

Economic selection index in small rural dairy farms

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SUPPLEMENTARY MATERIALS AND METHODS

The weight factors (\mathbf{b}) were estimated (in matrix notation) by: $\mathbf{b} = \mathbf{P}^{-1}_{11} \mathbf{G}_{12} \mathbf{V}$, where: \mathbf{P}^{-1}_{11} = inverse phenotypic (co)variance matrix among the selection criteria (e.g., MY, FY, PY, etc.); \mathbf{G}_{12} = genetic (co)variance matrix among the selection criteria (row) and the breeding goal (column); \mathbf{V} = vector of economic values of the selection goal expressed as monetary unit (dollar) per unit improved in each trait.

The relative importance (RI, in %) of each selection criterion, for its respective economic selection index, was estimated using the following equation:

$$RI = \frac{|b_j| \times \sigma_{g(j)}}{\sum_{j=1}^t (|b_j| \times \sigma_{g(j)})} \times 100, \text{ where: } \sigma_{g(j)} \text{ is the genetic standard deviation of the selection criterion } j \text{ used in the economic selection index.}$$

crit

The accuracy of the index (R_{IH}) was calculated as the correlation between the economic selection index (ESI) and the breeding goal (aggregated genotype, H), given

$$\text{by: } R_{IH} = \frac{\text{Cov}(\mathbf{ESI}, \mathbf{H})}{\sqrt{\sigma_{ESI}^2 \times \sigma_H^2}} = \frac{\sigma_{ESI}^2}{\sigma_{ESI} \times \sigma_H} = \frac{\sigma_{ESI}}{\sigma_H}, \text{ where } \sigma_{ESI} \text{ and } \sigma_H \text{ are the standard}$$

deviations of the ESI and of the breeding goal (aggregated genotype, H), respectively.

Meanwhile, $\sigma_{ISE} = \sqrt{\mathbf{b}' \text{Var}(\tilde{\mathbf{u}}_j) \mathbf{b}}$, where $\text{Var}(\tilde{\mathbf{u}}_j) = \mathbf{B}' \mathbf{P}_{11} \mathbf{B}$, where \mathbf{P}_{11} is the phenotypic (co)variance matrix among the selection criteria (e.g., MY, FY, PY, etc.) and $\mathbf{B} = \mathbf{P}_{11}^{-1} \times \mathbf{G}_{11}$. The standard deviation of the aggregated genotype (σ_H) was calculated as $\sigma_H = \sqrt{\mathbf{V}' \mathbf{C} \mathbf{V}}$, where \mathbf{C} is the genetic (co)variance matrix among the breeding goals (MY, FP, PP, LW, CI, and SCC).

The genetic superiority expected in the breeding goals (S_{ESI}) for one standard deviation in the selection using the ESI is given by $S_{ESI} = \mathbf{i} \times \mathbf{R}_{IH} \times \sigma_H = \mathbf{i} \times \frac{\sigma_{ESI}}{\sigma_H} \times \sigma_H = \mathbf{i} \times \sigma_{ESI}$, where i is the selection intensity. If i equals the unit (1), then $S_{ESI} = \sigma_{ESI}$. The genetic gain of each trait was calculated following the study by **Yamada et al. (1975)**, where $R_g = (1/\sigma^2_{ISE}) \mathbf{G}^* \mathbf{R} \mathbf{b}$, in which \mathbf{G}^* is the transpose matrix of genetic (co)variance among the selection criteria (row) and the breeding goal (column) and \mathbf{R} is the diagonal matrix of the n traits. Meanwhile, the matrix \mathbf{R} represents Wright's coefficient to provide the relation between the candidate to selection and the animal that provides the phenotype. In this study, every diagonal equal to 1 remained.