

184. Inbreeding depression in livestock: comparing trait groups and inbreeding measures

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Abstract

Inbreeding depression has been documented for many livestock populations. We compared inbreeding depression estimates (1) between trait groups, and (2) between different pedigree-based and genomic inbreeding measures. Inbreeding was found to affect all sorts of traits to a similar extent, independent of heritability and of whether a trait is a primary fitness trait or not. Inbreeding depression estimates were moderately to highly correlated between different pedigree-based and genomic inbreeding measures, but those based on genomic measures tended to have lower *P*-values, suggesting more power to detect inbreeding depression with genomic measures (assuming there is a true inbreeding depression effect). Among different genomic measures (based on genomic relationship matrix, regions of homozygosity, or percentage of homozygous markers), there were no consistent differences in *P*-values.

Introduction

Inbreeding reduces the mean performance of animals, a phenomenon known as inbreeding depression. Based on theory and laboratory experiments, inbreeding mostly affects primary fitness traits such as survival and fertility (Lynch and Walsh, 1998). These traits are under directional selection and the average dominance effect is expected to be favourable, because fixation occurs more quickly for loci with an unfavourable dominance effect (Lynch and Walsh, 1998). For livestock populations, one could argue that traits related to e.g. production may equally qualify as fitness traits, since there has been (artificial) selection for these traits for many generations. Hence, one may expect a similar degree of inbreeding depression for a wide range of traits in livestock.

The degree of inbreeding depression is typically quantified by linear regression of phenotypes on inbreeding coefficients. Inbreeding coefficients can be estimated from pedigree data, but are increasingly derived from genomic information, particularly SNP data. An advantage of genomic measures is that they provide estimates of realized inbreeding, instead of genealogical probabilities (Wang, 2016). Therefore, using genomic inbreeding coefficients may result in more accurate estimates of inbreeding depression (Caballero *et al.*, 2021). Among SNP-based measures, some may better capture inbreeding depression than others.

Many studies have reported (pedigree-based, and more recently genomic) estimates of inbreeding depression. In this paper, we summarize our recently published meta-analysis (Doekes *et al.*, 2021) and extend it with some additional literature and analyses. The aim was to determine and compare inbreeding depression estimates between different trait groups, as well as between different pedigree-based and SNP-based approaches.

Materials & methods

Data. A literature search in Web of Science and Scopus on inbreeding depression in cattle, pig, chicken, sheep, goat, horse and rabbit resulted initially in 766 studies published between 1990 to 2020. After filtering (for details, see Doekes *et al.* 2021) 154 studies remained with inbreeding depression estimated as linear regression coefficients (*b*-values), i.e. as the change in phenotypic mean per 1% inbreeding. From these studies, 2321 *b*-values were extracted. For each trait, the favourable phenotypic direction was determined,

and the sign of b -values was changed if needed to ensure that negative values reflected unfavourable effects. Estimates for traits with an optimum or an unclear favourable direction were removed ($n=197$).

Comparison between trait groups. Traits were divided into six groups: reproduction/survival, weight/growth, production, conformation, health and other traits (details on classification, see (Doekes *et al.* 2021)). For the comparison between traits and trait groups, b -values were divided by the corresponding trait mean (to get b_m) or trait standard deviation (to get b_s) and only pedigree-based estimates were used ($n=1,818$ for b_m and $n=1,259$ for b_s). A general linear model was run, in which a population effect (combined effect of study and breed) was fitted in addition to the trait group effect. Estimated marginal means (EMMs) for the different trait groups were obtained and compared. In addition, h^2 -estimates were extracted when available ($n=490$), compared across trait groups and correlated to b_m - and b_s -estimates.

Comparison between inbreeding measures. Inbreeding depression estimates were compared within 11 studies and within traits between pedigree inbreeding (F_{PED}), inbreeding based on ROH (F_{ROH}), inbreeding derived from a GRM (F_{GRM} , from VanRaden's method 2 and Yang's method), inbreeding derived from a GRM computed with allele frequencies of 0.5 ($F_{GRM0.5}$) and the percentage of homozygous SNPs (HOM). To account for scale differences of inbreeding measures, b_m and b_s were standardized, by multiplying them by the SD of the inbreeding measure in the corresponding population, such that they were expressed per 1 SD increase in inbreeding (rather than per 1%). Significance of b -values was also compared across inbreeding measures, with smaller P -values indicating a more significant association between inbreeding and phenotypic value.

Results

Across all studies and traits, the mean (median) pedigree-based b_m and b_s were -0.22 (-0.13) and -0.71 (-0.59), respectively. Distributions for b_m and b_s were roughly similar for different trait groups (Figure 1). The mean and median b_m and b_s were negative for each trait group, except for 'other traits'.

When correcting for population and ignoring the 'other traits', the EMM of b_m was most negative for production traits (-0.31) and reproduction/survival traits (-0.30), and least negative for conformation traits (-0.14). For b_s , the EMM was most negative for weight/growth traits (-1.07) and least negative for

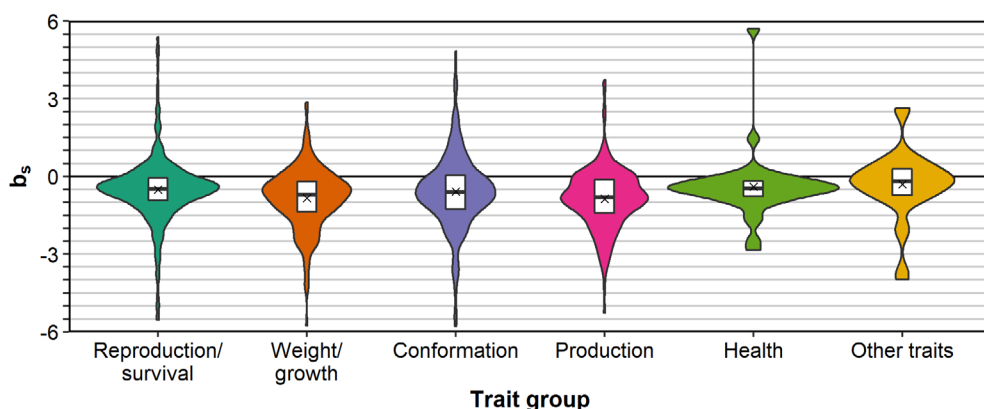


Figure 1. (adapted from Doekes *et al.*, 2021) Violin plots of inbreeding depression estimates per trait group, expressed as percentage of a trait's SD (b_s). Boxplots and the mean (\times) are also shown. There were 39 outliers outside the range of this figure.

reproduction/survival traits (-0.41). Pairwise differences of EMMs across trait groups were generally not significant.

Heritability estimates were on average 0.07 for reproduction/survival traits (n=141), 0.30 for weight/growth traits (n=126), 0.29 for production traits (n=109), 0.27 for conformation traits (n=95) and 0.17 for health traits (n=9). Correlation coefficients between inbreeding depression estimates and heritability estimates were close to zero (Figure 2).

Standardized b_m - and b_s -estimates generally showed moderate to (very) high correlations between different inbreeding measures. Correlations of b-values between $F_{GRM0.5}$ and HOM , between F_{PED} and F_{GRM} , between F_{ROH} and HOM , and between F_{GRM} and $F_{GRM0.5}$ were all ≥ 0.9 . Correlations were lowest between F_{ROH} and F_{GRM} (0.27 for b_m and 0.52 for b_s) and between F_{GRM} and HOM (0.24 for b_m and 0.47 for b_s).

Inbreeding depression estimates for SNP-based inbreeding measures had lower P -values than estimates based on pedigree inbreeding in more than 80% of direct comparisons (Table 1). Among the SNP-based measures, there were no consistent trends, i.e. which measure had the lowest P -value largely differed across studies and also across traits within studies.

Discussion

The mean (median) b_m of -0.22% (-0.13%) and b_s of -0.71% (-0.59%) are similar to the mean b_m of -0.14% and b_s of -0.56% that were previously reported by Leroy (2014) for a subset of 57 studies. Across trait groups, there were some small differences, but those differences were not consistent for b_m and b_s and did not suggest that primary fitness traits such as survival and reproduction exhibit more inbreeding depression than other traits.

Inbreeding depression estimates for SNP-based inbreeding were generally more significant than those based on pedigree inbreeding. Some other studies, which were not included in our analysis, also support this finding. Baes *et al.* (2020), for example, reported more significant inbreeding depression for genomic inbreeding than for pedigree inbreeding for six traits in a sample of ~15,000 Holstein cows (genomic inbreeding was most likely F_{GRM} though this is not explicitly stated). Lozada-Soto *et al.* (2021) recently estimated inbreeding depression for heifer pregnancy and weight/growth traits in American Angus cattle and found smaller credible intervals for F_{GRM} and F_{ROH} than for F_{PED} . Thus, SNP-based measures appear promising for accurately estimating inbreeding depression.

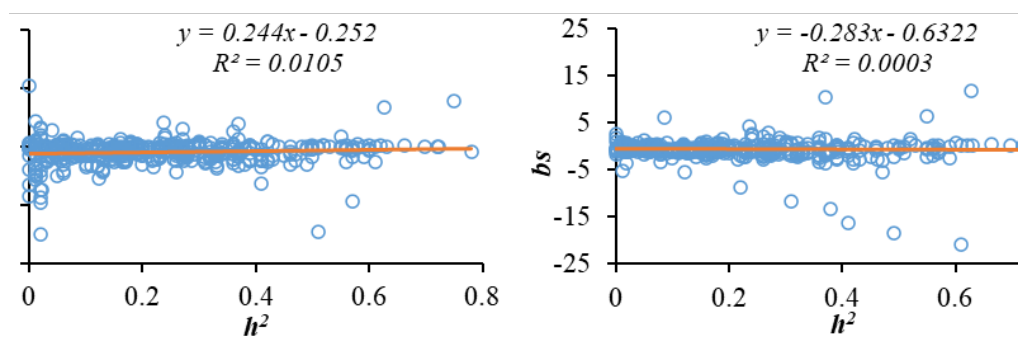


Figure 2. Relationship between inbreeding depression estimates expressed as percentage of a trait's mean (b_m ; left) or SD (b_s ; right) and heritability estimates (h^2).

Table 1. (adapted from Doekes *et al.*, 2021) Comparison of *P*-values of inbreeding depression estimates within 11 studies and within traits for each combination of two inbreeding measures, where both inbreeding measures had an unfavorable effect on the phenotype. There were no comparisons between F_{GRM} and $F_{GRMO.5}$ in the data set.¹

Measure 1	Measure 2	N studies	N comparisons	Comparisons where $P2 < P1$	
				N	% of total
F_{PED}	F_{ROH}	8	38	30	79
F_{PED}	F_{GRM}	1	7	7	100
F_{PED}	$F_{GRMO.5}$	4	26	21	81
F_{PED}	HOM	4	18	15	83
F_{ROH}	F_{GRM}	1	7	4	57
F_{ROH}	$F_{GRMO.5}$	5	40	15	38
F_{ROH}	HOM	4	34	19	56
F_{GRM}	$F_{GRMO.5}$	1	3	3	100
F_{GRM}	HOM	2	14	4	29
$F_{GRMO.5}$	HOM	1	20	10	50

¹ $P1 = P$ -value of measure 1; $P2 = P$ -value of measure 2.

Among the SNP-based measures, there were no consistent trends with regard to which measure yielded the lowest *P*-values. Caballero *et al.* (2021) performed a set of computer simulations to shed more light on the question which SNP-based measures are more accurate for estimation of inbreeding depression. They found that the answer largely depends on the population parameters. For example, while F_{ROH} is appropriate for populations with a small effective population size (in which relationships are tight and there is relatively less intense selection), it may be less appropriate for populations of larger effective population size.

Overall, we conclude that inbreeding depression in livestock populations is present for all sorts of traits to a similar extent and that SNP-based inbreeding measures tend to have more predictive power than pedigree-based measures.

References

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