**Table S2. Segregation ratio of male sterility in Progeny test A**

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