

**Title:** Bovine Genome Project

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**Objective:**

To participate in an international program directed at genetic mapping of the bovine and to collect phenotypic data on beef cattle so as to identify genes of importance to the economics, quality and health of beef cattle in Canada.

**What is to be done?**

To participate with United States Department of Agriculture, INRA (France) and the Roslin Institute in the U.K. in the bacterial artificial chromosome (BAC) library and fingerprinting as well as in expressed sequence tag (EST) sequencing of the bovine genome. Secondly, work is to be done in core animal breeding and phenotypic measurements of the Net Feed Intake project in Alberta, in particular, to map genetic data for positional localization of quantitative trait loci (QTL). A comparative analysis of improvement schemes utilizing marker assisted strategies will be involved in the concluding phase of this research.

**Why is it to be done?**

A map of the bovine genome is currently being developed as an international program involving many countries and institutions. It is important for Canada to be involved in this research to benefit from new tools that will allow us to use gene information (genomics) to identify high performing and quality cattle for breeding. This project will also capitalize on a major thrust in beef cattle breeding in Alberta that is already underway which is to identify high efficient cattle for selection. Industry funding needs to be a key component in leveraging funds from governments and other industries to allow a major project such as this one to proceed.

**What is to be done?**

The core program involves an ongoing commitment to the international program in BAC library fingerprinting and EST sequencing, with a view of completing an EST dataset for the bovine gastro-intestinal tract. For the Alberta based gene discovery component, phenotypic measurements are to be made on the top and bottom 8% of animals at the Edmonton Research Station of the University of Alberta as well as at the One Four ranch of the Lethbridge Research Station. Phenotypic measurements are taking place using calves placed on a high energy diet. Microsatellite-based genotyping is to be used to perform a QTL scan. Microarray analysis of gene expression is to take place in years 2 & 3 of the project.