We seek to identify the geographic regions that best explain the diversity in domesticated barley and associate genes or genomic regions with diverse environmental conditions.

Molecular tools and genetic resources for eyespot resistance in wheat.

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Eyespot is an important stem base disease of wheat caused by two species of fungi, *Oculimacula yallundae* and *Oculimacula acuformis*, both of which are widespread in northern Europe and the Pacific northwest USA. There are two main sources of resistance available; *Pch1*, a potent resistance gene introduced from *Aegilops ventricosa*, and the moderate resistance of the variety Cappelle Desprez.

Pch1 has not been used widely in European wheat varieties due to linkage between *Pch1* and yield-limiting genes. Breaking this linkage has proven difficult because of a low recombination frequency and a lack of molecular markers that function in both wheat and *Ae. ventricosa*. Utilising the *Brachypodium* genome sequence, we developed co-dominant Conserved Orthologous Sequence (COS) markers targeted to the *Pch1* region. These markers were used to identify recombinants and to locate *Pch1* on chromosome 7DL. By exploiting co-linearity between *Brachypodium*, rice and sorghum, we identified a candidate gene region as a prelude to the map-based cloning of the gene.

Resistance in Cappelle Desprez has been attributed to the partial resistance gene *Pch2*. We mapped *Pch2* resistance to *O. acuformis* as a QTL on the distal end of chromosome 7AL. However, it was not possible identify any resistance to *O. yallundae*. This indicates that *Pch2* operates specifically against *O. acuformis*, and that *Pch2* should not be relied upon as a stand-alone resistance in wheat varieties.

There is previous evidence of an adult-plant resistance on chromosome 5A of Cappelle Desprez. We showed this resistance to also be effective in seedlings and to provide protection against both pathogen species, indicating that it will be useful in commercial varieties. Two chromosome 5A recombinant populations were tested in seedling bioassays and field trials to locate a stable resistance QTL on 5AL and identify linked SSR markers for selection of the resistance.

In addition to characterising existing eyespot resistances, we screened 1,036 hexaploid genotypes from the Watkin's Worldwide Collection for resistance to *O. yallundae*. Some accessions exhibited a high level of resistance. Selected lines will be screened for resistance to *O. acuformis* and the genetic basis of any novel resistances will be determined.

Wheat Zapper, Illumina BSA, and radiation hybrids for synteny analysis of the scs region.

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Species cytoplasm specific (*scs*) genes are of great evolutionary importance because they guide the precise interaction between nucleus and cytoplasm. Recently, an *scs* gene of wheat (*Triticum* species) was localized to the pericentromere of chromosome 1DL. In an attempt to clone this gene, we generated a radiation hybrid (RH) *in vivo* population of ~1,500 individuals. EST-based markers were developed and used for genotyping the whole 1D chromosome. An online tool was developed to easily and rapidly study the colinearity between wheat and three sequenced plant species (*Sorghum bicolor*, *Brachypodium distachyon*, and *Oryza sativa*), namely the Wheat Zapper (http://wge.ndsu.nodak.edu/wheatzapper/). Employing this tool, together with functional analysis of the RH lines, we determined that the *scs* region corresponds to a region of paleofusion between two ancestral chromosomes corresponding to the modern Sb9-1, Bd3-2, or Os10-5. To