Barley inflorescence architecture mutants

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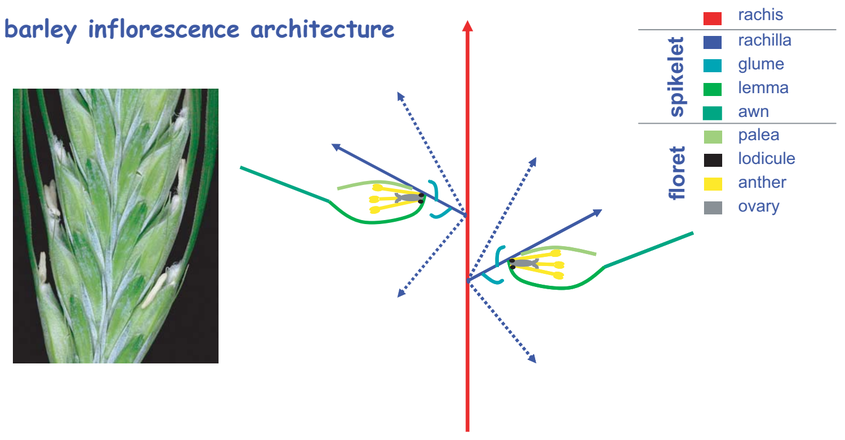
Introduction

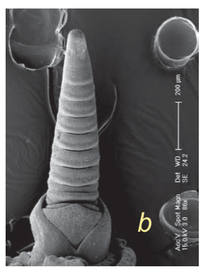
The four major cereal crops of the world, wheat, rice, maize and barley, display distinct patterns of inflorescence development.
Variation in inflorescence architecture can affect yield potential and as a result domestication of these grasses has involved selection for modified patterns of inflorescence development.
We are interested in identifying which genes control cereal inflorescence development.
Through a comparative approach, we want to use this information to explain the molecular basis underlying the distinct inflorescence architectures of different cereals and the differences between domesticated varieties and their wild progenitors.



Barley is the fourth most important crop in the world, the second most important in Europe and the most important in Scotland. The inflorescence of barley is distinct from other cereals and while wild barley has two rows of grain, some domesticated varieties have six.
The basic repeating unit of the inflorescence is the spikelet, a structure unique to grasses, in which the floret is borne. Barley develops three spikelets at each rachis node and each spikelet bears only one floret. In two row barley only the median spikelet is fertile and goes on to form grain (the lateral spikelets are much reduced). In 6-row barley the median and the lateral spikelets form grain.

Barley inflorescence development

Barley inflorescence development is poorly documented. Therefore we first dissected barley apices through a time course of development. Early in development, the vegetative meristem and emerging leaf primordia are clearly visible (a). Upon the switch to inflorescence development (b), the apex elongates and prominent double ridges appear. Later in the triple mound stage (c) the three spikelet meristems at each node become visible. Subsequently (d), the spikeletñspecific organ primorida (glumes and lemma) become clear, the floral meristem develops and gives rise to floret organs, eg. the three stamen primordia are clearly visible.

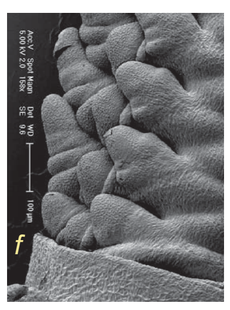


Screening for inflorescence architecture mutants

We screened an EMS-mutagenized population of barley (prepared by R. Waugh and colleagues at SCRI) for mutants with disrupted inflorescence architecture in summer 2003 and 2004.
We identified a range of mutants disrupted in spikelet meristem identity and determinacy. A selection are shown below and include a mutant that makes a single extra floret at the median spikelet (a), mulitflorous types (b,c) and a mutant that makes spikelet organs (glumes and reiterates lemmas), but fails to make the switch to floral meristem identity (d). Notably, this mutation only affects the median spikelet.
EMS has rarely been used with barley. This may account for the fact that some of the mutants we identified have not been reported before and are not maintained in barley stock centres.

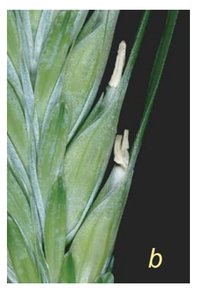
multispikelet

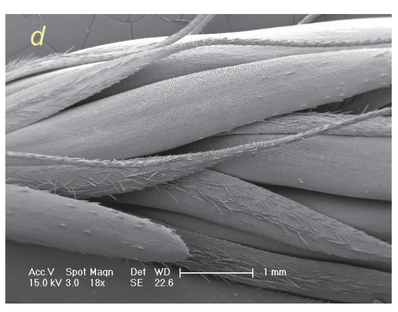
One mutant makes extra spikelets and we refer to it as *multispikelet* (*msp*). The mutant shows no other obvious phenotypes apart from spike morphology (a). Compared with wild-type (b), each rachis node in *msp* (c) gives rise to many more spikelets. SEM analysis reveals that *msp* is indistinguishable from wild type at the triple mound stage (d), but in subsequent development the median and lateral spikelets reiterates in *msp* (f,h), rather than progressing directly to floral meristem identity, as happens in wild-type(e,g). This mutant is therefore defective in spikelet meristem determinacy.

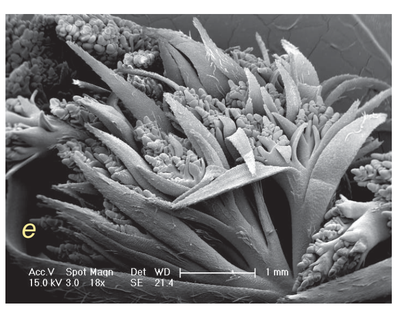


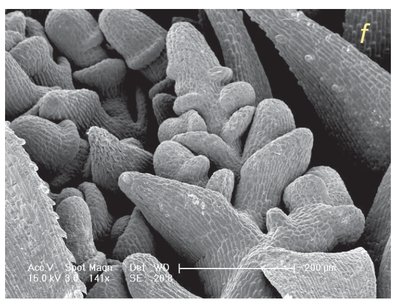
glumey

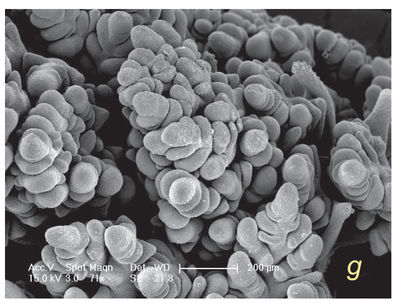
In contrast to wild type (a,b), the *glumey* (*gly*) mutant fails to make florets (a,c). SEM analysis of wild-type (d) and (at the same magnification) *gly* (e) revealed the presence of proliferating primordia in *gly* (e,f,g). This mutant reiterates glume primordia. The mutant is highly branched, indicating that the spikelet meristem produces axilliary meristems which also initiate further glume primorida and axilliary meristems. This mutant is therefore defective in spikelet meristem determinacy and the switch to floral meristem identity.





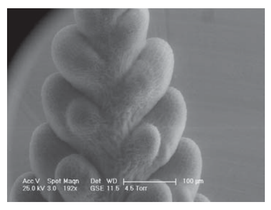






Future work

We have crossed heterozygotes of *gly* and *msp* to other barley varieties in order to map the mutant loci and have begun to characterize further inflorescence architecture mutants. In addition to conventional SEM, we have used environmental SEM to characterize our mutants and will examine the feasibility of using a CT scanner for imaging apices.



Acknowledgements

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