

Impact of genomic selection on genetic diversity in local European cattle breeds



From paper

SHORT SUMMARY FOR PRACTITIONERS:

Genomic selection (GS) uses DNA information to predict which animals will pass on the best traits to their offspring. GS has transformed cattle breeding over the past decades, but a key question is whether it also speeds up the loss of genetic diversity, particularly in smaller, local breeds.

This study examined changes in inbreeding before and after the introduction of GS five local European cattle breeds from three countries: Meuse Rhine Yssel (Netherlands), Norwegian Red (Norway), and Abondance, Tarentaise, and Vosgienne (France). The key finding is that genomic selection does not automatically increase inbreeding in local breeds. After the introduction of GS, inbreeding rates rose in two breeds but fell in the other three. The impact on genetic diversity depends more on how a breeding programme is managed than on GS itself.

What matters most is active diversity management. In Norwegian Red, limiting how much an animal contributes to the next generation helped reducing inbreeding. In Abondance, reintroducing cryopreserved semen from old bulls restored genetic diversity. In Meuse Rhine Yssel, a "cold sire system" reduced inbreeding rates over the last years.

GS is a powerful tool, but it must be paired with diversity management. Monitoring inbreeding levels, using a broad range of sires, and avoiding relying on too few popular bulls are essential, especially for smaller local breeds.

