Does genomic selection impact genetic diversity in local cattle breeds? Evidence from five European breeds

SHORT SUMMARY FOR PRACTITIONERS:

Genomic selection, which makes use of DNA information to identify top breeding animals early in their life, is increasingly used in local cattle breeds. While genomic selection accelerates genetic progress, concerns remain about rising inbreeding and loss of genetic diversity that have been observed in some breeds.
RUMIGEN researchers analysed over five years of data from five European dairy local cattle breeds (MRY, NRD, ABO, TAR, VOS), comparing inbreeding, diversity, and genetic progress before and after the introduction of genomic selection.

Key finding: the impact on inbreeding differed by breed. Inbreeding increased in MRY and TAR, decreased in NRD, ABO, VOS. Importantly, all breeds maintained or improved their genetic progress.

The main driver of diversity changes was not genomic selection itself, but genetic management. Genomic selection enables the screening of selection candidates and improves accuracies for younger sires, while shortening generation intervals. These effects could accelerate negative impacts on genetic diversity. However, breeds that carefully manage sire contributions, avoiding overuse of individual sires, maintained or even improved diversity while benefiting from genomic selection.

Practical recommendation: breed organisations should actively monitor and manage both the number of sires used and their genetic contributions each year.
For more on this topic, check out this paper.

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