Animal Research Programme – Genetic Improvement of Dairy Cattle

RMIS No: **5499**

Title: Genetics of predisposition to tuberculosis in Irish dairy cattle

Abstract

Infection with Mycobacterium bovis, the causal organism in bovine tuberculosis, remains an important infection of cattle in many countries. In Ireland, a tuberculosis eradication programme has been operating in the national cattle herd since the 1950s, with control costs being borne by both government and industry. Although human tuberculosis (with varying levels of M. bovis involvement) is now of minor importance in Ireland, it was recently the subject of an emergency declaration by World Health Organization following rapid increases in tuberculosis rates among people in Africa . There are substantial gaps in knowledge concerning the genetics of tuberculosis in cattle. Very little is known about the genetic background of the predisposition of cattle to tuberculosis. Earlier studies, on small numbers of animals, suggest heritability in the range of 0.06 to 0.19 for susceptibility to tuberculosis, which is lower than heritability estimates (0.48) from experimentally infected red deer. No study has yet evaluated the mode of inheritance of tuberculosis susceptibility in dairy or beef cattle, and the regulation of expression of polygenes across environments has also not been undertaken for cattle. There are several large animal- and herd-level datasets (animal breeding, disease control) in Ireland which represent an opportunity, unique internationally, to address some of these gaps in knowledge. Using these datasets, to which we have access, we aim to quantify the heritability (both direct and maternal heritability) for susceptibility to tuberculosis, as well as possible genetic associations with other economically important traits. The interaction between gene expression and environment will also be evaluated. Results from this study will provide scientists with an initial understanding of the genetics behind susceptibility to tuberculosis, and has the potential to identify Irish and foreign animals with relatives in Ireland that are genetically predisposed to infection with tuberculosis. The latter is advantageous for QTL discovery for tuberculosis susceptibility/resistance.

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