**Supplementary Table 1** Number of plants tested with markers to identify recombination events in the *Rag6* and *Rag3c* intervals each generation and the number of plants selected

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | *Rag6* | |  | |  | |  | | *Rag3c* | |  | | |
| Gen | Tested plantsa | | Flanking markers | | Selected plantsb | |  | | Tested plantsa | | Flanking markers | | Selected plantsb |
| F2 | 1161c | | Gm08-3, Gm08-28 | | 58/9 | |  | | 1161c | | Gm16-1, Gm16-9 | | 36/13 |
| F3 | 1533 | | Gm08-11, Gm08-27 | | 124/80 | |  | | 946 | | Gm16-1, Gm16-8 | | 18/75 |
| F4 | 1780 | | Gm08-12, Gm08-26 | | 21/10 | |  | | 797 | | Gm16-2, Gm16-7 | | 25/5 |
| F5 | 1277 | | Gm08-12, Gm08-25 | | 44/159 | |  | | 673 | | Gm16-2, Gm16-6 | | 96/67 |
| F6 | 1570 | | Gm08-12, Gm08-24 | | 111/156 | |  | | 1140 | | Gm16-2, Gm16-5 | | 89/58 |
| F7 | 2522 | | Gm08-14, Gm08-21 | | 93/55 | |  | | 1388 | | Gm16-2, Gm16-5 | | 76/9 |
| F8 | 1428 | | Gm08-14, Gm08-19 | | 72/81 | |  | | 694 | | Gm16-3, Gm16-5 | | 76/6 |
| F9 | 1209 | | Gm08-14, Gm08-17 | | 115/34 | |  | | 708 | | Gm16-3, Gm16-5 | | 92/23 |
| F10 | 1295 | | Gm08-15, Gm08-16 | | 1 | |  | | 911 | | Gm16-3, Gm16-5 | | - |

a At higher generations, among the tested plants, many of them shared pedigree because they were derived from same heterozygous recombinants. Additionally, some of the tested plants were recombinants that were carried over from the previous season to confirm their phenotype and genotype

b Selected plants included recombinants and heterozygotes, indicated by recombinants/heterozygotes. Some recombinant selections were carried over to the following seasons to confirm their phenotype and genotype

c Recombinants screening for *Rag6* and *Rag3c* started with 1161 F2 plants. Starting with the F3 generation, screening for recombinants of *Rag6* and *Rag3c* were separated as no interaction had been detected between *Rag6* and *Rag3c*

**Supplementary Table 2** Effectiveness of flanking markers in assisting selection for *Rag6* and *Rag3c* in breeding population 130103 and 130170

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Pop | Genotype | No. of lines | Flanking markersa | | | | | Mean | | Standard error |
|  |  |  | *Rag6* | |  | *Rag3c* | |  |  | |
|  |  |  | Gm08-15 | Gm08-17 |  | Gm16-2 | Gm16-5 |  |  | |
| 130103 | -/- | 21 | - | - |  | - | - | 2.98 | 0.12 | |
|  | -/*Rag3c* | 15 | - | - |  | + | + | 2.25 | 0.15 | |
|  | *Rag6/-* | 18 | + | + |  | - | - | 1.75 | 0.13 | |
|  | *Rag6/Rag3c* | 27 | + | + |  | + | + | 1.17 | 0.11 | |
| 130170 | -/- | 59 | - | - |  | - | - | 3.01 | 0.08 | |
|  | -/*Rag3c* | 68 | - | - |  | + | + | 1.94 | 0.07 | |
|  | *Rag6/-* | 64 | + | + |  | - | - | 1.58 | 0.08 | |
|  | *Rag6/Rag3c* | 56 | + | + |  | + | + | 0.79 | 0.08 | |

a + Implies allele from E12901; - Implies allele from the susceptible parent