Barley Genome Mapping: New Insights Into the Malting Quality of the World’s Oldest Crop

By Patrick M. Hayes

ABSTRACT

Recent developments in genetics - particularly in the areas of DNA marker technology and quantitative locus analysis - have provided insights into the genetic control of economically important traits in barley. The North American Barley Genome Mapping Project, a consortium of barley researchers in the US and Canada with extensive international linkages, has the long term goals of locating and characterizing genes of economic importance and using this information to develop superior varieties. In its first phase, the NABGMP has developed medium density chromosome linkage maps in a number of reference populations and used them to locate genes controlling a range of agronomic, malting quality, and stress resistance characters. A summary of effects across these populations provides an insight into the genetics of malting quality and reveals parallels with described biochemical pathways.

GENETICS OF MALTING QUALITY

Malting quality is determined by a number of component traits. Historically, plant breeding and biochemical analysis of these component traits have been “parallel” endeavors. For example, Sun and Henson (1991) used path coefficient analysis to describe relationships among key enzymes responsible for in vitro starch hydrolysis. From a crop improvement perspective, the situation is not so clear: expression of α-amylase activity, diastatic power, and malt extract under production conditions is the consequence of genotype, environment, and genotype x environment interaction. Impressive gains have been made in improving malting quality through conventional breeding procedures. Maintaining these rates of gain, and rapidly developing malting barleys with unique quality profiles, may be facilitated by a clearer understanding of the genetic basis of trait expression. Until recently, the quantitative inheritance of the components of malting quality necessitated statistical approaches to genetic analysis. Often, these tools were not directly applicable to variety development. New tools allow for mapping the genetic determinants of trait expression. This information can be used to develop breeding strategies, to implement marker assisted selection, and to build a fundamental understanding of genome architecture and expression.

The NABGMP

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SINTÉSIS

Desarrollos recientes en genetica - particularmente en las areas de tecnologia de marcacion de DNA y analisis cuantitativo de locus - nos han provisto de nuevos conocimientos referentes al control genetico de caracteristicas economicamente importantes en la cebada. El proyecto Norteamericano de Identificacion de Los Genes de La Cebada, un consorcio de investigadores de cebada en los Estados Unidos y Canada con extensas relaciones internacionales, tiene el objetivo a largo plazo de localizar y caracterizar los genes de importancia economica y usando esta informacion, desarrollar variedades superiores. En su primera etapa, esta asociacion ha desarrollado mapas de las uniones de densidad media en un numero de poblaciones referenciales y las usaron para localizar genes que controlan un rango de caracteristicas agronomicas, de calidad de malteado, y de resistencia de stress. Un resumen de los efectos en estas poblaciones proveen de informacion de la genetica para la calidad de la malta y revela paralelos con caminos bioquimicos descritos.
GENOME MAPPING

DNA marker technologies allow for the construction of genome linkage maps. Coupled with statistical tools, these maps can be used to locate the quantitative trait loci (QTL) that determine malting quality. Genome map-based strategies should allow for more systematic and efficient selection for the components of malting quality. The detection of QTL involves generating phenotype and genotype data sets and integrating the two through the statistical procedures of QTL analysis.

AN INTEGRATED VIEW OF THE BARLEY GENOME

Whether or not a QTL is detected is a function of, among other things, allelic variation present in the test population and the environments in which the test population is assessed. Thus, QTL, like estimates of components of genetic variance, will show germplasm and environmental specificity. However, estimates of genetic variance are single statistics that describe a population while estimates of QTL position are multiple values with a biological basis, i.e. chromosome position. Accordingly, integrating QTL position data cross genotypes and environments is a dynamic exercise that provides insights into the genetic basis of the interrelationships of the determinants of malting quality. Malting quality QTL effects reported in a range of barley genotypes were summarized and positioned on a "skeleton" linkage map (Figure 1). These positions can only be considered approximate: original reports should be consulted for more precise genome locations (Chalmers et al., 1993; Han et al., 1995; Hayes et al., 1993; Kjaer et al., 1991; Oziel et al., 1995; Tinker et al., 1994). Kernel weight and grain dormancy QTL are shown on the left axis of each chromosome map. QTL for grain protein, β-glucanase, the soluble to total protein ratio (S/T), diastatic power, α-amylase, and malt extract were then sequentially added at each position where significant effects were detected.

INTERPRETATION

This preliminary summary provides a number of intriguing insights into the genetics basis of malting quality. There are examples of QTL that are likely the consequence of cloned genes, cases where no QTL were detected in the vicinity of cloned genes, and cases where QTL were detected in regions where no cloned genes have been mapped. Coincident QTL for more than one trait may be due to linkage (the genetic determinants are in close proximity on the chromosome) or pleiotropy (the same gene controls multiple traits).

- The Amy2 locus on chromosome 1 is probably the determinant of the multiple QTL detected near the centromere of this chromosome: α-amylase is a component of diastatic power, and the role of α-amylase in starch hydrolysis would account for the malt extract QTL.
- No QTL were detected in the vicinity of AGL (an α-glucosidase locus) on chromosome 1, despite the importance of this enzyme in starch hydrolysis. It may be that in the
limited sample of germplasm contributing to this summary, all genotypes carry α-glucosidase alleles of similar activity. A wider cross (such as *Hordeum spontaneum* × *Hordeum vulgare*) may be required to detect genetic variation.

- The diastatic power QTL on the long arm of chromosome 4 is likely a consequence of the *Bmy1* locus. In the Steptoe X Morex and Dicktoo X Morex populations, the feed barley parents contribute favorable diastatic power QTL alleles in this region. Thus, feed barley varieties may carry favorable alleles for components of malting quality.
- Coincident QTL for a range of malting quality traits were mapped near the centromere of chromosome 7. No candidate cloned genes have been mapped to this region.
- Throughout the genome, there are examples of coincident and non-coincident QTL that are candidates for further characterization. For example, kernel weight QTL where there are no coincident starch-related QTL and grain protein QTL with no coincident QTL for S/T or any of the hydrolytic enzymes.

**PROSPECTS**

We will continue to integrate data from a range of germplasm in an effort to identify those regions of the barley genome that are critical for malting quality: ultimately we hope to develop a comprehensive analysis based on barley genotypes ranging from *Hordeum spontaneum* to elite germplasm from the principle malting barley production areas of the world. Sufficient marker saturation will facilitate prediction of which effects will be fixed and which will be segregating in various germplasm combinations. Characterization of germplasm - from ancestral to exotic - will allow for systematic accumulation of favorable alleles. No variety is perfect, and good genes may be hiding in the most unlikely backgrounds. These data are being used by North American barley researchers to rapidly and efficiently develop malting barley varieties with unique quality profiles.

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