

Amino Acid Responses of Wheat Cultivars under Glasshouse Drought Accurately Predict Yield-Based Drought Tolerance in the Field

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Abstract : Water limits crop productivity, so selecting for minimal yield-gap in drier environments is critical to mitigate against climate change and land-use pressures. To date, no markers measured in glasshouses have been reported to predict field-based drought tolerance. In the field, the best measure of drought tolerance is yield-gap; but this requires multisite trials that are an order of magnitude more resource intensive and can be impacted by weather variation. We investigated the responses of relative water content (RWC), stomatal conductance (gs), chlorophyll content and metabolites in flag leaves of commercial wheat (*Triticum aestivum* L.) cultivars to three drought treatments in the glasshouse and field environments. We observed strong genetic associations between glasshouse-based RWC, metabolites and Yield gap-based Drought Tolerance (YDT): the ratio of yield in water-limited versus well-watered conditions across 24 field environments spanning sites and seasons. Critically, RWC response to glasshouse drought was strongly associated with both YDT ($r^2 = 0.85$, $p < 8E-6$) and RWC under field drought ($r^2 = 0.77$, $p < 0.05$). Multiple regression analyses revealed that 98% of genetic YDT variance was explained by drought responses of four metabolites: serine, asparagine, methionine and lysine ($R^2 = 0.98$; $p < 0.01$). Fitted coefficients suggested that, for given levels of serine and asparagine, stronger methionine and lysine accumulation was associated with higher YDT. Collectively, our results demonstrate that high-throughput, targeted metabolic phenotyping of glasshouse-grown plants may be an effective tool for the selection of wheat cultivars with high YDT in the field.

Keywords : drought stress, grain yield, metabolomics, stomatal conductance, wheat

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