Phenotypic plasticity, yield stability and signature of stable isotopes of carbon and nitrogen in Safflower under saline environment

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INTRODUCTION

Salinity is one of the major factors contributing in land degradation, disturbance of soil biology, structure that leads to unproductive land with low crop yield potential especially in arid and semi-arid regions. The selection of appropriate crop genotypes and crop management practices that can play a pivotal role for adaptation and improvement under water scare and saline environment, are better options to mitigate effects of salinity (Munns and Tester 2008; Hussain et al. 2016). Moreover, selection of suitable agro-physiological and biochemical traits should be given priority in order to discover insight mechanism involved for abiotic stresses tolerance.

The present study was conducted to evaluate six safflower genotypes for detailed physiological, agronomical and isotopic responses under saline field condition that could provide a significant background regarding their adaptation and tolerance against salinity.

MATERIALS & METHODS

Six Safflower genotypes were grown at the research farm of International Center for Biosaline Agriculture (ICBA), Dubai, United Arab Emirates (25°5' N and 55°23' E). The field area has Hyperthermic Typic Torripsamment soil type. Nitrogen, phosphorus and potash fertilizers were applied @ 100 Kg/ha from fertilizer (20-20-20 NPK). The safflower seeds were manually sown during first week of November. The field plots measuring 2 m x 4 m (plot area of 8 m^2), was established in a split-plot design with three replications. The main factor was the salinity level (S1, 0 or Control; S2, 7 dS m^{-1} and S3, 14 dS m^{-1}) and sub factor was safflower genotypes (Fig. 1). There were four rows (each row of 4 m in length) in each plot with a row space of 0.5 m between them. The field experiment was equipped with a drip system (4 L hr^{-1} flow rate), 0.5 m distance between rows and 0.25 m between drippers. Irrigation was applied at rates equivalent to ET_0 plus 10% for leaching requirements. After harvest, all plots were irrigated at ET_0 plus 25% for additional leaching.

Agro-physiological data was collected as per standard procedure. Carbon isotope compositions ($\delta^{13}C$) and carbon isotope discrimination ($\Delta^{13}C$) were calculated as reported in Hussain and Al-Dakheel (2018).

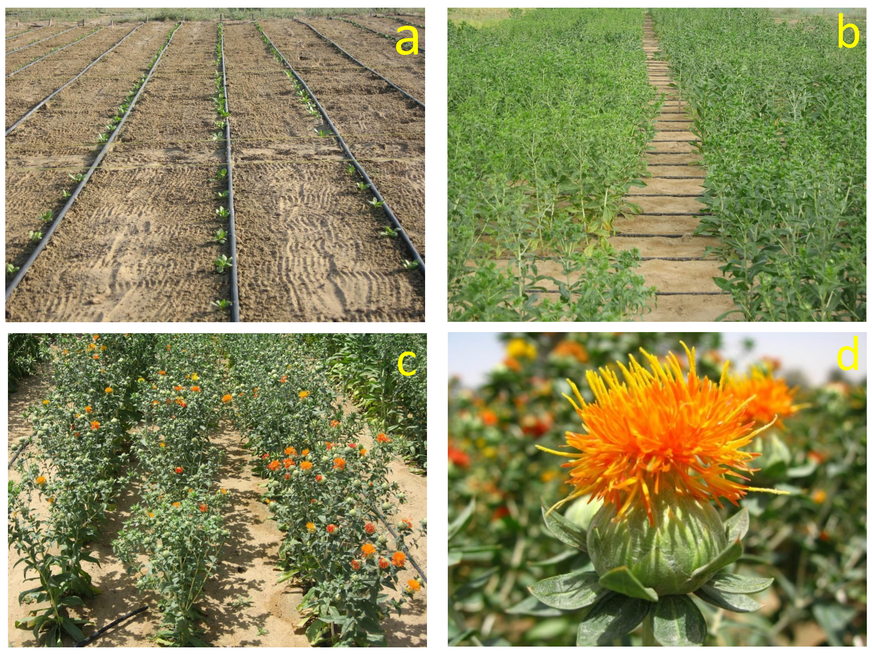

Fig. 1. Safflower production system management in marginal sandy desert soils at ICBA, Dubai, UAE. a: Irrigation systems and seedling growth of safflower. b: Safflower crop at vegetative stage. c: Safflower crop at flowering stage. d: Safflower capitula and flowers.

Fig.2. Isotopic Ratio Mass Spectrometer

RESULTS & DISCUSSION

Table 1

Variables	BN	PDM	CN
Genotypes			
Tolerant - PI248836	42.2b	9.7a	598b
Tolerant - PI167390	50.0a	10a	727.1a
M. Tolerant - PI253387	29.9d	8.9b	448.4d
M. Tolerant - PI250714	37.3c	7.5b	546.2c
Sensitive -PI253385	29.8d	6.8c	362.4f
Sensitive - PI239707	30.9d	8.6b	379.7e
Treatment			
S1 - 0 (Control)	43.6a	9.8a	599.3a
S2 - 7 dS m^{-1}	34.7b	8.3b	499.5b
S3 - 14 dS m^{-1}	31.6c	7.7c	432.1c
Level of significance			
Genotype (G)	.00	.00	.00
Treatment (T)	.00	.00	.00
G x T interaction	ns	**	ns

Table 2

Variables	SY	HI	iWUE
Genotypes			
Tolerant - PI248836	3.6a	36.7a	1.3d
Tolerant - PI167390	3.1a	30.4bc	1.7d
M. Tolerant - PI253387	2.7b	30.4bc	3.9b
M. Tolerant - PI250714	2.4bc	31.6b	2.5c
Sensitive -PI253385	2.3c	31.3b	4.6b
Sensitive - PI239707	2.2c	25.4d	7.1a
Treatment			
S1 - 0 (Control)	3.5a	35.8a	2.3c
S2 - 7 dS m^{-1}	2.6b	31.9b	3.6b
S3 - 14 dS m^{-1}	1.9c	25.1c	4.7a
Level of significance			
Genotype (G)	.00	.18	.00
Treatment (T)	.00	.00	.00
G x T interaction	ns	ns	ns

Abbreviations: BN, number of branches m^{-2}; PDM, Plant dry Biomass (t ha^{-1}); CN, number of capitula m^{-2}; SY, Seed yield (t ha^{-1}); HI, harvest index (%); $\delta^{13}C$, stable carbon isotope composition (‰). $\Delta^{13}C$, carbon isotope discrimination (‰).
Genotype values are the means of 9 measurements (three treatments and three replications per treatment), while treatment values are the means of the 54 measurements (six genotypes and three replications per genotype). Means followed by different letters are significantly different ($p \leq 0.05$) according to Tukey's honestly significant difference (HSD) test. M. Tolerant, Medium tolerant.
Treatments: S1 - 0, (control); medium salinity - S2, 7 dS m^{-1}; high salinity-S3, 14 dS m^{-1}; ns, not significant. G, Genotypes; T, Treatment.

The salinity caused significant reduction in the number of branches (BN) that was 38% less than the control. Plant dry biomass (PDM) was decreased by 15% and 21% following 7 and 14 dS m^{-1}, respectively, compared to control. Number of capitula (CN) decreased from 24% to 44% at 7 and 14 dS m^{-1}, than control, respectively (Table 1). PI248836 and PI6739 produced higher BN, PDM and CN as compared to other genotypes.
The seed yield (SY) was significantly higher in control plots and highest seed yield was recorded in genotype PI248836 and the lowest in PI239707. Harvest index (HI) was decreased due to water salinity by 10.24% and 32.6% at 7 and 14 dS m^{-1}, respectively as compared to control (Table 2). Harvest index greatly varied among the safflower genotypes and ranged between 36.7 – 25.4 % with highest HI observed in genotype PI248836 and the lowest in PI239707 (Table 2).
Among the genotypes, the $\Delta^{13}C$ values varied significantly ($p \leq 0.05$) and safflower genotype PI239707 had lowest Δ value (19.6‰), while PI248836 showed the highest Δ (25.6‰,) (Fig. 4).Safflower genotypes were separated into three grades according to their Δ values. The first grade included salt sensitive genotypes (PI253387 and PI239707), with the lowest Δ values, ranging from 19.6 to 22.2 ‰ but relatively high intrinsic water use efficiency (iWUE) (Table 2). These genotypes had relatively lower SY (2.2 – 2.3 t ha^{-1}). The second grade included genotypes with Δ values slightly higher than those from the first grade, ranging from 22.8 to 24.4 ‰. Seed yield in this category were quite variable, ranging from 2.4 to 2.7 t ha^{-1}. In the third grade, genotypes had the highest Δ values, ranging from 25.2 to 25.6 ‰ and also had highest seed yield with a range of 3.1 to 3.6 t ha^{-1} (Table 2).

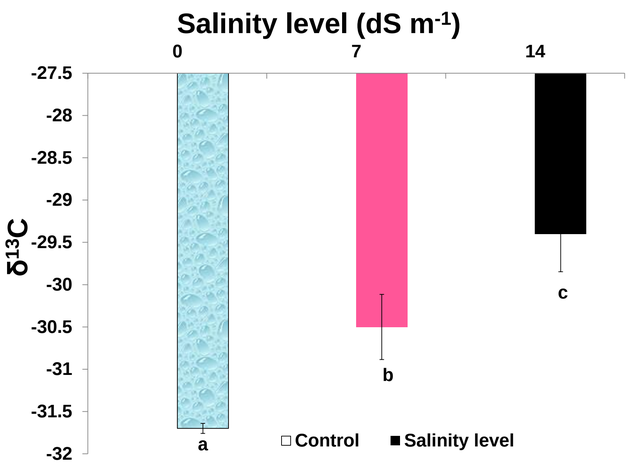

Fig. 3

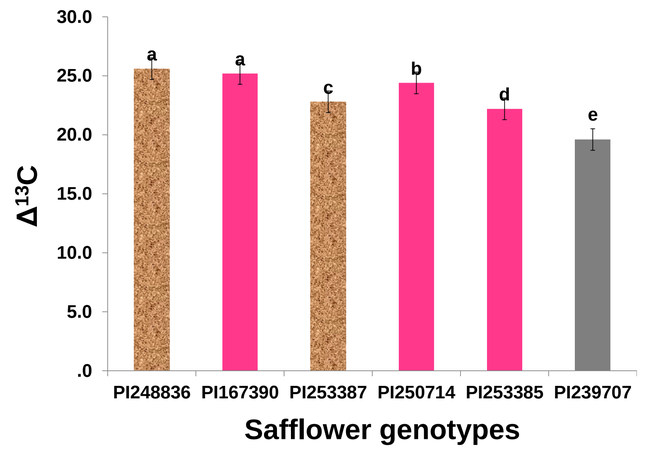

Fig.4

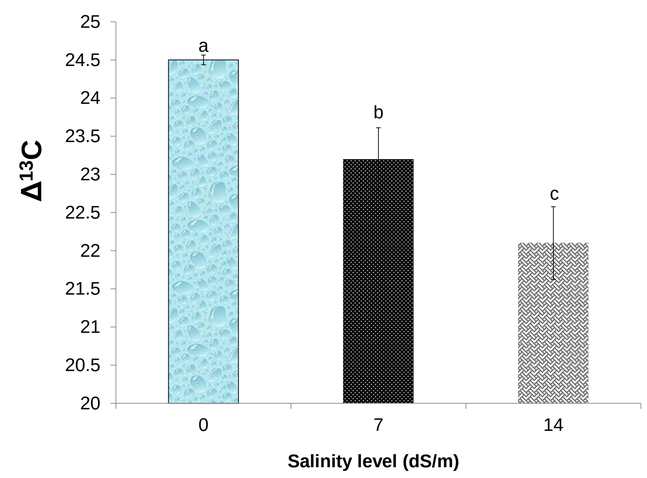

Fig. 5

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