Systematic evaluation of methylation profiling assays

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Advances in "omics" technologies has fuelled investigation into the epigenome as a tool to enhance livestock selection and breeding practices. DNA methylation is an important epigenetic mark that is essential for genomic stability and maintenance throughout development. Assays to profile DNA methylation are many and varied, offering a vast range of genome specificity and data yield options within a given budget. This study reviews four DNA methylation profiling assays and evaluates their potential for application within the livestock sector as tools to investigate the global methylation landscape, discover methylated sites associated with phenotypic outcomes and provide low cost, high throughput solutions for industry uptake. The assays assessed here are based on a range of platforms providing a balanced example of tools available for DNA methylation profiling; (1) whole genome bisulphite sequencing (WGBS); (2) reduced-representation bisulphite sequencing; (3) Oxford Nanopore Technology sequencing; and (4) methylation micro array technology via the recently released mammalian methylation BeadChip array. This study assesses the relative accuracy of these assays across seven of the ovine FAANG tissues, using WGBS datasets as the gold standard, and discusses the cost benefits with particular consideration for industry application. Overall, this research is directed towards the discovery of individual methylation markers or marker combinations which may be useful in the selection and breeding of livestock for continued improvement.