

COEFFICIENT OF VARIATION AS A MEASURE OF GENERAL RESILIENCE FOR YEARLING WEIGHT IN NELLORE CATTLE

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SUMMARY

Resilience can be defined as the capacity of the animal to be minimally affected by disturbances or to rapidly return to the state pertained before exposure to a disturbance (Colditz and Hine 2016). As indicators for general resilience have not yet been defined, our aim is to investigate the potential of the coefficient of variation (CV) as a measure of general resilience for yearling weight (YW). Using 138,590 Nellore cattle, sired by 560 Nellore bulls, we computed the CV based on within-sire progeny groups (PGs) that comprised of at least 10 progenies from the same sex, farm and year of birth. From this, we generated 5 datasets based on the size of the PG: maximum of 20, 30, 50, 100 and no limit. A two-trait single-step GBLUP model was adopted (mean YW and CV), considering the genotypes of the sires and the pedigree information relating to a given PG with its sire. Smaller groups resulted in higher estimates of heritability for both traits. Moreover, estimates of genetic correlations were positive yet of low magnitude, and closer to zero for PG with a maximum size of 20. We conclude that the use of the CV combined with the grouping, offers an opportunity to select animals that have high genomic estimated breeding values for YW with reduced CV.

INTRODUCTION

One of the current challenges of livestock production is to achieve successful intensification of production, without detrimental effects on animals, which requires healthy and easy-to-manage animals (Elgersma *et al.* 2017). Although highly important, few studies have investigated general resilience, a feature that can be defined as the capacity of the animal to be minimally affected by disturbances (Colditz and Hine 2016).

According to Berghof *et al.* (2019), indicators for general resilience to environmental disturbances have not yet been defined, and measuring this variable is difficult. Most studies regarding to resilience have been conducted at experimental level, which does not represent the reality of the production system. Also, most of these studies have focused on disease resilience and, although these studies can provide useful information in physiology, the results may not be representative of resilience under non-disease conditions.

Here, we propose to use coefficient of variation (CV) as an alternative to evaluate general resilience, based on within-family data across environments (sex-farm-year).

MATERIALS AND METHODS

Data for YW from 138,590 cattle, born between 1986 and 2016 and sired by 560 bulls, were extracted from the Alliance Nellore database. The number of progenies per sire averaged 247 and ranged from 10 to 12,612. Cattle were raised on pasture in herds from Brazil and Paraguay, and YW was measured at an average age of 533 days (ranging from 338 to 627 days).

The CV was considered as a measure of general resilience, which was computed based on within-sire progeny groups (PGs). We took the assumption that a PG size of 10 would be sufficient to estimate the mean and the CV, then each individual PG was comprised of at least 10 progenies from the same sire, sex, farm and year of birth. From this, we generated 5 datasets based on the size of the PG, considering the growth rate (age and weight) during the regrouping process, making the groups more homogeneous: (i) TS_20: PGs with more than 20 observations were splitted into other groups, respecting a minimum of 10 and a maximum of 20; (ii) TS_30: PGs with more than 30 observations were divided into groups with maximum size of 30; (iii) TS_50: PGs with more than 50 records were divided into groups with maximum of 50; (iv) TS_100: PGs with more than 100 were splitted respecting the maximum of 100; (v) No_TS: no limits were established, i.e. there was no regrouping.

Genotypic information from 560 sires genotyped with the Illumina® BovineHD chip was used. In the quality control of genotypes, non-autosomal SNPs, SNPs with minor allele frequency lower than 0.02, p-value for Hardy-Weinberg equilibrium test less than 10^{-5} and call-rate lower than 0.98 were removed, so that 405,442 SNPs remained for the analyses. All genotyped bulls had a call rate higher than 0.90, passing the quality control.

A two-trait single-step GBLUP animal model was adopted for the average YW and CV within PGs as the phenotypes, considering the genotypes of the sires and the pedigree information relating a given PG with its sire. Sex and year were used to create contemporary groups (CGs), fitted as fixed effects. In addition, the size of the PG (linear), the average age of the PG (linear and quadratic) and the heterozygosity (HET) of the sires were also included in the model as covariates.

RESULTS AND DISCUSSION

A summary of the number of PGs generated, mean and standard deviations for each dataset used in the bivariate analyses is reported in Table 1.

Table 1. Summary statistics of yearling weight (YW, kg) and coefficient of variation (CV, %) of progeny groups, and correlation estimates between sire's heterozygosity (HET) with YW and CV, in Nellore cattle

Groups*	N	YW		CV		Pearson correlation with HET			
		Mean	SD	Mean	SD	YW	P-value	CV	P-value
TS_20	10,290	300	45.9	7.08	2.62	0.123	0.004	-0.079	0.060
TS_30	8,951	300	44.6	7.80	2.44	0.120	0.004	-0.100	0.020
TS_50	8,459	300	44.3	8.11	2.33	0.118	0.005	-0.111	0.008
TS_100	8,341	300	44.1	8.19	2.29	0.116	0.006	-0.135	0.001
No_TS	8,327	300	44.1	8.20	2.29	0.116	0.006	-0.135	0.001

*TS_20: target size 20; TS_30: target size 30; TS_50: target size 50; TS_100: target size 100; No_TS: with no regrouping.

Estimates of correlation between sire's HET and the mean for YW, although low, were positive (Table 1). The opposite tendency was observed for the CV, being negative and more pronounced as the size of the PGs increased. Even though the estimates are discrete for both traits, the behavior of the estimates is desirable, i.e. the greater the heterozygosity the greater the YW and the lower the CV. Heterozygosity also has the potential to be used in mate selection in order to maximize heterozygosity in the offspring (de Cara *et al.* 2011). This could be achieved through the selection of parents that are opposite homozygotes for either as many loci as possible or for the relevant alleles for the trait of interest (Iversen *et al.* 2019).

Table 2 shows parameter estimates from the bivariate analyses and the different datasets. Smaller groups yielded higher heritability estimates for both traits. Moreover, although they are of low magnitude, estimates of genetic correlations were smaller for TS_20. Therefore, the creation of more groups by sire (within family) and consequently making the sizes of the groups more homogeneous, appears to be a sensible approach. In addition, despite being a non-favorable correlation, the use of the CV combined with the grouping, demonstrates that there is a chance of selecting animals that have high genomic estimated breeding values for YW and with reduced CV.

Table 2. Estimates of direct additive genetic variance (σ_a^2), heritability (h^2), and correlation (r) for yearling weight (YW) and coefficient of variation (CV) of progeny at each dataset in Nellore cattle

Groups*	YW		CV		$r_{yw,cv}$
	σ_a^2	h^2	σ_a^2	h^2	
TS_20	637.59	0.476	4.0201	0.556	0.0956
TS_30	509.39	0.411	2.5401	0.420	0.1339
TS_50	485.99	0.400	2.2209	0.399	0.1214
TS_100	476.98	0.396	2.0248	0.378	0.1497
No_TS	485.24	0.402	2.0006	0.376	0.1483

*TS_20: target size 20; TS_30: target size 30; TS_50: target size 50; TS_100: target size 100; No_TS: with no regrouping.

In Figure 1, animals that presented GEBVs above 1 standard deviation for YW and below 1 standard deviation for CV (16 sires) for the TS_20 dataset, are highlighted in blue. Selecting these sires would assist making progress towards both traits simultaneously: high and consistent growth.

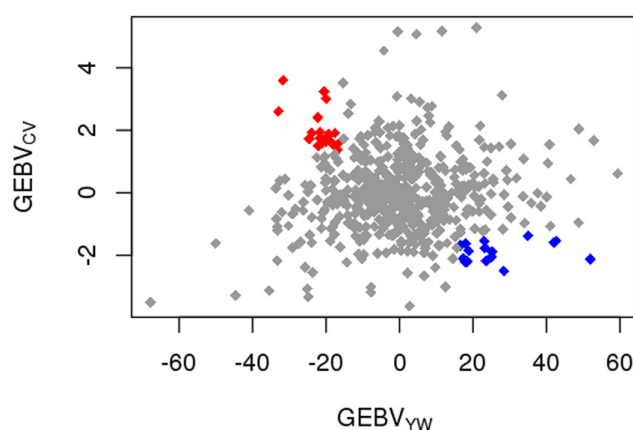


Figure 1. Scatter plot between genomic estimated breeding values for yearling weight ($GEBV_{YW}$) and for coefficient of variation ($GEBV_{CV}$) for all 560 Nellore sires. The blue lozenges represent the animals with favourable GEBVs for both traits, and the red lozenges represent animals with unfavourable GEBVs for both traits

The real-life nature of the data (within-family data) made this study particularly challenging, because bulls were used in different intensities through artificial insemination, presenting different sizes of progeny, and also some groups were in the same environment (sex-farm-year). While originally large in size, limiting the minimum size of the group (required to compute CV with some confidence) caused the exclusion of a lot of data, so further strategies are warranted.

CONCLUSIONS

TS_20 presented the highest heritability for YW and CV, and the smallest correlation between them, showing that the use of CV combined to the grouping strategy is feasible for studies considering within-family data, making possible the selection for weight and uniformity simultaneously. These are preliminary results of an ongoing study indicating that the use of CV is one alternative to select animals for resilience. Further research is warranted to test new variables and new strategies to assess general resilience.

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