



# THE HUNT FOR MODIFIERS OF THE *Tcb1* LOCUS

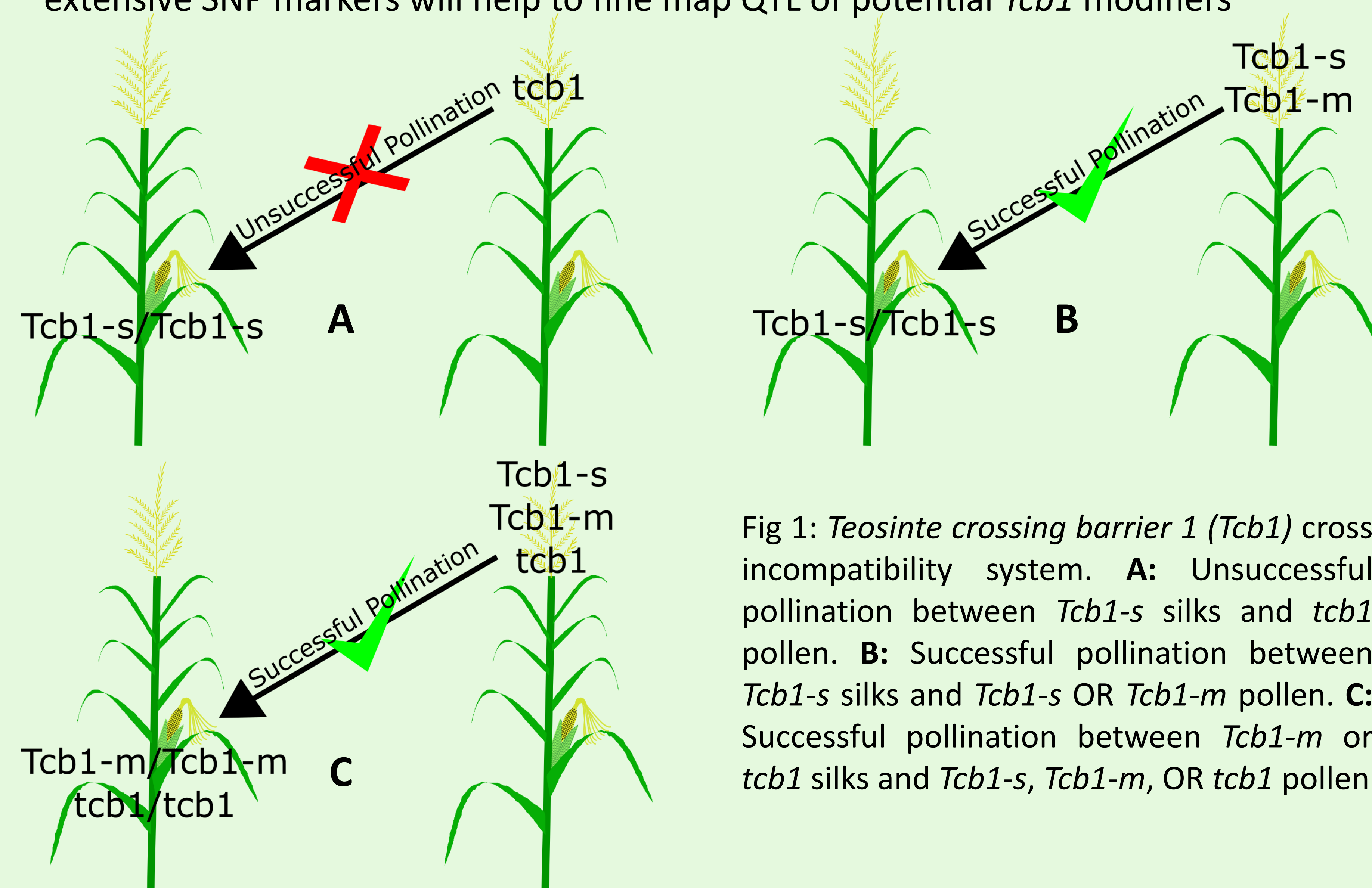
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## Introduction & Background

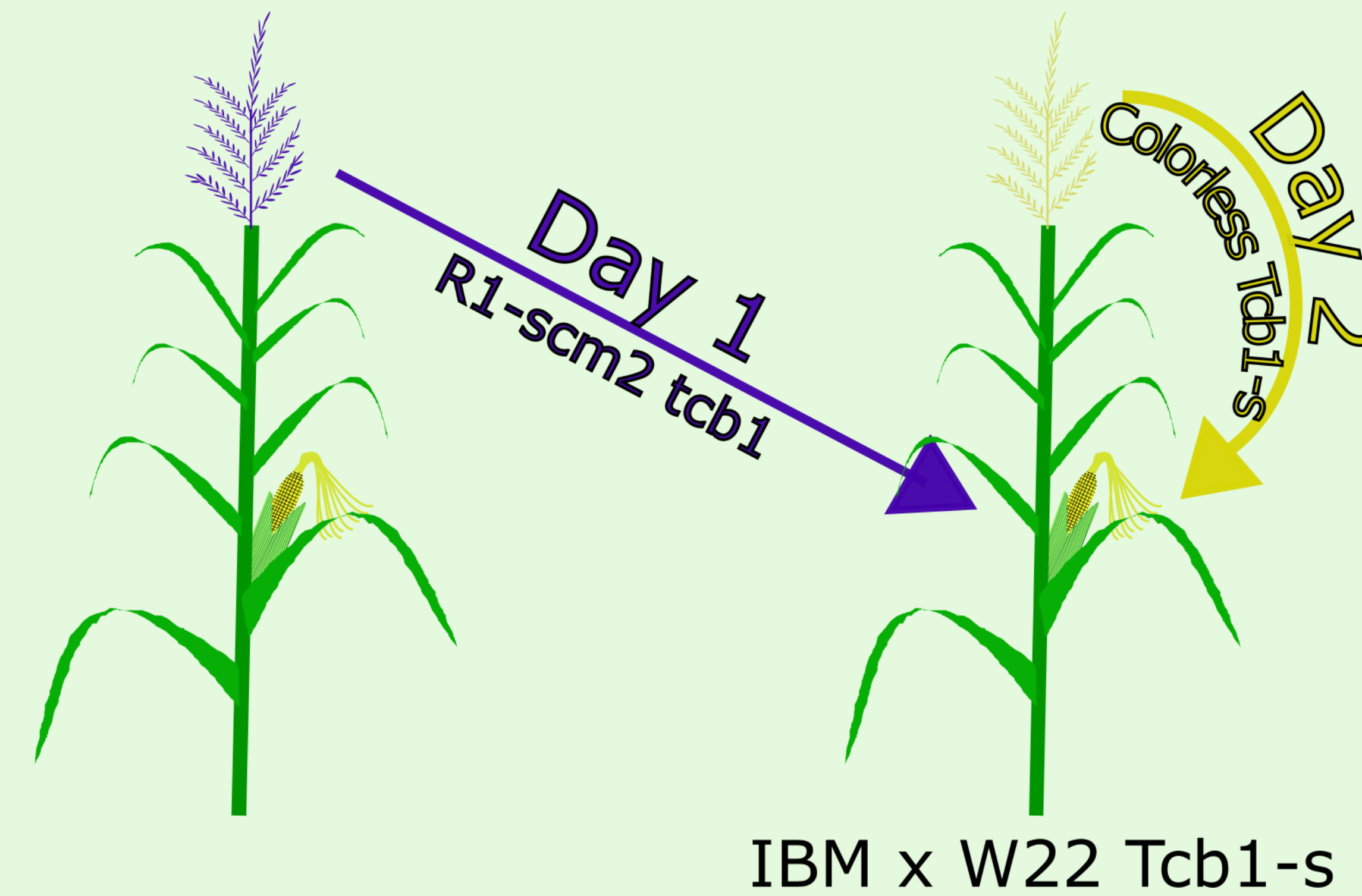
- Windborne contamination of organic maize by genetically modified pollen can decrease profits. Currently, farmers place barrier crops, separate fields, or displace planting times to prevent cross contamination
- An easier alternative would be to introgress one of three gametophyte cross incompatibility (CI) systems: *Gametophyte factor 1* (*Ga1*), *Gametophyte factor 2* (*Ga2*), or *Teosinte crossing barrier 1* (*Tcb1*)
- *Tcb1* was originally found in teosinte (*Zea mays* spp. *Mexicana*) and prevents fertilization from pollen with incompatible alleles (*tcb1*)
- *Tcb1* has three alleles: strong allele (-s), male allele (-m), and a null allele (**Fig 1**)
- F1's of many maize inbreds (e.g. B73) x W22 *Tcb1-s* show high incompatibility with *tcb1*; Mo17 x W22 *Tcb1-s* shows a weakened incompatibility
- Using an Intermated B73 x Mo17 (IBM) recombinant inbred line (RIL) containing extensive SNP markers will help to fine map QTL of potential *Tcb1* modifiers



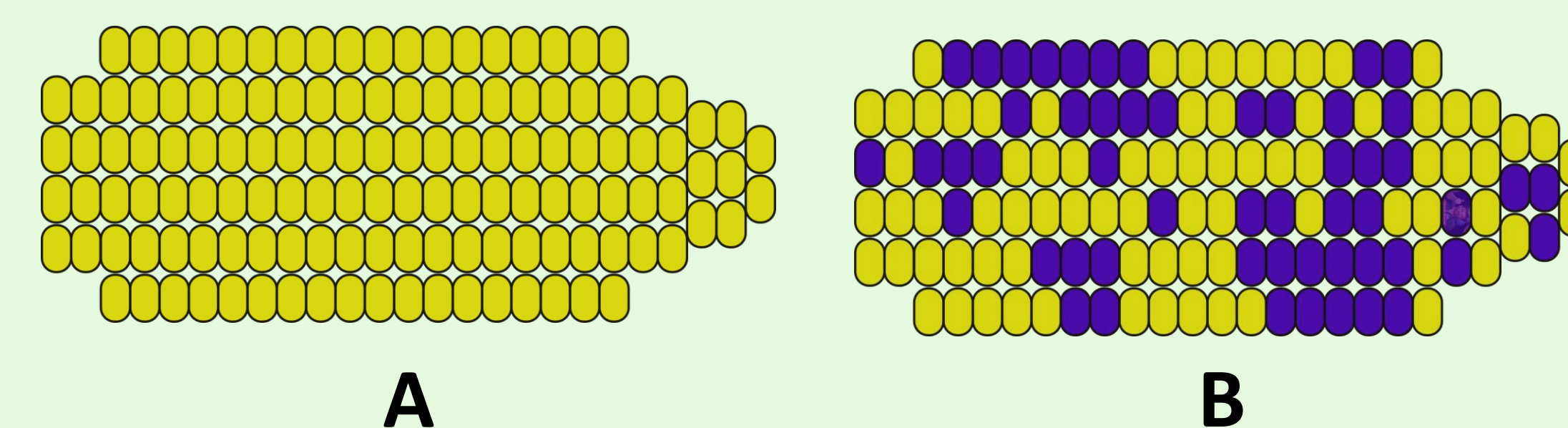
## Objectives

- Find QTL from *Tcb1* modifying loci
- From discovered QTL regions identify and isolate candidate genes
- Determine the molecular mechanism is for *Tcb1* cross incompatibility

## Materials and Methods



**Fig 2:** Pollination of IBM *Tcb1-s* silks with colored *R1-scm2 tcb1* pollen on day one (to test IBM x W22 *Tcb1-s* efficiency) and self-pollination with colorless *Tcb1-s* on day two



**Fig 3:** Predicted ear phenotypes of Fig 2 crosses. **A:** Strong effect of IBM x W22 *Tcb1-s* silks at rejecting colored *tcb1* pollen. **B:** Weak effect of IBM x W22 *Tcb1-s* silks at rejecting colored *tcb1* pollen

- Perform experiment in summer 2017 in Brookings, South Dakota
- Five plants from each IBM RIL will be crossed with *R1-scm2 tcb1* pollen and colorless self *Tcb1-s* pollen
- After harvest each RIL will be scored for the degree of *tcb1* contamination
- IBM contamination data will be associated with RIL markers to determine if QTL for *Tcb1* modifiers are present

## Expected Results

- Find QTL that cause *tcb1* to have lower efficacy in Mo17 F1s and identify those regions of the maize genome that support *tcb1* activity

## Future Work

- Isolate and sequence candidate genes to shed light on *Tcb1* incompatibility
- Quantify pollen tube growth in compatible and incompatible silks

## Acknowledgements & References



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