Supporting Information

for "*Diversity in stomatal and hydraulic responses to post-flowering drought in common (Phaseolus vulgaris) and tepary (P. acutifolius) beans*"

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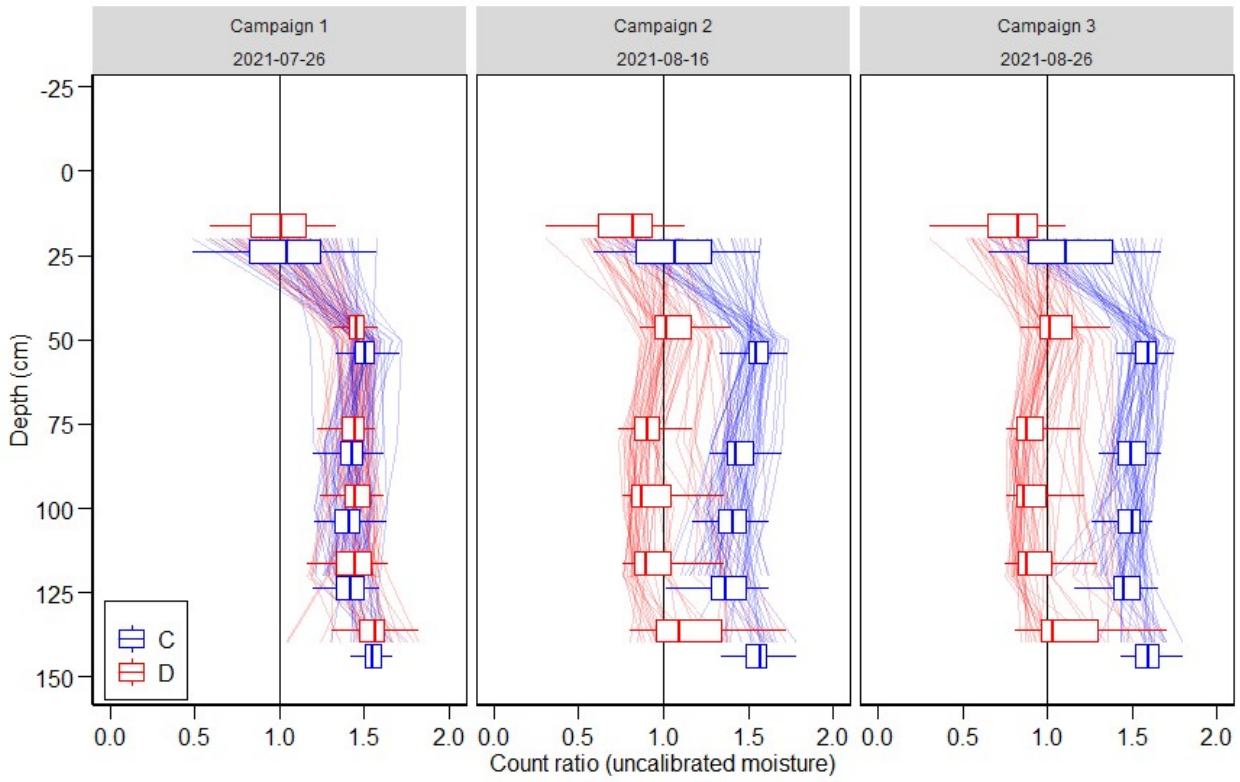

Figure S1. Cessation of irrigation in the drought treatment (D, red) caused significant reduction of soil moisture, compared to the control treatment (C, blue), at all soil depths below 25 cm. Measurements were made using a neutron backscatter detector moisture probe and are presented as count ratios. Irrigation was stopped in the drought treatment after Campaign 1. Individual lines represent plots (three per genotype). Results did not differ significantly among genotypes (not shown).

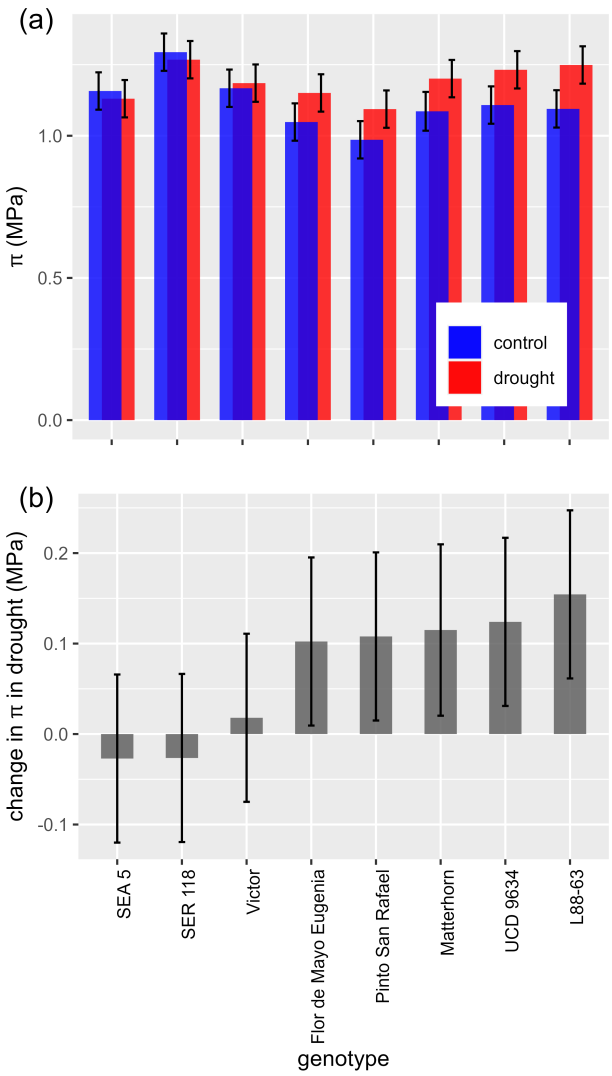

Figure S2. Osmotic pressure at full turgor (a), and its change under post-flowering drought (b), in the eight parents of the MAGIC population used in this study. These measurements were conducted in a second field trial, in 2022, whereas all other measurements reported in this study were conducted in 2021.

Methods S1. Details of field experimental configuration

The present study was part of a larger project to explore drought resilience of yield across the MAGIC population and in 20 tepary bean genotypes; thus, the 16 genotypes examined in detail herein were among 320 genotypes planted together in the field. On 04 June 2021, we planted all 320 genotypes at the Plant Sciences Field Facility at UC Davis in Davis, CA (38.534^{o}N, 121.775^{o}W), in planting beds 1.52 m wide and aligned along a north-south axis, with two rows of seeds planted in each bed (spaced 0.66 m apart). Each planting bed was divided into 16 plots, each 3.05 m long, with unplanted lanes (1.22 m long) separating the plots along each planting bed. Every second planting bed was left unplanted, to avoid confounding effects of competition for soil moisture between adjacent plots. Within each bed, the northern- and southern-most plots were planted with a buffer to minimize edge effects.

Three replicate plots per treatment were planted for each genotype. Replicate plots were grouped spatially into blocks, such that each block contained every genotype, and there were three blocks per treatment. Genotypes were located randomly within each block. Blocks were separated from each other by two beds (one unplanted and the other planted with a reference genotype as buffer).