A laboratory and field survey of leaf feeding resistance in diverse maize inbred lines

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Using a common garden plot in Northern Florida (Mission Road Field, FSU) that was established for an unrelated genetic study, we assessed natural levels of insect damage exhibited by a highly diverse population of inbred maize lines (Liu et al., Genetics 165:2117, 2003). The field contained families for seed propagation from two sets of maize diversity lines developed by E. S. Buckler, J. Holland, M. McMullen and Goodman. The two sets of lines grown in 2008 are referred to by us as the “MDS” set (260 of the 283 lines from Order 185771, Feb 2007) and the “DL25” set (25 of the 26 lines from Order 179535, Apr 2006) originally provided by the USDA, ARS, NCRPIS, ISU, Ames, IA. The MDS lines were planted in families of 16, 12, or 8 plants each and the DL25 lines were planted in two different locations within the same field in families of 24 or 14 plants each.

Cursory inspection of insect damage prior to pesticide treatment revealed potential line-dependent variation in herbivory damage, primarily from lepidoptera exposure. To investigate the possible genotypic basis for this observed variation, we measured field damage in the DL25 and MDS lines and carried out laboratory bioassays on a selected subset of them. The DL25 lines, plus a common-parent, B73, have been used to develop a nested association mapping (NAM) population (Yu et al., Genetics 178:539). A general objective of the study described here was to determine which lines and corresponding NAM recombinant inbred lines might be useful for subsequent genetic analyses of complex quantitative traits related to maize-lepidoptera interactions.

Data was collected from our DL25 set, B73, B97, CM103, CML228, CML247, CML277, CML322, CML333, CML52, HP301, It14H, Ki11, K3, Ky21, M162W, M37W, Mo17, Mo18W, Ms71, NC350, NC358, On43, Oh7B, P39G-B, Tx303, and Tzi 8. Insect surveys revealed that the damage present on plants in our plot was caused primarily by two species of caterpillars, Spodoptera frugiperda (J. E. Smith), the fall armyworm, and Spodoptera ornithogalli (Guenée), the yellowstriped armyworm. The amount of damage sustained by plants was quantified using a rating scale of 0-4, with larger ratings indicating that damage was present on a greater proportion of leaves from an individual plant.

Leaf damage varied significantly among lines according to analysis of covariance as shown in Figure 1 (F=5.48, df=25, P<0.001; using MIXED procedure; SAS version 9.2; SAS Institute, 2008). Additionally, planned contrasts found that five lines were significantly more damaged and five were significantly less damaged compared to the population average (Fig. 1). A spatial covariance matrix was incorporated into the ANCOVA to account for autocorrelation because, within each of the two blocks in the plot, all individuals of a maize line were planted in “family groupings” located along contiguous stretches within rows.

Induced and constitutive antibiosis resistance laboratory phenotype data was collected from herbivore growth rate bioassays for nine (B73, CML52, HP301, IL14H, KY21, M162W, M37W, NC350, Tzi 8) of the 26 maize lines present in the field plot, plus

\[ \text{Figure 2. Constitutive antibiosis resistance, assayed by relative growth rates (ln(final mass) – ln(initial mass)) of fall armyworm caterpillars (±SE) fed leaves from different greenhouse-lab grown maize lines. Faster growth rates denote less resistance. Each caterpillar was allowed to feed on the newest expanded leaf of a plant (excised) for 48 h in a no-choice situation. Plants had been grown in a greenhouse under standard conditions and were stage V4 (4 leaf-collar stage). Means represent least squares means produced from an ANOVA model incorporating a main effect of line. Significant differences were found between NC350 and four lines (B73, CML52, IL14H, M37W) when p-values of multiple comparisons were adjusted with a Bonferroni correction. Average sample size was 39.9.} \]

Sorghum bicolor and teosinte (Balsas, Zea mays ssp. parviglumis). The subset of nine from the DL25 lines was chosen in order to encompass as much phenotypic and genetic variation as possible, using our field damage estimates and knowledge of phylogenetic relationships. Second instar fall armyworm caterpillars were fed foliage from herbivore-damaged or undamaged plants (V4/4-leaf-collar stage) grown under greenhouse conditions, and their weight gain over a 48-hour period was measured. An ANOVA on caterpillar growth rates revealed significant variation in constitutive resistance among the lines, as shown in Figure 2 (Main effect of line: F=2.74, df=10, P=0.0028), but provided no obvious evidence of induced resistance (Main effect of leaf damage: F=0.09, df=1, P=0.76; Damage x Line interaction F=1.21, df=10,P=0.33). According to multiple comparisons, caterpillars grew significantly slower when fed NC350, compared to all other lines except Tzi 8. Four of these differences remained significant after a highly conservative Bonferroni p-value correction (Fig. 2). Furthermore,
levels of constitutive resistance in the laboratory were significantly related to the amount of damage that was sustained by lines in the field, as shown in Figure 3 (Likelihood ratio test: deviance=1.267, df=7, P=0.033).

The concordance between the patterns of resistance observed in the field versus laboratory suggests that constitutive resistance expressed by the lines is important for deterring leaf damage. To the extent that this relationship holds up, these types of herbivore growth rate bioassays may provide an efficient method to pre-screen germplasm for resistance prior to more extensive field trials. Despite the fact that our observations of damage in the field were predicted by laboratory measures of resistance, follow-up studies will still be needed in order to confirm whether levels of resistance in these lines are stably expressed across seasons, locations, and developmental stages. This study confirms our suspicion that these maize diversity lines could be used to learn more about the genetic basis of herbivore resistance and the effect of genetic variation in plant defense on ecological dynamics.

New alleles of chlorophyll111 found in lemon white endosperm stocks in the Maize COOP phenotype-only collection

--Jackson, JD

This report summarizes allele testing of lemon-white endosperm stocks characterized only by phenotype in the Maize Genetics COOP Stock Center collection. Here pale kernels linked to pale-green or albino seedlings characterized all stocks. Many had previously given negative results in tests with w3 and y9. The cl1 Clm1-3 stock used in crosses here carries a dominant modifier of cl1 that allows for viable green plants, making crosses with a homozygous stock possible. Crosses were made as follows: [+/lw+] @ X cl1 Clm1-3 or +/+/lw* X cl1 Clm1-3. Ears were scored for the segregation of pale yellow kernels.

New designations have been assigned to these alleles and they have been placed in the main collection. Stocks with this same phenotype that were found to complement cl1 Clm3 will be tested for allelism with other stocks linked to pale endosperm.

New alleles of white3 found in viviparous stocks in the Maize COOP phenotype only collection

--Jackson, JD

This report summarizes allele testing of various viviparous and lemon-white endosperm stocks characterized only by phenotype in the Maize Genetics COOP Stock Center collection. Here pale kernels linked to pale or albino seedlings characterized all stocks. Many had previously given negative results in tests with vp9 and y9. The w3-y11 stock used in crosses here is homozygous viable. Crosses were made as follows: [+/vp+] @ X w3-y11 and +/+/vp* X w3-y11. Ears were scored for the segregation of pale yellow kernels. In most cases, pale-yellow kernels were selected from positive allele test ears and planted in the field for observation.