and increasing inbreeding may have a negative effect on future productivity. Australian Wagyu comprises of Japanese Black, Red and others. Japanese Black is the predominant strain. This study focused on Australian Japanese Black cattle. The aims of this study were to assess the inbreeding status and genetic diversity of Australian Japanese Black cattle.

MATERIALS AND METHODS

Pedigree was extracted from the Australian Wagyu BREEDPLAN database. Individual animals were classified by Australian Wagyu Association Herdbook registration status, content grade or colour code. There were 151,730 animals registered as Australian Wagyu cattle and of these, 97,182 were Japanese Black. Pedigree completeness is an important factor for estimating effective population size (N_e) as it directly relates to the inbreeding coefficients determined and can be assessed in three parameters: 1) maximum number of generations traced (G_x); 2) complete generation equivalent or the number of equivalent complete generations (G_e); 3) number of fully traced generations (G_f). These parameters were calculated using the function *summary.Pedig()* from the R package *optiSel* (Wellmann 2019).

Inbreeding coefficient and effective population size. Inbreeding coefficient (F_i) for each animal in the pedigree was calculated using the *pedInbreeding()* function from the R *optiSel* package (Wellmann 2019). The standardized inbreeding rate per generation was computed as

$\Delta F_i = 1 - \sqrt{(1 - F_i)^{t_i}}$, where t_i was the number of complete generation equivalent (G_e) of animal i (Gonzalez-Recio *et al.* 2007). The ΔF_i values of individuals of the reference population were averaged to form $\overline{\Delta F}$. The effective population size N_e was calculated as $N_e = \frac{1}{2 * \overline{\Delta F}}$.

* A joint venture of NSW Department of Primary Industries and University of New England

F-statistics. Wright's (1965) F-statistics were separately calculated for each year period. Following Wright's notation, three parameters were involved in F-Statistic calculations, 1) F_{it} is the individual inbreeding coefficient relative to the entire population (equivalent to F_i); 2) F_{st} is the inbreeding coefficient of the subpopulation relative to the entire population expected under random mating, it was computed from a hypothetical population produced by matching sires and dams of the registered animals in each time period (eg year) at random. For each year period, 20 hypothetical populations were generated, and mean F_{st} from 20 samples was used for each year of the examined period to estimate a reliable mean F_{st} ; 3) F_{is} is the inbreeding coefficient of an individual relative to its own subpopulation and indicates how the mating departs from random, it was obtained as $F_{is} = (F_{it} - F_{st}) / (1 - F_{st})$, as F_{it} was estimated as F_i and F_{st} was derived from the simulation.

Generation interval. Generation interval was computed for four genetic pathways, sire to male progeny (L_{mm}), sire to female progeny (L_{mf}), dam to male progeny (L_{fm}) and dam to female progeny (L_{ff}). This was based on the birth dates of animals in each year and the birth dates of their parents. The annual average generation interval (L) was subsequently calculated as $L = \frac{L_{mm} + L_{mf} + L_{fm} + L_{ff}}{4}$.

RESULTS AND DISCUSSION

Pedigree completeness. Pedigree completeness by year of birth was determined by counting generations including **maximum (G_x)**, **complete equivalent (G_e)** and **fully traced (G_f)** and are presented in Figure 1. Pedigree completeness has increased over time and reached a high level in 2000 with a G_e of 5. Japanese Black cattle had a deep pedigree with the average maximum, equivalent complete or fully traced number of 15.1, 4.3 or 7.3 generations, respectively.

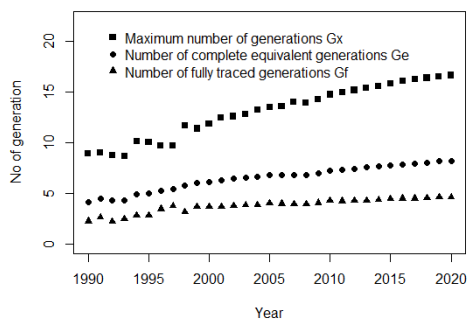


Figure 1. Mean number of generations (maximum G_x , complete equivalent G_e and fully traced G_f) recorded by birth year

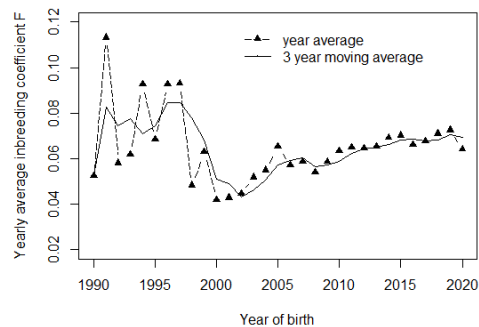


Figure 2. Average inbreeding coefficients by birth year for Japanese Black cattle

Generation interval. The average generation interval was 6.4 years. After 2000, the average generation interval for the Japanese Black population was 8.4 and 7.9 years for sire to male progeny and sire to female progeny, respectively and about double the size for dam to male progeny and dam to female, i.e. 4.8 and 4.6 years, respectively. Average generation intervals increased from 2.4 years in 1984 to 8.7 years in 2008, followed by a reduction to 7 years in 2011 and afterwards increased to 8.3 years in 2017. From 2005, the mean generation intervals remained steady between 6.8 and 8.7 years. This trend might reflect the development of Australian Wagyu (or Australian Japanese Black) during the herd building phase, where less cows were culled and more old ancestors, mostly males, were retained. Nomura *et al.* (2001) reported that generation intervals for Japanese Black in Japan

ranged from 8.3 in 1985 to 10 years in 1997. The generation interval for American Wagyu has been estimated at 5.14 years (Scraggs *et al.* 2014).

Inbreeding coefficient. Mean inbreeding coefficients F by birth year fluctuated markedly before 2000, then the inbreeding coefficient increased steadily from 4.2% to 7.2% in 2019 (Figure 2). Similarly, a gradual increase in inbreeding coefficient was reported in Japanese Black cattle in Japan, from 4.7% in 1985 to 5.4% in 1997 (Nomura *et al.* 2001). The average inbreeding coefficient from 1994 to 2011 was 4.8% for American Wagyu cattle, suggesting Australian Japanese Black cattle shared a similar breeding path as that of US Wagyu cattle (Scraggs *et al.* 2014). Large variation in inbreeding levels was observed across herds. The inbreeding coefficient within individual herds ranged from 0.0 to 18% with 45 of 513 herds having average inbreeding coefficients greater than 10% (mean $F = 12.5\%$), suggesting an urgent need to control inbreeding in these herds.

Changes in F-statistics. The changes in F-statistics are shown in Figure 3. There was evident difference between F_{st} and F_{it} prior to 1998, suggesting that matings in the early period were mainly operating within subgroups or subpopulations. Both F_{st} and F_{it} had increased steadily since 1998 and the differences decreased gradually, leading to a negligible difference, indicating that matings across the population was dominant. F_{is} decreased from 1997 to a low level. $F_{is} > 0$ or with a large value suggests existence of evident subpopulations. This finding indicated that subpopulations had disappeared in current Australian Japanese Black cattle. This was most likely due to deliberate mating decisions by breeders that avoided mating close relatives. Similarly, Nomura *et al.* (2001) found that F_{is} in Japan had decreased from 2 or more to 0.5 by 1997 and concluded that subdivision between prefectures no-longer existed in Japan. Honda *et al.* (2004) analysed 25 subpopulations (i.e. populations of prefectures) of more than 2,000 Japanese Black cows and found that 17 of the subpopulations shared very high similarity because of high migrations amongst these subpopulations and the other 8 subpopulations with relatively low migration rates showed their unique genetic structures. Estimated F_{it} in this study was in line with the reported values in American Wagyu (Scraggs *et al.* 2014), where F_{it} values in US Wagyu cattle fluctuated markedly before 2000, then remained at approximately 5%.

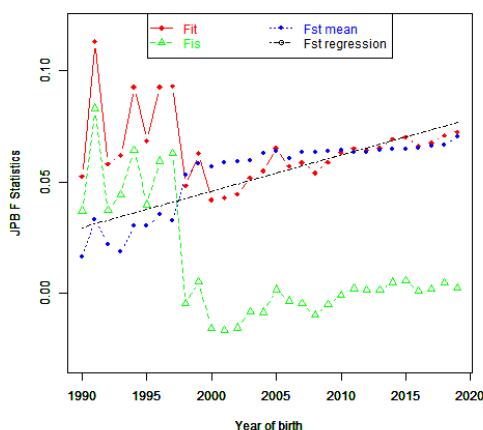


Figure 3. Change of F-statistics (%) in pedigree for Japanese Black from 1990 to 2018: the actual overall inbreeding coefficient (F_{it}), the inbreeding coefficient expected under random matings (F_{st}) and inbreeding due to population subdivision (F_{is})

Effective population size. N_e increased and peaked at 59 in 2000, followed by a decrease to 41 in 2005, afterwards N_e remained stable at approximately 43. The overall estimated N_e was 43.4 for

the Japanese Black population. This estimate was higher than estimates of N_e from the early Japanese Black cattle in Japan (mean=27.1, range 13.4 to 52) (Nomura *et al.* 2001) and that for American Wagyu (the average was 13.4 from 1994 to 2011, with a maximum of 48 in 2002). The estimates of N_e varied largely across years. Detailed N_e by year was not reported in American Wagyu (Scraggs *et al.* 2014). The method used in estimating N_e in Japanese Black (Nomura *et al.*, 2001) and American Wagyu (Scraggs *et al.* 2014) were vulnerable to sampling. The comparison of N_e between Australian Japanese Black with the results from Japan or America remains inconclusive. A number of studies on effective population sizes in cattle (e.g. Meuwissen & Woolliams 1994) suggested that the effective population size of Australian Japanese Black is at the lower range of the published results for beef cattle breeds, for example, 45 to 117 in Brazilian Zebu (Faria *et al.* 2009), 64 to 127 in Irish dairy and beef breeds (McParland *et al.* 2007), 116 in US angus (Decker *et al.* 2012) and 244 to 558 in European Charolais subpopulations and 345 to 2,459 in European Limousin subpopulations (Bouquet *et al.* 2011).

CONCLUSIONS

The most recent animals in the Australian Japanese Black population had adequate pedigree completeness with the average maximum, equivalent complete or fully traced number of generations of 15.1, 4.3 or 7.3, respectively. Generation intervals from Sire to male or female progeny were almost twice those for Dam to male or female progeny, particularly for individuals after 2000. Average generation interval and complete generation equivalent were 6.4 and 5.9 for Japanese Black populations, respectively. Inbreeding coefficients increased rapidly from 2000 to 2019 (4.2% to 7.2%). The current levels of inbreeding are not indicative of an immediate problem with genetic diversity, but the change is large, almost doubling from 2000 to 2019. It is advisable for Wagyu breeders to continue monitoring inbreeding levels and to develop breeding strategies to balance genetic gain and increased rates of inbreeding. The computed effective population sizes (N_e) in the last period (2016 to 2020) was 43.4 in the Japanese Black population, which is on the low end of similar estimates in other beef breeds. F_{is} -statistics estimates showed low or negative F_{is} , suggesting that subpopulations were no longer evident in Australian Japanese Black.

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