

Comparative proteomic analysis and plant salinity response of two quinoa genotypes

Walid Derbali¹, Arafet Manaa², Bernhard Spengler¹, Rahma Goussui², Zainul Abideen³, Parviz Ghezellou¹, Chedly Abdelly², Christoph Forreiter⁴, and Hans-Werner Koyro⁵

¹Justus-Liebig-Universität Giessen Fachbereich 08 Biologie und Chemie

²Borj Cedria Biotechnology Centre

³University of Karachi

⁴University of Siegen Department Chemistry and Biology

⁵Justus Liebig Universität Giessen

December 1, 2020

Abstract

The aim of this study was to investigate the effect of NaCl salinity (0, 100 and 300 mM) on the individual response of the quinoa varieties Kcoito (Altiplano Ecotype) and UDEC-5 (Sea-level Ecotype) with physiological and proteomic approaches. UDEC-5 showed an enhanced capacity to withstand salinity stress compared to Kcoito. In response to salinity, we detected overall the following differences between both genotypes: Toxicity symptoms, plant growth performance, photosynthesis performance and intensity of ROS-defense. We found a mirroring of these differences in the proteome of each genotype. Among the 700 protein spots reproducibly detected, 24 exhibited significant abundance variations between samples. These 24 proteins were involved in energy and carbon metabolism, photosynthesis, ROS scavenging and detoxification, stress defense and chaperone functions, enzyme activation and ATPases. A specific set of proteins predominantly involved in photosynthesis and ROS scavenging showed significantly higher abundance under high salinity (300 mM NaCl). The adjustment was accompanied by a stimulation of various metabolic pathways to balance the supplementary demand for energy or intermediates. However, the more salt-resistant genotype UDEC-5 presented a beneficial and significantly higher expression of nearly all stress-related altered enzymes than Kcoito. Salinity, halophyte, quinoa, proteomic, photosynthesis, antioxidant, salt resistance, oxidative stress.

Hosted file

Proteomic 011220.pdf available at <https://authorea.com/users/380522/articles/496456-comparative-proteomic-analysis-and-plant-salinity-response-of-two-quinoa-genotypes>

Table 1: Effect of NaCl treatments (0, 100 and 300 mM) on substomatal CO₂ concentration (*C_i*), transpiration rate (*E*), stomatal conductance (*g_s*), net CO₂ assimilation (*A_n*) and water use efficiency (*WUE*) of UDEC-5 and Kcoito genotypes. Means (n = 6 per treatment ± SE.) values with different letters are significantly different (*P* < 0.05).

Treatments NaCl (mM)	<i>C_i</i>	<i>E</i>	<i>g_s</i>	<i>A_n</i>	<i>WUE</i>
	UDEC-5				
0	256.55 ±31.5 <i>a</i>	2.80 ±0.61 <i>a</i>	0.21 ±0.05 <i>a</i>	16.01 ±1.91 <i>a</i>	5.83 ±0.99 <i>a</i>
100	232.09 ±11.8 <i>a</i>	1.82 ±0.11 <i>b</i>	0.10 ±0.03 <i>b</i>	13.28 ±1.03 <i>b</i>	7.28 ±0.39 <i>a</i>
300	214.57 ±11.1 <i>b</i>	1.41 ±0.07 <i>c</i>	0.11 ±0.02 <i>b</i>	11.96 ±0.93 <i>c</i>	8.47±0.28 <i>b</i>
	Kcoito				
0	259.15 ±25.8 <i>a</i>	2.47 ±0.44 <i>a</i>	0.19 ±0.01 <i>a</i>	16.61 ±0.42 <i>a</i>	6.86 ±1.23 <i>a</i>
100	277.17 ±21.8 <i>a</i>	1.77 ±0.24 <i>b</i>	0.12 ±0.08 <i>b</i>	12.21 ±1.04 <i>b</i>	6.95 ±1.02 <i>a</i>
300	236.76 ±21.5 <i>b</i>	1.31 ±0.31 <i>b</i>	0.07 ±0.04 <i>b</i>	8.96 ±1.03 <i>c</i>	6.64 ±1.12 <i>a</i>

Hosted file

PCE Table 2 final.pdf available at <https://authorea.com/users/380522/articles/496456-comparative-proteomic-analysis-and-plant-salinity-response-of-two-quinoa-genotypes>

Figure 1

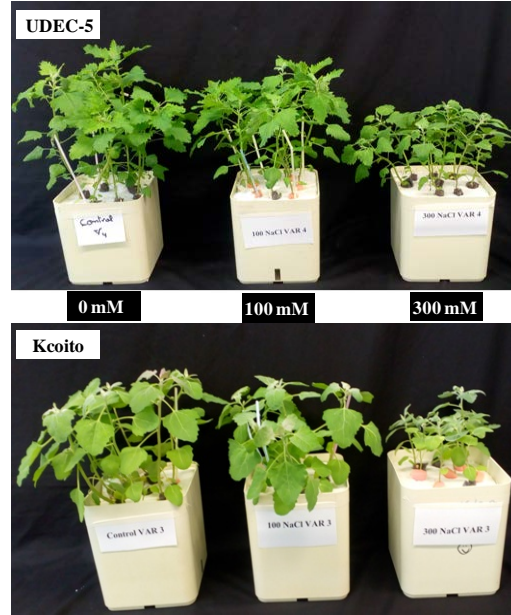


Figure 2

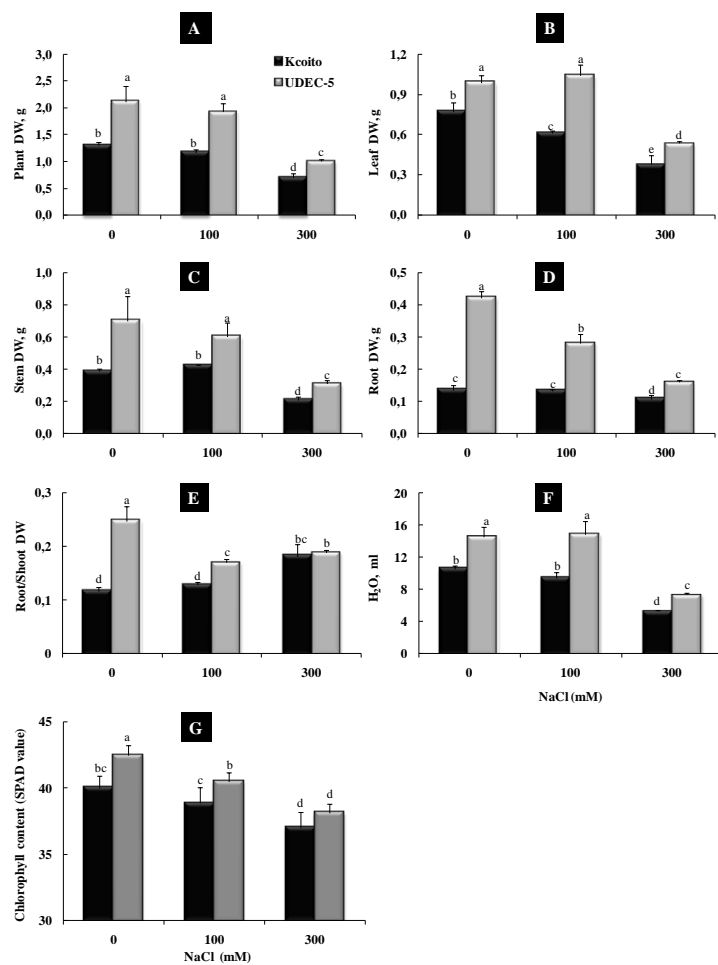


Figure 3

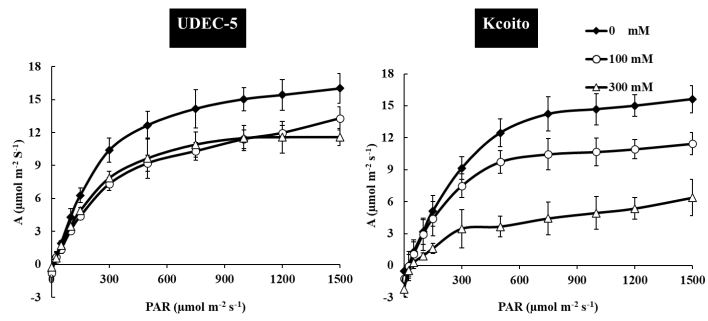


Figure 4

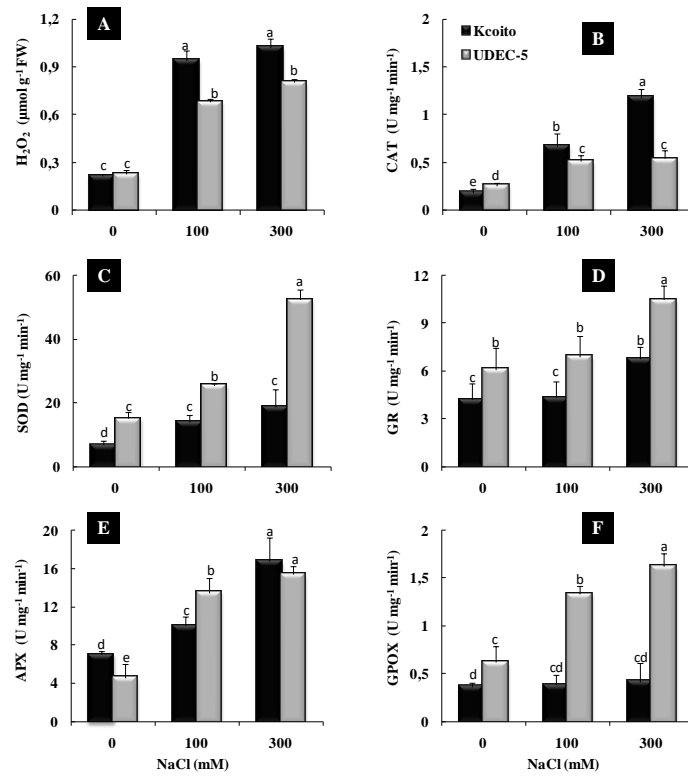
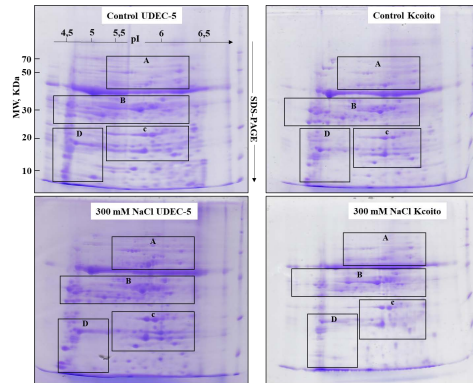


Figure 5



Hosted file

Figure 6 final.pdf available at <https://authorea.com/users/380522/articles/496456-comparative-proteomic-analysis-and-plant-salinity-response-of-two-quinoa-genotypes>

Figure 7.

