Mapping Harmful Genomic Regions to Reduce Inbreeding Depression in Local Cattle Breeds

SHORT SUMMARY FOR PRACTITIONERS:

Inbreeding can cause a concentration of rare recessive mutations potentially harmful in livestock herds when homozygous (i.e. two identical copies). This is known as inbreeding depression, and it is a main concern for small cattle breeds where the pool of unrelated animals is limited.

This study identified specific regions in the genome (the full set of an animal's genetic material) that are most strongly linked to inbreeding depression in five local cattle breeds from 3 countries: Abondance, Tarentaise and Vosgienne from France, Meuse-Rhine-Yssel (MRY) from The Netherlands, and Norwegian Red Cattle from Norway.

Researchers pinpointed 108 regions in the cattle genome that, when an animal inherits two identical copies from the two parents (more likely when related), are associated with poorer performance in traits like milk yield, fat and protein content, or conception rate. This is known as genetic load.

Key practical takeaway for farmers and breeding managers: Rather than only trying to reduce overall inbreeding level, it is now also possible to directly control genetic load and avoid to produce calves homozygous in these high-risk regions. This is particularly valuable for small or local breeds, where some degree of inbreeding may be unavoidable, but the worst genetic risks can now be managed more precisely.

Ultimately, this work supports the development of smarter, more sustainable breeding programs maintaining both productivity and long-term herd health.

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