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Genetic control of stomatal conductance in maize and conditional effects to water deficit and evaporative demand as revealed by phenomics

(submitted by Santiago Alvarez Prado <santiago.alvarez-prado@inra.fr>)

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Plants tend to decrease transpiration under water deficit and/or high evaporative demand by closing stomata. Stomatal conductance is central for the trades-off between hydraulics and photosynthesis. We aimed at deciphering its genetic control and that of its responses to evaporative demand and water deficit, a nearly impossible task with gas exchanges measurements. Whole-plant stomatal conductance was estimated via inversion of the Penman–Monteith equation from data of transpiration and plant architecture collected in a phenotyping platform. We have analyzed jointly 4 experiments with contrasting environmental conditions imposed to a panel of 254 maize hybrids. Estimated whole-plant stomatal conductance closely correlated with gas-exchange measurements and biomass accumulation rate. Sixteen robust quantitative trait loci (QTLs) were identified by genome wide association studies and co-located with QTLs of transpiration and biomass. They accounted for 58% of the additive genetic variance and 40% of the genotype × environment interaction. Light, vapour pressure deficit (VPD), or soil water potential largely accounted for the differences in allelic effects between experiments, thereby providing strong hypotheses for mechanisms of stomatal control and explaining part of the observed genotype × environment interaction. Light positively affected the allelic effects of three QTLs (e.g. $R^2 = 0.74$), whereas VPD and water deficit negatively affected the allelic effects of other four QTLs. The combination of SNP effects, as affected by environmental conditions, accounted for the variability of stomatal conductance across a range of hybrids and environmental conditions ($R^2 = 0.86$). This approach may therefore contribute prediction of stomatal control in diverse environments and to breeding for water efficient maize.

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Genetic mechanisms for bud suppression during maize domestication

(submitted by Dong Zhaobin <dongz@berkeley.edu>)

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Many domesticated crop plants have been bred for reduced axillary branching compared to their wild ancestors. In maize this has been achieved through selection for gain of function alleles of the TCP transcription factor teosinte branched1 (tb1) nearly ten thousand years ago. Despite its importance, the precise genetic mechanism for how tb1 was able to achieve bud suppression is unknown. By raising an antibody to TB1 and performing chromatin immunoprecipitation and high through-put sequencing (ChIP seq) on very young axillary bud tissue, we identified the genetic pathways necessary for TB1 function. For example, TB1 targets several hormone pathways to effect axillary bud suppression, including auxins and gibberellins, but also targets genes controlling sugar metabolism whose products are necessary to feed the growing bud. Interestingly, TB1 also targets several previously described genes in the domestication pathway including teosinte glume architecture1 (tga1) and grassy tillers1 (gt1). This fact places tb1 near the top of the domestication hierarchy, demonstrating the critical importance of this gene during the domestication of maize from teosinte.

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