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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| 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 |