Mapping loci that modify the efficacy of *Teosinte crossing barrier 1*

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*Teosinte crossing barrier 1* (*Tcb1*) is a genetic cross-incompatibility factor that is responsible for blocking non-self-type pollen in silks. Originally found in teosintes, *Tcb1-s* (*strong allele*) has been introduced into modern maize varieties conferring resistance to *tcb1* pollen. Previous studies using a similar cross incompatibility system, *Gametophye factor 1* (*Ga1-s*) suggest that the cell wall modification enzyme *ZmPme3*, a pectin methylesterase, along with multiple modifying QTL loci contribute to the effectiveness of silks at resisting foreign pollen types. In *Tcb1,* little is known about the genetic modifiers and, more importantly, what the underlying biological mechanism is for this cross incompatibility. Cross-incompatibility systems like *Tcb1* and *Ga1* can be beneficial to breeders and farmers when only certain pollen types are desired on specialty maize crops. It was observed that nearly all the F1's of various inbreds, including B73, crossed by W22 *Tcb1-s* demonstrate strong incompatibility with *tcb1* pollen. One exception was Mo17, whose F1s had weaker resistance. In this study we used recombinant inbred lines (RILS) from the intermated B73-Mo17 (IBM) population crossed with homozygous W22 *Tcb1-s* plants to test the efficacy of the various F1s at blocking *tcb1* pollen. The F1s were tested by first challenging the *Tcb1-s* silks with *R1 C1 tcb1* pollen and the next day pollinated the same silks with *r1 c1* *Tcb1-s* pollen. The resulting ears were scored for the percentage of colored kernels. Six quantitative trait loci (QTL) were detected on chromosomes 1, 3, 5, and 7 that explained 28.9% of the phenotypic variability. Most modifying QTL loci showed simple additivity effects and epistatic interactions between loci. Further exploration into these genomic regions and the underlying candidate genes is underway, these results could shed light on the genetic and physiological mechanisms controlling *Tcb1.*

A row of trees in the background

Description generated with high confidenceA close up of a map

Description generated with high confidence

> summary(out.fq)

fitqtl summary

Method: Haley-Knott regression

Model: normal phenotype

Number of observations : 77

Full model result

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Model formula: y ~ Q1 + Q2 + Q3 + Q4 + Q5 + Q6

df SS MS LOD %var Pvalue(Chi2) Pvalue(F)

Model 6 14.06081 2.343469 9.359507 42.86583 1.113397e-07 4.084648e-07

Error 70 18.74110 0.267730

Total 76 32.80192

Drop one QTL at a time ANOVA table:

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df Type III SS LOD %var F value Pvalue(Chi2) Pvalue(F)

1@28.0 1 2.0279 1.7179 6.182 7.575 0.005 0.00753 \*\*

1@324.0 1 0.4868 0.4288 1.484 1.818 0.160 0.18186

3@21.0 1 1.2024 1.0397 3.666 4.491 0.029 0.03762 \*

3@107.0 1 1.9384 1.6456 5.909 7.240 0.006 0.00891 \*\*

5@426.0 1 1.2296 1.0626 3.749 4.593 0.027 0.03558 \*

7@4.0 1 2.5974 2.1702 7.918 9.702 0.002 0.00267 \*\*

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1