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Placement of the *lw5 lw6* duplicate factor loci to chromosome arm.

--Stinard, PS

The EMS-induced lemon white mutant *w*-N176* was recently characterized as being due to a duplicate factor pair *lw5-N176A* and *lw6-N176B* (Stinard, P. 2013. MNL 86:32). Because we were able to putatively associate all other known lemon white loci with gene models in the DOXP/MEP isoprenoid biosynthetic pathway except for CDP-ME synthase (ISPD) (Stinard, P. 2013. MNL 86:29-31), we hypothesized that the *lw5 lw6* duplicate factor loci correspond to the two gene models in maize encoding CDP-ME synthase: GRMZM5G856881 and GRMZM2G172032 on 3L and 8L respectively. We isolated separate lines homozygous mutant for one factor and homozygous nonmutant for the other factor (*i. e. lw5-N176A Lw6* and *Lw5 lw6-N176B*) in order to determine whether *lw5* and *lw6* map to these chromosome arms using B-A translocations.

A method for mapping duplicate factor pairs using B-A translocations is described by Stinard (1991. MNL 65:17). In this technique, two single factor lines are crossed to B-A translocation stocks, and the resulting F1 lines that are heterozygous for the B-A translocation and one of the factors, and homozygous nonmutant for the other factor, are crossed onto lines segregating for both mutant factors. If the F1 B-A translocation line uncovers the mutant phenotype in the resulting cross, then the factor that is homozygous nonmutant in the F1 B-A translocation line must be located on the chromosome arm involved in the B-A translocation.

Using this approach, we were able to confirm that *lw5* maps to chromosome arm 3L (three arm-locating crosses), and that *lw6* maps to chromosome arm 8L (three arm-locating crosses), as predicted. These map locations do not definitively associate *lw5* and *lw6* with the two predicted gene models for CDP-ME synthase located on these same chromosome arms, but they are consistent with the hypothesis outlined by Stinard (2013. MNL 86:29-31).