



# RESEARCH FACTS

RESEARCH & TECHNOLOGY DEVELOPMENT FOR THE CANADIAN BEEF INDUSTRY

## Beef Science Cluster



## New Technologies to Breed Better Barley

### Project Title:

The development of molecular markers for improved fiber quality in barley

### Researchers:

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### Project Code:

FRG.01.10

### Completed:

March 2013

### Background:

The nutritional value of barley grain comes from its seed starch content, but a great deal of barley is used for silage, greenfeed or swathgrazing. Therefore, it is important to know the nutritional value of the cut plant. Nutritional value largely depends on how digestible the fiber (lignin, cellulose and hemicellulose) in the stem and leaves are. Barley varieties with higher whole plant digestibility allow cattle to obtain more nutrients per tonne of feed.

Some barley varieties have more digestible fiber than others. For example, researchers at Alberta Agriculture Rural Development Lacombe developed the hull-less six-row barley variety "Falcon", which has 8% less neutral detergent fiber than the closely related hull-less six-row variety "Tyto", and even less than hulled barley. This means that breeders can select for improved digestibility. If genomic technologies can be used to identify the chromosomal locations and molecular markers linked to fiber digestibility, selection should be easier and faster.

Finding genetic markers that are linked to the improved digestibility in Falcon will help in transferring this unique silage quality trait to new elite varieties with greater whole plant feed quality.

### Objectives:

To

1. determine the heritability of fiber digestibility,
2. identify markers and map sites on the chromosome (QTL's) that affect fiber digestibility,
3. determine how these interact with each other,
4. validate markers that could help select for fiber digestibility in barley, and
5. identify genes that may affect fiber digestibility.

### **What They Did:**

Falcon was crossed with several other hulled, hull-less, six-row or two-row feed varieties (such as Tyto, Kasota, AC Virden, Seebe and Manny). Each cross produced about 200 recombinant inbred lines (RIL) that were grown in field plots during 2010-2012. Each line was phenotyped for silage quality by NIR spectroscopy (IVFD, NDF, ADF, Lignin, protein and starch). Two populations (Falcon X Tyto and Falcon X AC Virden) were then genotyped with DNA genetic markers, and these markers were mapped to barley's seven pairs of chromosomes. The NIR quality data was compared to marker genotype data to identify groups of linked markers (or QTLs) that appeared to affect silage feed quality. These markers were then validated by testing their ability to predict silage quality in the other Falcon-cross populations.

### **What They Learned:**

The Falcon parent in both RIL populations (Falcon/Tyto and Falcon/Virden) was consistently lower in ADF, NDF, lignin and higher in protein, starch and IVFD. Many markers were found in the RIL populations, but when the markers were mapped to chromosomes it turned out that Chromosomes 2H and 4H in the Falcon/Tyto population showed little genetic variation. Large regions on these chromosomes appear to have been "fixed" during the breeding process. These may represent blocks of genes that may be important for yield, disease resistance and feed quality.

Many different markers for silage feed quality were observed across the barley genome in both genetic populations. Clusters of markers (called QTL's) for silage quality were found in three regions of the Falcon/Tyto map (2H, 1H and 7H). The 2H QTL was correlated with an improvement in silage quality (higher starch content and decreased NDF, ADF and lignin), and explained 36% of the phenotypic variation in starch content and digestibility. The 1H and 7H QTLs reduced quality (lowered starch and increased ADF, NDF and lignin), but had smaller effects on starch content and digestibility.

Three regions within the Falcon/Virden map were also observed to have clusters of QTLs for silage quality (3H, 4H and 5H), with less important QTLs on 1H and 7H. The 3H and 4H regions both had QTLs that were linked to increased starch and/or IVFD and reduced ADF, NDF and/or lignin.

### **What it Means:**

This team found chromosome regions with overlapping clusters of QTLs for silage quality in each genetic mapping population. These regions may represent gene clusters or "hot spots" containing genes that control lignin, protein and/or starch production (which ultimately determine digestibility). The researchers are currently validating the DNA markers to ensure that they will work equally well in other crosses. Identifying reliable DNA markers will allow more rapid and economical selection for barley silage quality.

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### **Proudly Funded By:**



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