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Characterisation of inflorescence development in *Zea  
mays* with four developmental mutants

A thesis presented in partial fulfilment of the

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## Ad endum

P. 9 The beginning of section 1.3.3: "Floricaula" should be spelt "FLORICAULA"

P. 11 paragraph 3. The logic of the regulation 'AP1 and TFL1 negatively regulate FCA' contradicts previous statements, which suggest that FCA negatively regulates TFL and positively regulates AP1.

Page *et al.* (1999) State that:

- "Mutations involved in the *FCA* gene strongly delay the floral transition resulting in plants with much larger numbers of rosette leaves and cofilenceses".
- "Mutations in the *TFL1* gene result in the conversion of the indeterminate apical meristem into a determinate floral meristem (Shannon and Meeks and Wagner, 1991). They can also cause an acceleration in flowering time, the extent differing in different alleles (Alvarez *et al.*, 1992)
- "In the LD cabinet conditions, the *ap1-1* mutant flowered earlier and with fewer rosette leaves than the *Ler* parent (in agreement with (Schultz and Haughn, 1993)."

When *FCA* is combined in double mutants with *TFL1* and *AP1*:

- "the flowering time of the double mutants, *fca-1 tfl1-2* and *fca-4 tfl1-2* was later than the respective *fca* parents. Cofilenceses and cauline leaf number on the main inflorescence of the double mutants was similar to the *fca* parent. The number of floral nodes produced was less than the *fca* parent but >six fold greater than the *tfl1-2* mutant. Production of the terminal flower was suppressed in the double mutants but did occur eventually in all cases....The late flowering phenotype was epistatic to the early flowering conferred by the *tfl1* alleles and the formation of the terminal flower was significantly delayed."
- "the *fca-1 ap1-1* double mutant plants flowered at a similar time to the *fca-1* parent, with a similar number of rosette leaves, but the *fca-4 ap1-1* plants flowered considerably later than *fca-4*. The characteristic determinate branched flowers previously described for *ap1-1* mutations (Bowman *et al.*, 1993) were present and these formed a dense mass of floral-like structures at the inflorescence apex in the late flowering backgrounds.....In summary, all *fca* alleles enhanced the *ap1* inflorescence phenotype but did not significantly affect floral development in the *ap1* flowers. As *ap1-1* is a strong allele this suggests that *FCA* functions to promote the formation of flowers in pathways that act redundantly with *AP1*. the early flowering phenotype of *ap1-1* mutations indicates that *AP1* functions as a repressor of the floral transition and epistasis of the late flowering phenotype of *fca-1* over the early flowering of *ap1-1* suggests that it acts via inhibiting *FCA* function.

Furthermore Page *et al.* (1999) state:

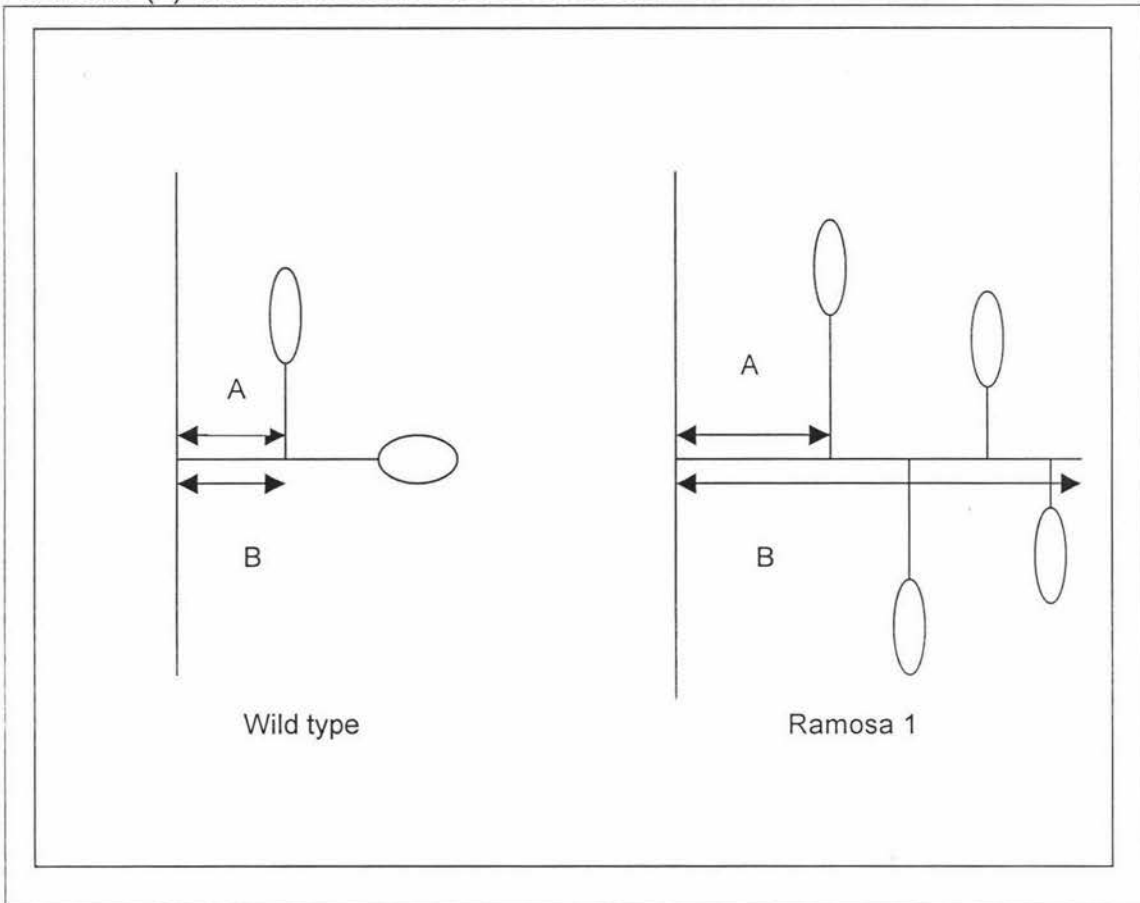
- "The results are consistent with *AP1* and *TFL1* negatively regulating *FCA* function..."

Therefore any suggestion that *FCA* negatively regulates *TFL* and positively regulates *AP1* is incorrect based on the double mutant analysis of Page *et al.* (1999) and any implications I have made should therefore be disregarded.

Evans (1940) should be Evans, M.W. and Grover, F.O. (1940)

P 33 and P34 the small unexplained numbers and octagons present in the figures are outliers with the number referring to the individual in that dataset which is the outlier.

P 41 Figure 3-19 refers to the distance from the central culm to the base of the first spikelet axis (A). Figure 3-20, however, refers to the distance from the central culm to tip of its axis (B) and was devised to show the indeterminate nature of this axis.



P 43 "wild type siblings" should be deleted from figure caption

P 67 The red in the pie charts is the mean percentage of the tassel that branched and the blue is the mean percentage of the tassel that is spikelet pairs.

P 73 The branches in fig. 3-51 and 3-52 are subtended by two glumes and arise in place of the upper floret with a single floret on the surface away from the cob. The branches produce two secondary structures similar to spikelet pairs along its flanks perpendicular to the axis of the inflorescence axis. These structures are most likely derived from the loss of determinacy of the spikelet meristem which then reverts to a developmental program similar to a branch meristem and produces spikelet pairs in an alternate phyllotaxy.

P 107 in response to the question whether the map location of the *ids1* mutant is known. The reference Chuck *et al.* (1998) did not give a map position nor did Neuffer *et al.* (1997). However, the Maize DB (<http://www.agron.missouri.edu/>) lists *ids1* locus as being on the long arm of chromosome 1 while *bd1* is located on chromosome 7 (Neuffer *et al.*, 1997).

A explanation on how to interpret boxplots has been included in Appendix1 on page 118

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## Abstract

The genetic control of inflorescence development has been studied in great detail in the model dicotyledonous plants *Arabidopsis thaliana* and *Antirrhinum majus*. In contrast, little is known about the genetic regulation in monocotyledonous species. Using maize (*Zea mays*) as a model system, the phenotypes were documented for the *branched silkless1* (*bd1*) and *ramosa* (*ra1*, *ra2*, and *ra3*) inflorescence mutants that are characterised by abnormally branched ears. A comparison of the adult morphology and developing inflorescences using scanning electron microscopy in mutant and normal maize reveals that there are at least five reproductive meristems that can be identified in maize: the inflorescence meristem, the branch meristem, the spikelet pair meristem, the spikelet meristem, and the floret meristem. The abnormal branching in *bd1* and the three-*ramosa* mutations is the result of the failure to determine the fate of specific types of reproductive meristems in both tassels and ears. Both *RA1* and *RA3* are required for the determination of spikelet pair development in branch primordia. *RA2* is necessary for determinate growth in spikelet pair meristems. *BD1* is required for determinate growth of spikelet meristems by specifying a determinate floral meristem identity. The classification of the different types of reproductive meristems and the genes that regulate their development is essential to understanding the genetic programs that underlie inflorescence morphogenesis in maize and other *Gramineae*.

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