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Presentation Summary

### **Extreme Population-Dependent Linkage Disequilibrium Detected in Inbreeding Plant Species, *Hordeum vulgare***

The nonrandom association of alleles at two or more loci on a chromosome is defined as Linkage disequilibrium. Information gained from LD can determine the resolution power of association-based mapping strategies. In human or mammalian genetic studies knowledge of LD has been important in refining high-resolution gene mapping and cloning studies for complex disease genes. In plants this same information can be utilized, but biological systems and population history influencing LD need to be evaluated before association-based mapping strategies can be applied. Initial studies of LD in plant systems have been done on maize, Arabidopsis, and rice. Information gained from these studies suggest that the decay of LD occurs at a slower rate in inbreed systems due to the decrease in recombination. Linkage disequilibrium can only be decayed by recombination and in inbreed systems there are fewer heterozygous individuals which means there are fewer opportunities for recombination.

Studies of LD in inbreed crop plants are needed to build upon information gained from Arabidopsis. To characterize the extent of LD in inbreed crop species this study analyzed inter and intragenic associations across four gene loci within 212 kb of the barley hardness locus. A total of 74 cultivated, 34 wild, and 23 landrace accessions were used. Estimates of nucleotide polymorphism, neutrality, recombination, and linkage disequilibrium were calculated. To determine the level of LD four regions of the hardness locus was analyzed, such as *hinb*, *hina*, *GSP*, and *PG2*. When analyzing the four gene regions they found that in general the cultivated accessions had high association, wild accessions had low association, and landrace accessions had an intermediate association compared to the wild and cultivated accessions.

Estimates of association were also determined among the different gene regions, which are nonuniformly distributed across the 212 kb sequence. High levels of association were found to stretch across the entire region in the cultivated sample. LD decreases as a function of increasing distance in both ancestral samples. There is also an undulating pattern in the levels of association among the different between-gene comparison groups in all three sample sets studied. The presence of either singular or nested transposable elements has previously been implicated as a mechanism for recombination suppression in several eukaryotic genomes and, therefore, could have an impact on local levels of LD. Several of the results in the paper suggest recombination suppression, although the presence/absence of repetitive DNA cannot solely account for the punctuated pattern of LD observed across the entire sequenced region.

One other plausible explanation for this punctuated pattern of LD is the presence of contrasting gene histories within the same local chromosomal region. The different patterns of nucleotide diversity observed among the genes analyzed suggested varying intensities of selection as selection within the domesticated germ plasm. This work represents a detailed study into the levels and patterns of local or short-range LD within an inbreeding crop species and suggests that LD-based approaches will be a powerful tool for identifying the allelic variants that contribute to complex traits in crop plants.