

Application of genomic evaluations for heifers and dairy cows

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Efficient genomic selection for artificial insemination (AI) bulls using high-density SNP arrays is widely implemented in the dairy industry. However, its effectiveness relies on a large reference population, which is intrinsically limited in the Israeli herd. Regressing phenotypes on dense SNP arrays involves markers (p) vastly exceeding available samples (n). This high-dimensional regression ($p > n$) poses a strict statistical challenge, requiring dimensionality reduction methods.

While limited in genotyped bulls, the Israeli herdbook has accumulated over 9,000 genotype records from dairy cows and heifers, originally collected for parentage confirmation and culling decisions. We hypothesized that integrating these female genotypes with AI bull data would enhance prediction power, yielding more reliable Genomic Estimated Breeding Values (gEBVs) for both sexes.

Our primary objectives were to:

- Develop an algorithm for enhanced genomic evaluations to optimize culling and mating decisions.
- Evaluate the economic value of this system for genetic improvement and herd management.
- Train specialized personnel to advance this research domain.

Methods and Results: Utilizing the innovative APEX software, we computed gEBVs via the Single-Step Genomic Best Linear Unbiased Prediction (ssGBLUP) method, enabling blending female and male data. We demonstrated that incorporating contemporary cow genotypes constructs a statistically powerful reference population tailored to the Israeli breeding program. Conversely, historical, low-density data did not improve predictions. Furthermore, fine-tuning the polygenic weight parameter and the data sampling timeframe significantly improved accuracy and mitigated genomic inflation (overestimation).

To resolve persistent overestimations in the ssGBLUP model for fat and protein yields, we integrated Deregressed Proofs (DRP) and international Interbull data. This integration, alongside optimized marker-contribution weightings, significantly enhanced prediction accuracy and effectively eliminated overestimation. Finally, evaluating inbreeding coefficients revealed that employing a Genomic Relationship Matrix (GRM) yields significantly more accurate predictions than traditional pedigree-based methods (correlation of 0.70 vs. 0.56), while maintaining modest computational overhead.

Conclusion: These findings confirm that integrating the annually growing pool of female genotypes into genomic evaluations yields highly accurate estimates, comparable to major international populations (e.g., the Dutch CRV). This research accelerates genetic progress, optimizes herd management, enhances the global competitiveness of Israeli milk production, and successfully trains the next generation of industry experts.