## Use of flanking loci to characterise variation at the Mla disease resistance locus in barley.

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## Introduction

The Mla locus in barley is one of several loci that confer gene-specific resistance to the powdery mildew fungus, Blumeria graminis f. sp. hordei The locus exhibits considerable functional variation with over thirty alleles described. A 261 -kb contig spanning the Mla gene family has been sequenced in the cultivar Morex (Wei et al, 2002, Plant Cell 14: 1903-1917).

At least seven alleles at this locus ( $M 1-a 1, M 1-a 3, M I-a 6, M 1-a 7, M 1-a 9, M I-a 12$ \& $M I-a 13$ ) have been used in past breeding programmes in Northwest Europe in attempts to introduce resistance to powdery mildew.. These resistance gene introgressions suffered from classic boom and bust cycles as the fungus developed virulence to the specific resistance alleles introduced.

Although the gene is no longer a major target of selection in modern breeding programmes the introduction of the various alleles has had a profound impact on the variation present in this genomic region in modern elite barley varieties.. This study was initiated to study the effect of the introgression of the MI-a alleles into elite germplasm and we present preliminary results here.

## Haplotype surrounding MI-a locus

Although the gene is cloned and the surrounding BAC sequence known, the application of this genomic sequence to the study of variation at the locus is complicated by duplication within the MI-a locus itself and duplication between the region and homologous loci elsewhere in the genome.

In order to circumvent the problems inherent in studying the variation at the MI-a locus we have characterised the variation within the genomic region around Ml -a through sample sequencing at a number of single copy loci flanking the locus. The results from two single copy genes on BAC clones flanking the locus ( $\sim 500 \mathrm{~kb}, \sim 0.35 \mathrm{cM}$ apart) are presented in the table opposite.

The derived primers were used on DNA from stock accessions previously described as type designations of particular MI-a alleles (Jørgensen, 1993). The resulting derived sequences of the two flanking loci indicate that severa $\mathrm{MI}-\mathrm{a}$ alleles reside within identical haplotypes (MI-a1, MI-a5, MI-a7, MI-a10, $\mathrm{MI}-\mathrm{a} 11$ and $\mathrm{MI}-\mathrm{a} 30$ ) that possibly indicates a recent diversification of these alleles from a common ancestor.

Other flanking haplotypes (such as that for $\mathrm{ml}-\mathrm{a}$ ) indicate possible recombination between the two flanking loci. This recombination may relate to the known derivation of the null allele ml -a from an unequal crossing over event within the MI-a locus (Halterman, and Wise, 2004, Wei et al., 2002). The in stability of the locus in heterozygotes and loss of resistance has previously been described (Wise and Ellingboe, 1985).


Table of the SNP haplotypes at two loci flanking MI-a locus for past and current Northwest European barley cultivars showing range o MI-a alleles

## Genotyping Barley varieties for MI-a alleles

The integration of the sequence information has enabled the genotyping of barley lines for MI-a alleles by proxy through the genotyping of closely physically linked loci. When used on a range of current and past northwest European barley varieties the flanking sequences correctly predicted the Ml -a allele in previously characterised cultivars (Jørgensen and Jensen , 1983) and gave an indication of which allele had been inherited in current uncharacterised material for which pedigree information was known.

In addition the characterisation of MI-a alleles within recent European barley material indicted not only the presence of the seven introgressed alleles but also four other haplotypes which presumably were present in ancestral Northwest European barley landraces. These four European haplotypes include the functionally characterised weak allele MI-a8 (Jørgensen, 1993). Interestingly other barley cultivars that have been characterised as MI-a8 such as the variety Golden Promise have a different haplotype (denoted MI-a X). This could be due to the genotype of the Heil Hanna No. 3 plant used for this study not carrying $\mathrm{MI}-\mathrm{a8}$ or alternatively that the Japanese isolate used to functionally characterise MI -a8 could possibly have carried avirulence to two old European MI-a resistance alleles.

Given the maintenance of linkage disequilibrium (LD) over $\sim 0.35 \mathrm{cM}$ around the Ml -a locus in elite material that has allowed us to genotype for MI-a by proxy, we are currently investigating how far this LD ex tends. Initial studies with primers derived from AF085164 the receptor-like kinase LRK10 gene (Feuillet and Keller , 1999) ~3cM distal of MI-a indicate a near complete maintenance of the donor haplotype in current barley varieties. This corresponds to past findings of correlations of allelic states at $\mathrm{MI}-\mathrm{a}$ and the flanking hordein seed storage proteins (Shewry et al 1979) We are continuing this with other genes on 1 HS to determine whether there may be selection acting on alleles at other loci brought in via linkage drag with the introgressions of the MI-a alleles.

## Summary

The use of flanking loci has enabled an investigation of the relationships between MI-a alleles and highlighted a possible role of recombination in their evolution

These loci have also allowed us to follow complex breeding history of Northwest European barleys that includes repeated introgression of resistance alleles

The characterisation of older European barley lines has also indicated that the functionally characterised $\mathrm{Ml}-\mathrm{a} 8$ allele may encompass two separate sequence haplotypes.

## References

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