DROUGHT TOLERANCE PHENOTYPING IN SUNFLOWER INBRED LINES (*Helianthus annuus* var. *macrocarpus* (DC) Cockerell)

GRANDON Nancy[1]*, MARTIN Eugenia[2], CICCONI Emanuel[3], DIAZ Carolina[4], MAMANÍ Eva[1], YACHETTA Gaspar[5], CASALANGUIDA Maximiliano[5], MECCHIA Luis[5], MORENO Ma. Valeria[1].

[1]Laboratorio de Biotecnología, INTA-EEA Manfredi. Ruta Nac. Nº 9. Km 636. (5988) Manfredi, Córdoba, Argentina. [2]IICAR-CONICET. Campo Experimental Villarino, CC Nº 14 (S2125ZAA). Zavalla, Santa Fe, Argentina. [3]Asesor técnico. [4]Estadística. Grupo Economía, INTA-EEA Manfredi. [5]Instituto A. P. Ciencias Básicas y Aplicadas. Universidad Nacional de Villa María. Av. Arturo Jauretche 1555. (5900) Villa María, Córdoba, Argentina. *E-mail: grandon.nancy@inta.gob.ar.

INTRODUCTION

Sunflower (*Helianthus annuus* var. *macrocarpus*) is the fourth most important sources of vegetable oil in the world and the second most important in Argentina. In the last years, the crop moved to marginal areas due to extension of soybean cultivation. The most important limitation of this area are the low rainfall and drought period, which affects the crop yield. In this way, in latest years, different studies were done with accessions from the Sunflower Germplasm Bank of Manfredi Experimental Station of Instituto Nacional de Tecnología Agropecuaria (INTA), to obtain a better knowledge about drought tolerance in sunflower.

The aim of this study was phenotyping seven sunflower inbreed lines (ILs) for drought tolerance under controlled conditions.

MATERIALS AND METHODS

Phenotyping of seven inbred lines (ILs) (B59, HA64, HA89, HAR4, R419, R423 and R432) was conducted in the greenhouse during vegetative stage, under well-watered (WW) and water-deficit (WD) conditions. Water deficit (70% of WW condition) was induced at V8 stage for a period of 16 days following an alpha lattice design with six replicates. Both WW and WD plants were weighed and water loss replaced daily. Traits evaluated were: gain of leaf area (GLA), total water use (TWU), net assimilation rate (NAR), water use efficiency (WUE) and transpiration rate (TR) response to vapor pressure deficit (VPD) (slope and breakpoint). At the end of the experiment, shoots and roots were harvested and dry mass was determined after oven-drying the samples at 105°C for 24 hs. Statistical analysis was performed by InfoStat (Di Rienzo et al., 2011) and SAS University Edition 3.6 (SAS, 2016) software.

Phenotyping under controlled conditions.

Alpha-lattice design.

Pots were weighed and watered manually.

RESULTS

Significant differences between genotypes and between treatments were found for all traits. Moreover, significant genotype for treatment interaction was observed for NAR, WUE and breakpoint in the VPD response. Under WD conditions, all genotypes showed lower GLA (average decreased of 18%) and TWU (average decreased of 23%) than WW treatment (Figure 1). For the GLA trait, HA64 genotype was the unique IL, which showed significant differences between both water conditions (a decrease of 27%). Whereas NAR (average increased of 9%) and WUE (average increased of 32%) showed higher values for WD treatments (Figure 2). In this way, HA64 and HAR4 were unique ILs that showed significant differences between both WW and WD treatments (an increase higher than 23%) for both traits.
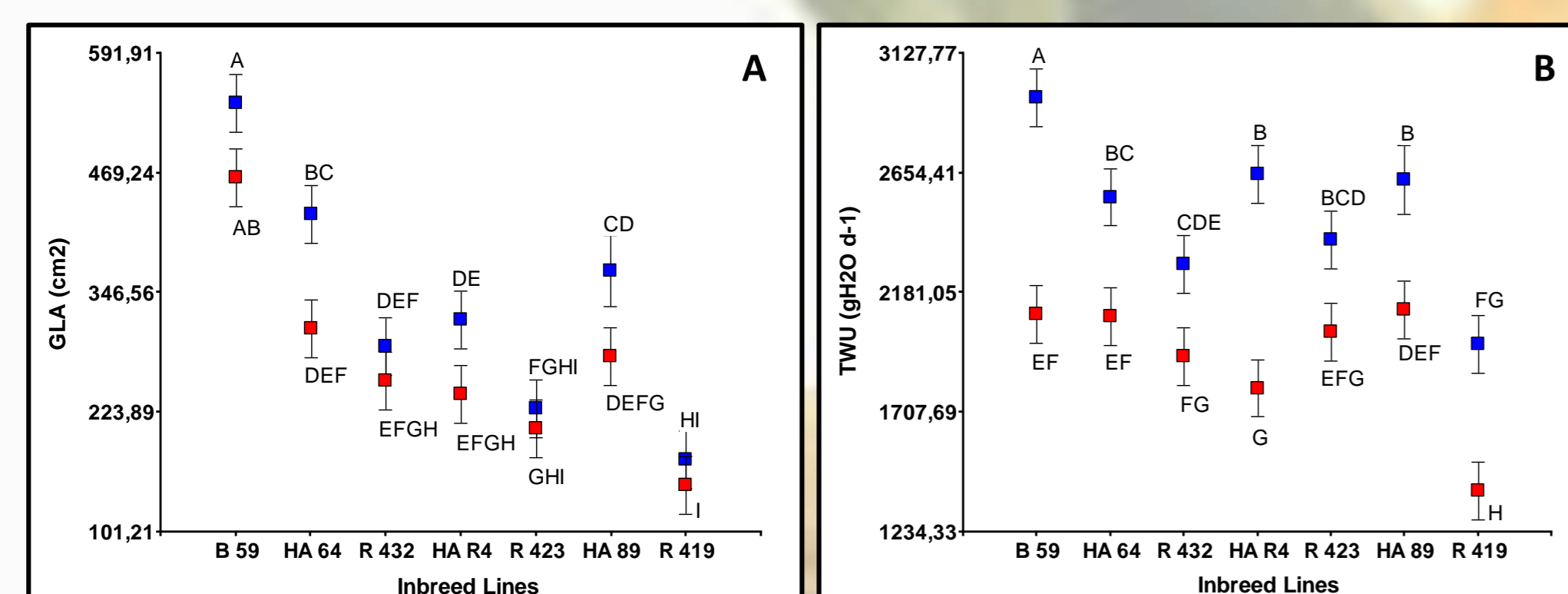
Figure 1: A) GLA and B) TWU traits for seven inbreed lines evaluated under well-watered (WW) (blue spot) and water-deficit (WD) (red spot) conditions. Data are means ± SE of six replicates. Values with the same letter are not significantly different (p ≥ 0.05).
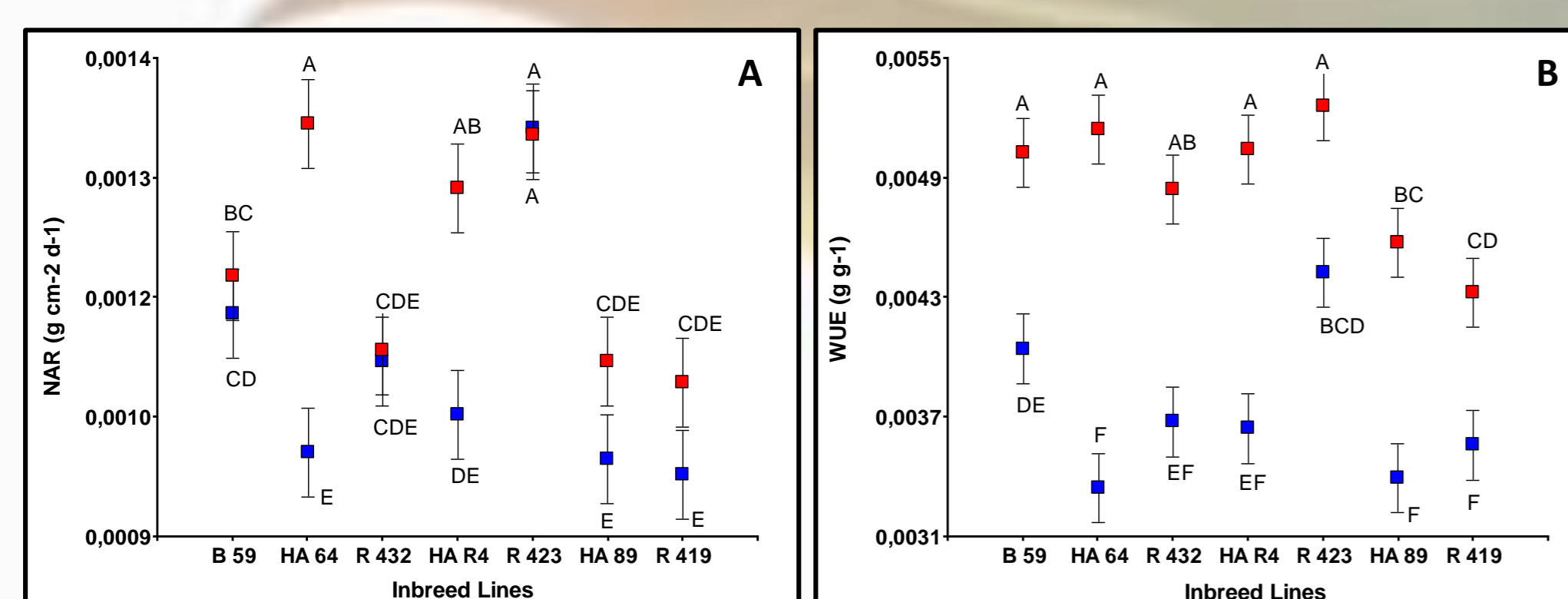
Figure 2: A) NAR and B) WUE traits for seven inbreed lines evaluated under well-watered (WW) (blue spot) and water-deficit (WD) (red spot) conditions. Data are means ± SE of six replicates. Values with the same letter are not significantly different (p ≥ 0.05).

Furthermore, all genotypes showed reduction of the slope and breakpoint in VPD response on the WD treatment (average decreased of 6% and 5%, respectively) (Figure 3). Thus, ILs that presented higher slope showed lower breakpoint (HA64 and R432, fucsia line) (Figure 3 and 4A). On the other hand, ILs that presented lower slope showed higher breakpoint (HA89 and R419, turquoise line) (Figure 3 and 4A); probably because their stomata would be less sensitive to water deficit (Turner et al., 1985), reducing like this the TR to a higher value of VPD than the other genotypes. The Transpiration rate (TR) response to increasing vapor pressure deficit (VPD) was determined by non-linear regression between ILs (Figure 4A) and treatments (Figure 4B).
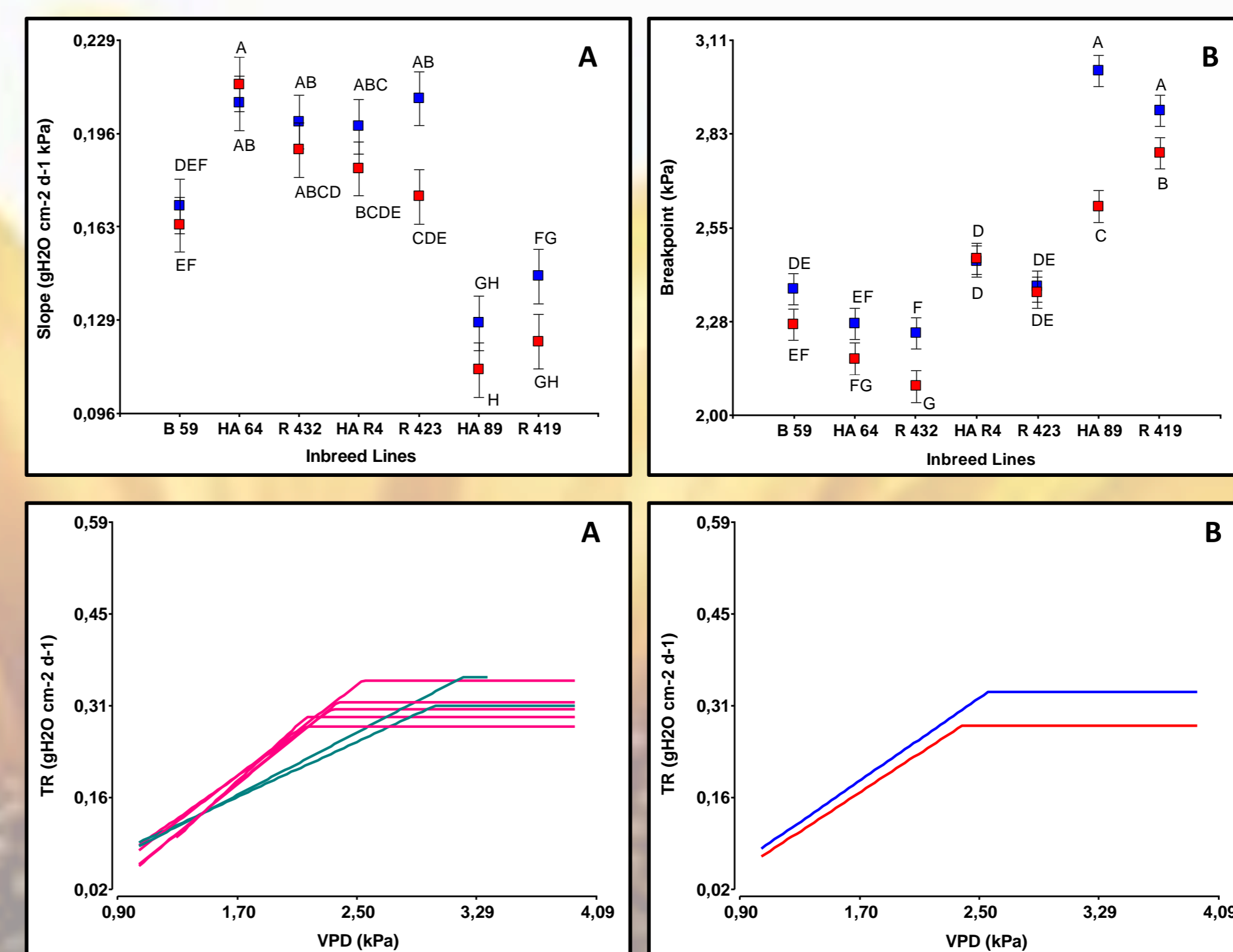
Figure 3: A) Slope and B) Breakpoint in the VPD response for seven inbred lines evaluated under well-watered (WW) (blue spot) and water-deficit (WD) (red spot) conditions. Data are means ± SE of six replicates. Values with the same letter are not significantly different (p ≥ 0.05).
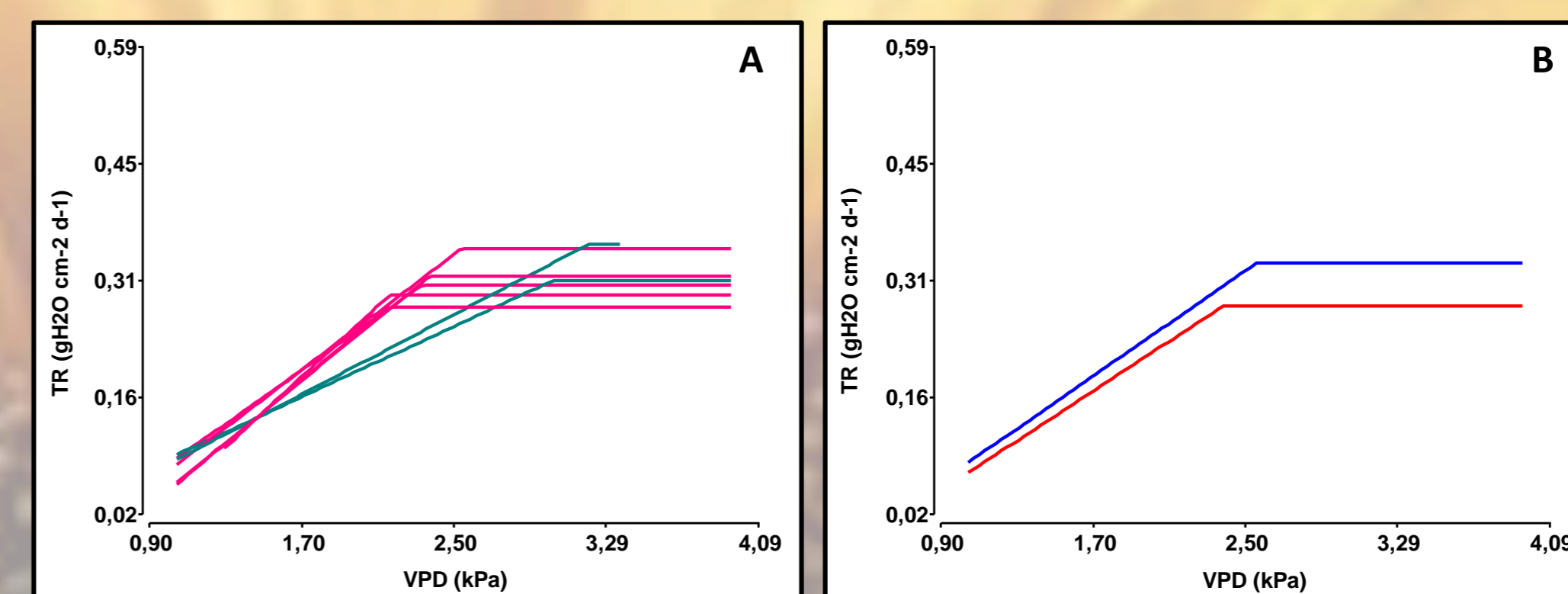
Figure 4: Transpiration rate (TR) response to increasing vapor pressure deficit (VPD), A) for seven inbred lines evaluated and B) for well-watered (WW) (blue line) and water-deficit (WD) (red line) conditions.

PCA analysis was performed and explains the 80% of the total variability (Figure 5). PC1 discriminated HA89 and R419 from the other ILs due to a lower slope and higher breakpoint, whereas PC2 discriminated all genotypes by treatment based on WUE and TWU values. In this regard, plants under the WD condition showed lower water consumption and were more conservative with the water in the tissues. The correlation between traits was analyzed by Pearson correlation coefficients (Table 1). A significant positive correlation was found between GLA and TWU (r=0.60, p<0.0001), and between NAR and WUE (r=0.77, p<0.0001). On the other hand, a significant negative correlation was found between slope and breakpoint in the VPD response (r=-0.73, p<0.0001).
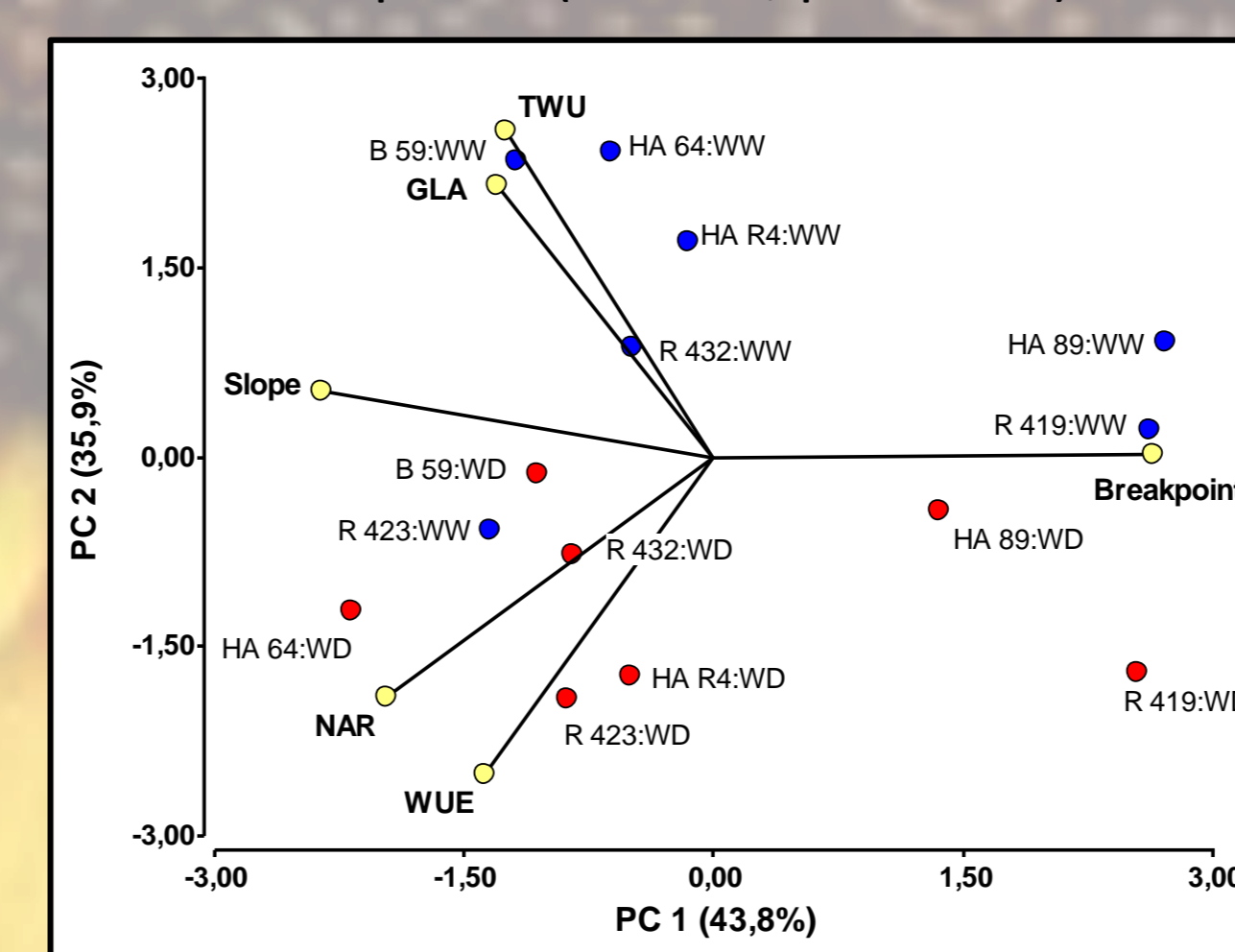
Figure 5: PCA based on six traits evaluated in seven inbred lines under well-watered (WW) (blue spot) and water-deficit (WD) (red spot) conditions. GLA: Gain of Leaf Area, TWU: Total Water Use, NAR: Net Assimilation Rate, WUE: Water Use Efficiency.

Traits	WUE	Slope	Breakpoint	TWU	GLA	NAR
WUE	1	0,957	0,003	0,004	0,975	**0,000**
Slope	-0,01	1	**0,000**	0,017	0,172	0,003
Breakpoint	-0,32	**-0,73**	1	0,029	0,022	0,001
TWU	-0,32	0,26	-0,24	1	**0,000**	0,292
GLA	0,00	0,15	-0,25	**0,60**	1	0,786
NAR	**0,77**	0,32	-0,36	-0,12	0,03	1

Table 1: Pearson correlation coefficients (r) between six traits evaluated in seven inbred lines in lower diagonal and p-value in upper diagonal. GLA: Gain of Leaf Area, TWU: Total Water Use, NAR: Net Assimilation Rate, WUE: Water Use Efficiency.

CONCLUSION

According to traits evaluated, ILs were classified as high (HA64 and HAR4), intermediate (B59, R423 and R432) and low transpiration efficiency (HA89 and R419). Moreover, the large genotypic variation among ILs analyzed in this study, offer potentially parental inbred lines with contrasted response to drought tolerance to generate future mapping populations.

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