

Project number: MKDC-0201-5246

Project leader: Buckley, F

Full title: Evaluation of Norwegian Red and Norwegian Red x Holstein-Friesian dairy cattle under Irish production circumstances.

ABSTRACT

Interest is increasing in the potential use of alternative dairy breeds other than the Holstein-Friesian (HF) and/or crossbreeding. These interests arise from the reduced reproductive performance and survival of the modern HF dairy cow in Irish production circumstances. A recent study in the Republic of Ireland has reported pregnancy rate to first service to be 48%, considerably lower than the target of 60% for compact seasonal calving. There is growing evidence that crossbreeding can offer considerable merits in terms of fertility and survival. At present dairy farmers within Ireland are 'experimenting' with alternative breeds. However, they have no means of comparing the genetic level of the sires of these alternative breeds with the HF. The objective of this study is to provide estimates of key genetic parameters, that are needed before an Across-Breed evaluation can be put in place for the Irish dairy industry. The breed of choice is the Norwegian Red (NRF). Irish farmers will thus be able select from the top sires within the EBI across two breeds, and gain information on the potential advantages from crossing the two breeds (heterosis). This study will also provide considerable phenotypic and genetic information that will be of significant benefit to the newly initiated molecular genetics program at Teagasc Moorepark.

In addition to phenotypic data, genetic information will also be generated on all the animals in the crossbreeding study through the Animal Biotechnology Programme, a joint venture between Moorepark DPRC and Moorepark Production Research Centre. The incorporation of molecular technologies into this crossbreeding study is a key issue. Molecular aspects of the crossbreeding study include (a) signature profiling where a collection of informative molecular markers are tracked through all animals and results allied to phenotypic data and (b) gene discovery of economically important traits via a candidate gene approach. This study will provide considerable phenotypic and genetic information that will be of significant benefit in the selection of superior animals for breeding which is very much part of Teagasc new vision for Agriculture Research. No costs (budget) have been included for any molecular

MAIN DATES

Start date: 01 September 2002

Proposed completion date: 31 December 2009

DESCRIPTION

Specific objectives of the project:

- To generate data which will facilitate the estimation of parameters pertinent to the provision of genetic evaluations for NRF sires and HFxNRF crosses in Ireland i.e. to put in place an "Across-breed Evaluation". At minimum this requires estimates of the relative breed effects (for the HF and NRF breeds) and the estimated level of heterosis (obtained when the two breeds are crossed) for the range of traits currently represented in the Irish Economic Breeding Index (the EBI). These are milk yield, fat yield, protein yield, calving interval and survival.
- To provide conversion factors for Interbull-type across-country evaluation that will allow the prediction of breeding values for other NRF sires not included in the study.
- A number of other economically and biologically important criteria will be monitored including measures of calving ease, calf vitality, growth rate, temperament, body condition score, live weight, intake, routine fertility measures including pre-breeding utero-ovarian measurements, udder health, bloods samples for various metabolites and for the DNA depository at Moorepark etc.
- It is envisaged that this study will provide a comprehensive and diverse source of phenotypic and genotypic data, given the different selection goals within the HF and the NRF breeds. This study will be a valuable asset allowing the integration of molecular technologies into a production breeding program. It is hoped that associations will be made between phenotypic variations of economically important traits and genotypic variations in causative genes. As such, it will provide an appreciable resource for SNP detection/discovery and indeed gene discovery - see RMIS projects 5198 and 5199 for example.

Expected benefits of the project:

High levels of involuntary culling, slippage in calving pattern, veterinary intervention, hormonal treatment and reduced annual milk production are costly to the Irish dairy enterprise. The relative importance of fertility performance in particular in Ireland compared to other countries is higher due to our seasonal calving system. Reducing the rate of involuntary culling due to poor health and reproductive performance has improved ethical as well as financial implications for the Irish dairy farmer. Providing genetic evaluations for alternative breeds/crossbreeds will identify more high profit sires. This will lead to a more efficient and satisfying dairy enterprise encouraging young farmers to remain in dairy farming, strengthening communities and maintaining employment in rural areas.

Previous studies have shown that selection for milk yield increases gross feed efficiency especially in early lactation. However, this calculation takes no account of the nutrients required for heifer rearing and dry periods, nor does it consider the polluting potential of young stock and culled cows. The reduced life-span of cows in the herd means that there are fewer lactations in which to 'repay' the nutrients used in rearing and an increased number of polluting young stock and cull cows to dispose of. These additional cull cows represent a significant potential source of pollution that has to be disseminated, through rendering, as well as a direct cost for example through schemes such as the Over Thirty Months Scheme (OTMS). Thus, on a life-time basis, and from the perspective of herd and environmental sustainability, it may be more efficient to have moderately yielding cows that produce milk for over 5 lactations rather than high yielding cows that last for only 2-3 lactations.

A genetic index for dairy cattle will be developed through signature profiling. We define this as a process where every animal is graded for the presence or absence of polymorphisms in several genes known to influence economically important phenotypic traits (fertility, disease resistance, body condition and milk production). The aim is to track several combinations of allelic variations simultaneously, while gathering phenotypic data on animal performance. Initially a number of genes with known polymorphisms associated with phenotypic variation will be investigated. The list will be expanded as more genes are discovered and mutations in promoter regions or coding regions which affect expression or amino acid sequence of the protein will be investigated.

A fundamental long term component of this project will be gene discovery for economically important traits. The majority of economically important traits in livestock are complex, continuously distributed phenotypes which are influenced by multiple gene dispersed across the genome. We believe a candidate gene approach will maximise our likelihood of success. This is where a known mapped gene is chosen for analysis because it may be linked with a particular phenotype. A new field of comparative genomics has emerged which uses genomic information in one species to find homologous genes or chromosomal segments in another species. For example, human genes identified as playing a role in lactation, fertility, growth rate or disease susceptibility may have similar or homologous counterparts in the dairy cow. It is a relatively simple task to find and characterise these genes in any mammalian species using the human sequence or chromosome segment as a molecular signpost. This work will be facilitated by the large number of animals in the crossbreeding study and the natural genetic variation which exists between the two chosen breeds.

It is envisioned that in the long term, molecular discoveries made during this study will be used to assist in the selection of animals for future breeding which will play a big part in Teagasc new vision for Agriculture Research. In this way higher genetic merit animals will be identified and may be targeted for use in future breeding programmes.

COLLABORATIONS AND LINKAGES

<u>Country code</u>	<u>Name of institute</u>	<u>Scientist name</u>
NL	ID-DLO	Dr. Luc Janss and Dr. Roel Veerkamp
NO	Matforsk	Dr. Torstein Steine