

BWYPEX: Discovery, Approval and Management of Genetic Abnormalities in Cattle

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Genetic abnormalities in cattle continue to challenge animal welfare, reproductive efficiency, and the long-term sustainability of breeding programs. Advances in genomic technologies have significantly improved the ability to detect and manage deleterious variants. However, effective control depends not only on scientific discovery but also on robust reporting systems, clear governance structures, and coordinated industry engagement. Developed as part of the ICAR Brian Wickham Young Persons Exchange Program (BWYPEX), this report integrates perspectives from North America, Europe, and Oceania to examine how genetic abnormalities are identified, analysed, validated, and managed within cattle populations.

The review summarises current methods to detect defects, including phenotype-based reporting and genotype-based surveillance, and evaluates how information flows from farms into national or breed-level analytical systems. Evidence across regions demonstrates that successful systems are characterized by clearly assigned stakeholder responsibilities and transparent industry-wide communication. The report further describes the scientific and procedural steps required to establish a newly identified genetic abnormality, including evaluation of supporting scientific evidence, cost-effective research strategies, development of standardized nomenclature, establishment of biobanks, and the design of gene tests and/or haplotype-based diagnostics to facilitate population-level control. Key management considerations, such as intellectual property frameworks, biobanking strategies, and long-term monitoring, are highlighted as critical determinants of effective implementation.

Despite differences across countries, shared principles emerge, including centralized or clearly mandated authority, supportive environments for reporting, integration of causal variant testing into routine genotyping platforms, and proactive communication strategies. Collectively, these findings provide a structured roadmap for developing national systems to record and identify genetic abnormalities while strengthening international collaboration in their management.