Sire Proof Interpretation Table for Linear Type Traits – April 2026

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- Conformation

Linear type traits play an important role in the genetic improvement of your herd. Bull proofs for these traits should therefore be considered during selection.



To aid in the understanding of sire proofs for type traits and their relationship with the expected average daughter classification scores in first lactation, Lactanet created interpretation tables for all seven breeds.

The updated tables for April 2026 tables can be found below.

Key Points to Remember:

- Genetic evaluations for type traits typically range from -15 to +15
- Type traits with an intermediate optimum are published with a letter code.
- “Average for Proof=0” column is the calculated average linear score of daughters in first lactation for a sire with a proof of zero (the average bull for the breed)
- “Per 5-pt Proof Increase” column represents how much of an increase in daughter performance is expected on average when comparing daughters of two sires whose proofs differ by 5 points.

- For traits with an actual measurement recorded during classification the interpretation in terms of the measure is below its linear trait and denoted by the units of measure following the trait name

- For proofs published with a letter code, a ‘proof increase’ is representative of movement in the direction of the descriptor of the higher linear score.

- Knowledge of both where the breed population and the potential female mate stands is important for selecting the direction for selection for intermediate optimum traits and effectively using genetic evaluations for type traits in a breeding program.

- Table values are averages and actual individual daughter scores in a herd may differ due many genetic and non-genetic factors.

For more information on type trait evaluations and the interpretation tables, see our previous article “Interpreting Sire Proofs for Linear Type Traits”.

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Allison enjoys sharing her knowledge of the dairy cattle genetic improvement landscape with all audiences from the technical to the end-user for the successful

understanding and application of genetic selection tools.