

New *nana plant1* (*nal*) alleleBest NB<sup>1</sup>, Hartwig T<sup>1B</sup>, Budka JS<sup>1</sup>, Schulz B<sup>1A</sup>, Weil C<sup>2</sup>, and Dilkes BP<sup>3</sup><sup>1</sup> Department of Horticulture & Landscape Architecture; Purdue University; West Lafayette, IN<sup>2</sup> Department of Agronomy; Purdue University; West Lafayette, IN<sup>3</sup> Department of Biochemistry, Purdue University; West Lafayette, IN<sup>A</sup> current address Plant Science and Landscape Architecture; University of Maryland; College Park, MD<sup>B</sup> current address Department of Biology; Carnegie Institution for Science; Stanford, CA

The maize gene *nana plant1* encodes a 5 $\alpha$ -steroid reductase, orthologous to the *Det2* gene of Arabidopsis, involved in brassinosteroid biosynthesis [1]. We screened the Maize TILLING Population (W22 background) in Summer 2010 and identified a mutant with the *nana plant* phenotype in line 04INW22CW0376. This row was segregating for wild type and *nana* consistent with a 3:1 segregation ratio although too few plants were available for chi-squared testing. Since there were phenotypic similarities between *nal* and our mutant (04INW22CW03763), we performed an allelism test crossing a plant homozygous for *nal-4* with heterozygous plants from 04INW22CW03763. A total of 333 individuals from 5 independent crosses were planted in the greenhouse and visually phenotyped for plant height (Figure 1). All families segregated for mutant *nal* and wild-type phenotypes indicating a failure to complement *nal-4* (Table 1). The segregation ratio was close to 1:1 and failed a chi-squared test for goodness of fit when all data were summed due to an underrepresentation of the mutant class (Table 1). This is consistent with our previous observations in which the homozygous recessive class either failed to germinate or establish as seedlings, resulting in too few mutants in field plots (unpublished). Failure of 04INW22CW03763 to complement *nal-4* indicates that 04INW22CW03763 contains a new allele of *nal*, which we refer to as *nal-5*. The phenotype of this allele is similar to the other *nal* alleles and causes severe dwarfism and a tasselseed phenotype; however, the molecular nature of the *nal-5* allele is currently unknown. An isogenic W22 lineage containing this allele is available. In addition, the original line may be available from the Maize TILLING collection [2].

**Table 1.** Allelism test results from 5 independent crosses of *nal-5/+* maternal plants with *nal-4/nal-4* paternal plants.

Cross	WT	<i>nal</i>	TOTAL	$\chi^2$ p-value
1	33	30	63	0.7046
2	40	24	64	0.0455
3	35	32	67	0.7140
4	44	24	68	0.0153
5	37	34	71	0.7218
TOTAL	189	144	333	<b>0.0137</b>

**Figure 1.** From left to right: WT, *nal-4/nal-4*, and *nal-5/nal-4* 14 d old seedlings grown in the greenhouse.



References:

[1] Hartwig T, Chuck GS, Fujioka S, Klempien A, Weizbauer R, Potluri DPV, Choe S, Johal GS, Schulz B (2011) Brassinosteroid control of sex determination in maize. PNAS 108: 19814-19819.

[2] Weil CF, Monde RA (2009) EMS mutagenesis and point mutation discovery. In: Kritz AL, Larkins BA (eds.) Molecular Genetic Approaches to Maize Improvement. Biotechnology in Agriculture and Forestry 63: 161-171.