**Table S4. Segregation ratio of male sterility in Progeny test C**

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| --- | --- | --- | --- |
| Inheritance model | No. of combination  | Genotype of maintainer line and restorer line | Progeny test C |
| F1 genotype | F2 phenotype (mf:ms ratio) | Test result (All F2 lines) |
| 1 gene with multiple alleles  | 1 | *BrMscMsc* × *BrMsaMsa*  | *BrMsaMsc* | no segregate (1:0) | All lines mf |
| 2 dominant genes  | 2 | *Brmsms rfrf* × *BrMsMs RfRf* | *BrMsms Rfrf* | segregate (13:3) | All lines segregated |
| 2 dominant genes  | 3 | *Brmsms rfrf* × *BrMsms RfRf* | *BrMsms Rfrf*  | segregate (13:3) | Partial lines segregated |
|  |  |  | *Brmsms rfrf* | no segregate (1:0) |  |
| 2 dominant genes  | 4 | *Brmsms rfrf* × *Brmsms RfRf* | *Brmsms Rfrf* | no segregate (1:0) | All lines mf |
| 1 gene with multiple alleles  | 5 | *BrMscMsc* × *BrMsaMsa*  | *BrMsaMsc* | no segregate (1:0) | All lines mf |
| 2 dominant genes  | 6 | *Brmsms rfrf* × *BrMsMs RfRf* | *BrMsms Rfrf* | segregate (13:3) | All lines segregated |
| 2 dominant genes  | 7 | *Brmsms rfrf* × *BrMsms RfRf* | *BrMsms Rfrf*  | segregate (13:3) | Partial lines segregated |
|  |  |  | *Brmsms rfrf* | no segregate (1:0) |  |
| 2 dominant genes  | 8 | *Brmsms rfrf* × *Brmsms RfRf* | *Brmsms Rfrf* | no segregate (1:0) | All lines mf |