Mapping large genomic variants in 14 French cattle breeds

From paper

SHORT SUMMARY FOR PRACTITIONERS:

This study developed a comprehensive map of structural variants (SVs) across 14 French cattle breeds, covering both dairy and beef types. SVs are defined as genomic variants larger than 50 base pairs, such as insertions or deletions of genetic material. In addition to smaller variants, SVs may have a stronger influence on important traits as fertility, milk production, and disease resistance, making them valuable targets for breeding improvement.

The study utilized two whole genome sequencing technologies: long-read (176 animals) and short-read (571 animals). After evaluation of multiple SV detection and genotyping tools with optimised parameters, a reference panel of over 55,000 SVs, including 25,191 deletions and 30,118 insertions, was created from the 176 long-read sequenced animals. Subsequently, SVs of 571 animals were genotyped using their short-read data based on the reference panel. This catalogue of genotyped SV covering 14 breeds is publicly available for the research and breeding community.

The key practical outcome is a ready-to-use genetic resource that can be applied in genomic selection programmes. By providing a catalogue of genotyped SVs using standard short-read data, the study enables to integrate the SV information into future genomic analyses and potentially into selection programmes. Given the availability of SV reference panel, the work shows that SV genotyping can be performed reliably using only short-read data, making it widely applicable without requiring expensive long-read sequencing for every animal.

Breeds covered include Holstein, Montbéliarde, Normande, Charolais, Limousine, and nine others, making this one of the most comprehensive SV resources available for French cattle to date.

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