

# Nanopore sequencing for livestock epigenetic profiling



*From paper*

## **SHORT SUMMARY FOR PRACTITIONERS:**

This study explored whether Oxford Nanopore Technology (ONT) sequencing can be used as an alternative or complement to the current standard method — reduced representation bisulphite sequencing (RRBS) — for detecting DNA methylation marks in livestock. DNA methylation is an epigenetic modification that can influence how genes are expressed, and identifying these marks across the genome could improve our understanding of traits like fertility, health, and productivity in farm animals. Semen samples from three fertile and three sub-fertile bulls were sequenced using both methods and compared.

The key finding is that ONT detected far more methylation sites across the genome than RRBS, particularly in regions away from gene promoters, while RRBS gave better coverage of promoter regions specifically. Both methods successfully identified methylation differences between fertile and sub-fertile bulls, including markers linked to economically important traits such as milk yield, body weight, and scrotal circumference — a key indicator of bull fertility and sperm quality.

The practical recommendation is that combining both techniques provides the most complete picture of the epigenetic landscape. For breeding programmes, this means that ONT sequencing could be incorporated alongside existing tools to identify new epigenetic biomarkers for bull fertility and other productive traits. These markers were used to develop an "EpiChip" — a cost-effective screening tool that is currently being used on farms to improve selection decisions, health-related decisions and reproductive outcomes.

