Four-point linkage data for *ae1 yg3 pr1 gl8* on 5L.

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Yg*-N1582 is a dominant yellow-green seedling and mature plant mutant with good expression as a heterozygote, and good viability as a homozygote. It is of particular interest due to its potential use as a marker in haploid inducer lines (Sachs, M; Stinard, PS. 2013. MNL 86:28). *Yg*-N1582* was physically mapped to an interval (173-175Mb (AGPv3)) between *ae1* and *pr1* on chromosome 5, and GRMZM2G165521 was proposed as a potential gene candidate (Sorgini, CA. 2018. Utilizing maize genomics for pre-breeding insights. Ph.D. dissertation, University of Illinois). Due to its distinct location and the lack of mutants with similar phenotype in the vicinity of that location, the locus of *Yg*-N1582* was assigned the gene symbol *yg3* (*yellow-green3*), and the variation was renamed *Yg3-N1582*. In order to confirm the physical location of *yg3* between *ae1* and *pr1*, a classical test of linkage was performed. The results of a four-point linkage test for *ae1, yg3, pr1*, and *gl8* on chromosome 5 are presented in Table 1. The linkage test was set up as a backcross as indicated in Table 1. Kernels from the backcross ears were visually scored for *ae1* and *pr1*, planted separately in the sand bench based on kernel phenotype, and the resulting seedlings scored for *yg3* and *gl8*. The following linkage relationship was established (distances expressed in centiMorgans): *ae1* - 3.9 - *yg3* - 2.1 - *pr1* - 0.7 - *gl8*. These data are consistent with previously reported linkage data for *ae1*, *pr1*, and *gl8*, and confirm the placement of *yg3* between *ae1* and *pr1*.

Table 1. Four-point linkage data for *ae1 - yg3 - pr1 - gl8*.

Testcross: [+ *Yg3-N1582* + + X *ae1* + *pr1 gl8*] X *ae1* + *pr1 gl8*.

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Reg.         Phenotype                    No.      Totals

0            +   Yg3 +   +            2756
             ae1 +   pr1 gl8          2733        5489

1            +   +   pr1 gl8           122
             ae1 Yg3 +   +             105         227

2            +   Yg3 pr1 gl8            59
             ae1 +   +   +             62         121

3            +   Yg3 +   gl8            22
             ae1 +   pr1 +             21          43

1+2          +   +   +   +              1
             ae1 Yg3 pr1 gl8            0           1

2+3          +   Yg3 pr1 +              1
             ae1 +   +   gl8            0           1

1+3          +   +   pr1 +              0
             ae1 Yg3 +   gl8            0           0

1+2+3        +   +   +   gl8            0
             ae1 Yg3 pr1 +             0           0

Total                                           5882
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% recombination *ae1 - yg3* = 3.9 $\pm$ 0.3
% recombination *yg3 - pr1* = 2.1 $\pm$ 0.2
% recombination *pr1 - gl8* = 0.7 $\pm$ 0.1