**Table S3. Segregation ratio of male sterility in Progeny test B**

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| --- | --- | --- | --- |
| Inheritance model | No. of combination  | Genotype of ms plant and restorer line | Progeny test B |
| ms plant genotype from Test cross A | maintainer line genotype | progeny phenotype (mf:ms ratio) | Test result (All progeny lines) |
| 1 gene with multiple alleles  | 1 | *BrMsbMsb* × *BrMsaMsa* | *BrMsbMsb* | *BrMscMsc* | no segregate (0:1) | All lines ms |
| 2 dominant genes  | 2 | *BrMsMs rfrf* × *BrMsMs RfRf* | *BrMsMs rfrf* | *Brmsms rfrf* | no segregate (0:1) | All lines ms |
| 2 dominant genes  | 3 | *BrMsMs rfrf* × *BrMsms RfRf* | *BrMsMs rfrf*  | *Brmsms rfrf* | no segregate (0:1) | Partial lines segregated |
|  |  |  | *BrMsms rfrf*  | *Brmsms rfrf* | segregate (1:1) |  |
| 2 dominant genes  | 4 | *BrMsMs rfrf* × *Brmsms RfRf* | *BrMsMs rfrf*  | *Brmsms rfrf* | no segregate (0:1) | Partial lines segregated |
|  |  |  | *BrMsms rfrf*  | *Brmsms rfrf* | segregate (1:1) |  |
| 1 gene with multiple alleles  | 5 | *BrMsbMsc* × *BrMsaMsa* | *BrMsbMsb* | *BrMscMsc* | no segregate (0:1) | All lines ms |
| 2 dominant genes  | 6 | *BrMsms rfrf* × *BrMsMs RfRf* | *BrMsMs rfrf* | *Brmsms rfrf* | no segregate (0:1) | Partial lines segregated |
|  |  |  | *BrMsms rfrf*  | *Brmsms rfrf* | segregate (1:1) |  |
| 2 dominant genes  | 7 | *BrMsms rfrf* × *BrMsms RfRf* | *BrMsMs rfrf* | *Brmsms rfrf* | no segregate (0:1) | Partial lines segregated |
|  |  |  | *BrMsms rfrf* | *Brmsms rfrf* | segregate (1:1) |  |
| 2 dominant genes  | 8 | *BrMsms rfrf* × *Brmsms RfRf* | *BrMsMs rfrf* | *Brmsms rfrf* | no segregate (0:1) | Partial lines segregated |
|  |  |  | *BrMsms rfrf* | *Brmsms rfrf* | segregate (1:1) |  |