POPULATION GENETICS

Rich pastures for cattle genomics

The availability of high-density SNP panels and effective genotyping platforms has done wonders for human population genetics. The same now promises to be true for livestock. One paper reports an approach to maximize SNP discovery in cattle, whereas another has taken advantage of dense-SNP catalogues to map five inherited cattle disorders.

Van Tassell and colleagues have developed a quick and cheap method to detect >60,000 SNPs in the cow genome and simultaneously estimate their frequencies. The method involves the deep sequencing of genomic libraries that derive from selected target populations, and that have been pooled and reduced in complexity. Beyond the benefits to bovine genetics, this approach is applicable to any species with a partially sequenced genome.

The disease-mapping protocol developed by Charlier and colleagues relied on dense-SNP genome scans on cases and controls, followed by computationally detecting those regions of the genome that were homozygous in the cases. Important regions of the genome were thus identified, which on further investigation led to the identification of the causative mutation in three recessive disorders (congenital muscular dystonia 1 and 2, and ichthyosis foetalis).

The practical consequences of these developments are immediate in terms of rapidly fine-mapping disease loci and breeding them out, not to mention the assistance in characterizing their human homologues. Cows are set to join dogs as important models for clarifying genotype–phenotype relationships.

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ORIGINAL RESEARCH PAPERS
van Tassell, C. P. *et al.* SNP discovery and allele frequency estimation by deep sequencing of reduced representation libraries. *Nature Methods* 24 Feb 2008 (doi:10.1038/nmeth.1185) | Charlier, C. *et al.* Highly effective SNP-based association mapping and management of recessive defects in livestock. *Nature Genet.* 16 Mar 2008 (doi: 10.1038/ng.96)