

Abstract by Bruce Moran - Investigating the hepatic transcriptome in dairy cattle with divergent genetic merit for fertility traits using Next Generation Sequencing

Fertility in dairy cows has declined during the last 50 years. This represents a major barrier to efficient milk production, especially in seasonal calving systems where reproductive performance is a key driver of profitability. The Economic Breeding Index (EBI) was introduced in Ireland in 2000 and non-production traits were incorporated in 2001. The EBI currently has 6 sub-indices, with the fertility sub-index accounting for 34.8% of the total weighting. The fertility sub-index is comprised of 2 traits; survival (11.5%) and calving interval (23.2%). Animals with similar genetic merit for high milk production traits (top quartile nationally) and similar proportions of Holstein ancestry (>75%) but with extremes of good (Fert+) or poor (Fert-) genetic merit for fertility traits (top 20%, bottom 5% nationally) were identified by screening the national dairy cattle database in collaboration with the Irish Cattle Breeding Federation. This facilitated the establishment of a herd with similar genetic merit for milk production and phenotypic milk yield, but divergent genetic merit for fertility traits and phenotypic fertility performance. This animal model is a unique and powerful tool to elucidate the underlying physiological basis of subfertility in the Holstein dairy cow. Initial publications show calving interval, body condition scores and services to conception were all significantly different between the two groups. Molecular biology was used to show that insulin, insulin-like growth factor 1 (IGF1) and progesterone profiles between the Fert+ and Fert- animals are also significantly different (Cummins et al. 2012). This gives the current study a very good basis.