The semi-dwarfing gene sdw1 in European spring barley

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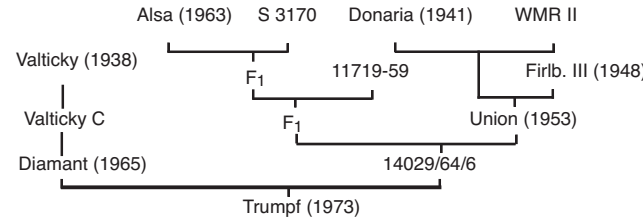
Introduction

The mutation sdw1 in barley confers a semidwarf phenotype that is sensitive to exogenous GA unlike the dominant GA insensitive dwarfing genes found in bread wheat. sdw1 is utilised in the majority of spring barley cultivars grown in North-West Europe. It is present, for example in all but one of the spring varities on the current UK recommended list.

Although multiple sources of the mutation are known most current varieties carry the gene from one particular source, the mutation in the Czech variety Valticky that produced the variety Diamant in 1965. Its prevalence is due in part to the great success of the high malting quality variety Trumpf (Triumph) bred in Germany in 1973 that included Diamant in its parentage. The success of Trumpf and its subsequent wide use as a parent has ensured the use of the Diamant source of sdw1 in North -Western European spring barleys.

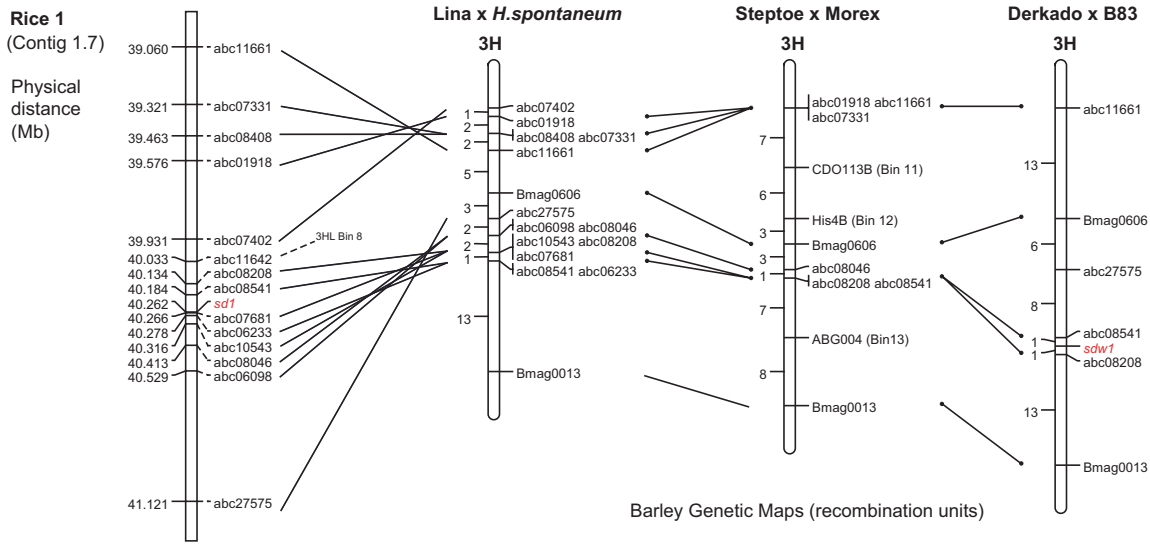


Pedigree of Trumpf (adapted from Fischbeck G., Barley Genetics VI, 1992)

Use of barley-rice synteny for the mapping of sdw1 region

The map position of sdw1 on the long arm of 3H(3) allows the genomic sequence of the broadly homolgous rice chromosome 1 to be used to provide markers that delineate the sdw1 region in barley and also gives more detailed data on the syntenic relationship between these two species in this genomic region.

The presence of the recently cloned sd1 gene (coding for gibberellin 20-oxidase) on the long arm of rice chromosome 1 gave the focus of a candidate gene for this study. Mutations at the rice gene sd1 have been widely used in the 'Green Revolution' and give a dwarf phenotype that is also sensitive to exogenous GA as is sdw1 in barley.



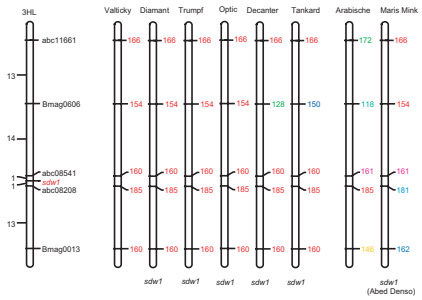
Barley Genetic Maps (recombination units)

The genomic sequence of rice PACs from the sd1 genomic region was used to find putative homologous barley sequences from the assembly of public barley ESTs in HARVEST (S.Wanamaker & T.Close). Primer pairs were then designed to these barley sequences targeting either polymorphisms show in the HARVEST assemblies or to regions likely to contain polymorphisms, (3'UTRs and introns). Markers (SNPs, indels and SSRs) were verified/discovered through the sequencing of PCR products from several mapping parents and the polymorphisms mapped in the relevent populations.

The use of the rice chromosome 1 sequence to generate barley markers was successful in populating the marker-poor region of sdw1 on the barley genetic maps. It appears that the co-linearity in rice may be interrupted by two rearrangements in this region in barley. However two markers that showed homology to genes on the same rice PAC as sd1 were shown to map with a recombination unit of sdw1 mapped from the phenotypic scores on the Derkado x B83 population. The comparison of the barley genetic maps shows some variation in recombination frequency as well as a loss of polymorphism as the crosses become narrower.

Introgression

The mapping of polymorphic markers in the sdw1 region has allowed us to genotype a range of elite spring barley varieties. These studies indicate that a region between the genomic SSRs, Bmag0606 and Bmag0013, is conserved from Diamant in some modern varieties such as Optic.



Although some recombination can be observed the haplotype across this region is indicative of the presence of the sdw1 gene from Diamant. Alternative haplotypes are observed in non-sdw1 lines or in varieties with sdw1 from a different sources.

Future work

We are presently engaged in cloning sdw1 in order to fully characterise the mutant alleles from the various sources available. To this end we have screened a 3x genome coverage subset of the Morex BAC library with a probe derived from abc07681 which is homologous to a gene which is less than 1.5 kb from the gibberellin 20-oxidase sd1 gene in rice. This hybidisation highlighted four BAC clones which are presently being fingerprinted and subcloned.

Other work will include a further elucidation of the rice/barley synteny in this region with particular emphsasis on the region distal to sdw1. The putative translocations relative to rice are also of interest and will continue to be investigated. In particular confirmation of breakpoints indicated on the barley genetic maps will be sought using physical mapping approaches. In addition we will be utilising the markers that this study provides within an ongoing genotyping survey of elite barley germplasm in order to elucidate the patterns of linkage disequilibrium within modern barley varieties.

Acknowledgements

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