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*Full Length Research Paper*

# Assessing biomass and grain yields stability of a restricted collection of Batini barley landraces from Oman under salinity stress

**Abdullah J. Al-Dakheel, Makram Belhaj Fraj***

ICBA, International Center for Biosaline Agriculture, PO Box 14660, Dubai, United Arab Emirates

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**Batini barley landraces from Oman are thought to exhibit salinity tolerance because of their wide cultivation in several salt affected areas. This field study evaluated the biomass and grain yields of 21 Batini landraces and 4 breeding lines from an international collection over three cropping seasons under three irrigation water salinity levels corresponding to electrical conductivities of 2, 8 and 14 dS $m^{-1}$. These entries were selected from larger collections based on previous evaluations. Biomass and grain yields were 6.06 and 1.99 t $ha^{-1}$, respectively, averaged across all salinity levels, with regression coefficients ranging between -0.01 and -0.2. Superior landraces maintained their biomass and grain yields at levels of 3-8 and 1.7-3 t $ha^{-1}$, respectively, whereas salinity stress reduced the yield of unstable entries by 70%.**

**Keywords:** Genetic resources, *Hordeum vulgare* L., salt-tolerant germplasm.

## INTRODUCTION

Salinity is a major abiotic stress affecting agricultural production in marginal environments, reducing economic yield of crops and impacting farmers' livelihood (Munns et al., 2006). Barley (*Hordeum vulgare* L.) is among the most salt-tolerant glycophytes and is widely grown in dryland agro-ecosystems of developing countries in the West Asia North Africa (WANA) region. It is a major component of the cropping systems in the region due to its high resilience and is an important stable source of forage (grain and straw). Therefore, improving barley yield in these environments is an important objective to cope with both increasing livestock demands and environmental stresses.

Batini landraces are usually grown in saline environments and were chosen because of their expected adaptation to salinity. These landraces were collected from farmers' fields in the coastal Batinah region of Oman, where they are primarily grown for animal feed as both green forage and for dual-purpose end-use (straw and grain harvest at maturity) under subsistence production. The barley entries were collected and identified prior to this study based on their characterization under controlled conditions. Most research on these landraces has focused on the quantification of biomass variation during early seedling growth (Jaradat et al., 2004a,b; Al-Maskri et al., 2006). These studies showed that Batini landraces are variable for several morphological traits. On average, 66% of the total Batini landraces were considered to be tolerant to salinity.

The general objective was to identify barley entries having high and stable yields over the range of irrigation water salinities that may be experienced by farmers. Salt-tolerant entries can be used as a genetic resource for barley improvement targeted at salt-prone environments in the region.

## MATERIALS AND METHODS

Drawing upon work on Batini landraces by Jaradat et al. (2004a,b) and on breeding lines from the International Center for Agricultural Research in the Dry Areas (ICARDA) by Al-Dakheel et al. (2001), a selection of

*Corresponding author Email adresses: m.belhaj@biosaline.org.ae, Tel.: +971 4 336 1100: fax: +971 336 1155.

**Table 1.** Details of the 25 barley entries evaluated under salinity stress.

| Origin of the entry | Number of screened entries | Entry holder | Subpopulation or elite germplasm code* | Entry code |
|---|---|---|---|---|
| Omani landrace | 21 | ICBA | Batini 1 (13)† | 9; 12; 14; 18; 23; 40; 45; 48; 55; 59; 60; 64; 65 |
| | | | Batini 2 (5) | 78; 79; 99; 100; 110 |
| | | | Batini 4 (3) | 165; 170; 178 |
| Observation nursery | 2 | ICARDA | BON (2) | 241; 252 |
| Special heat nursery | 2 | ICARDA | SHN (2) | 270; 271 |

* Batini subpopulation and ICARDA's elite germplasm codes according to Jaradat et al (2004a) and to ICBA codes, respectively.
† in parentheses, total number of evalued entries per subpopulation or elite germplasm.

germplasm was evaluated in the field for potential suitability for the region.

Jaradat et al. (2004a,b) identified 7 subpopulations (Batini 1-7) within the Batini landraces. Twenty one landraces (4 from Batini 1, 13 from Batini 2 and 3 from Batini 4) were tested in this study, along with 2 breeding lines from each of ICARDA's Barley Observation Nursery (BON, 328 entries) and Special Heat Nursery (SHN, 320 entries) as shown in Table 1. These breeding lines were selected based on previous screening for salinity tolerance at the United Arab Emirates University Research Station in Al-Ain over four cropping seasons (1999-2003) under similar salinity levels (Al-Dakheel et al., 2001).

The work was conducted at the International Center for Biosaline Agriculture (ICBA) in Dubai, United Arab Emirates (25°13'N and 55°17'E) over three cropping seasons (2003/2004, 2004/2005 and 2005/2006). The climate is arid desert with dry and hot conditions from April to November (Karim and Al-Dakheel, 2006). The soil is a Carbonatic, Hyperthermic Typic Torripsamment with a negligible level of inherent soil salinity (0.2 dS $m^{-1}$).

The entries were grown using three irrigation water salinity levels corresponding to electrical conductivities of, 2, 8 and 14 dS $m^{-1}$ (denoted as S1, S2 and S3, respectively). The lowest salinity water available is 2 dS $m^{-1}$ (SAR = 4 mmol/l with Na and Cl concentrations lower than 11 meq/l and pH = 8.5). This salinity level precludes a control treatment with non-saline water, but corresponds to the prevalent salinity in the non-affected areas of the region. The higher salinities were obtained by mixing this water with highly saline chloruro-sodic groundwater (with ECw up to 25 dS $m^{-1}$, SAR>26 mmol/l with Na and Cl concentrations higher than 190 meq/l and pH=7.6) in the proportions required to achieve the target levels. Throughout each cropping season, each salinity level was checked twice a week by a portable EC meter (TetraCon® 325 Cond 197i, WTW, USA).

Prior to plot establishment, the site was prepared by harrowing to ensure an even seedbed and the incorporation of 10 tons $ha^{-1}$ of organic manure compost (41% organic matter, 1.64% moisture, pH=7.7, C/N=16.5, 1.5% N, 1.65% K and 1.22% Na, Al Bayadir®, Jabel Ali, Dubai, UAE). Irrigation was applied using a drip system with 0.5 m distance between rows and 0.25 m between drippers. The plot covered 8 $m^2$ (2 x 4 m) with the row spacing being of 0.5 m (corresponding to the drip system) to enable manual weeding. The plots were hand-seeded with equal number of seeds (200 seeds $m^{-2}$) per entry since the germination rate of the seeds, as tested prior to the experiment, did not differ between entries. The plots were sown around mid November to avoid autumn high temperatures and desiccating winds. N-P-K fertilizer (20-20-20% Growfert Solub™ fertilizer) was applied at a rate of 100 kg $ha^{-1}$ split into applications of 50, 30 and 20 kg $ha^{-1}$ at the early vigor, mid stem elongation and heading stages, respectively. Physiological maturity extended from late March to late April.

The experimental plan was a split-plot design with three replications. The main-plot factor was the salinity level and the subplot factor was the entry tested. All observations were made on 1m of row in the two central rows. 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 leaching requirement over two days. The plots were harvested at maturity and measurements made of biomass yield (BY) and straw yield (SY) at 0% moisture, and grain yield (GY) at 15% moisture The entries were evaluated based on their reduction in grain and biomass yield relative to their values at the lowest water salinity available (2 dS $m^{-1}$).

An analysis of variance (ANOVA) was carried out for SY, BY and GY according to split-plot design. The stability of the selected genotypes was analyzed. Stability assessment aims at characterization of the observed yield variation for each entry under different environments

**Table 2.** Analyses of variance for straw yield (SY, t $ha^{-1}$), biomass yield (BY, t $ha^{-1}$) and grain yield (GY, t $ha^{-1}$) in the collection of 25 entries assessed (21 landraces of the Omani and four ICARDA's breeding lines) at three salinity levels: S1 (2 dS $m^{-1}$), S2 (8 dS $m^{-1}$) and S3 (14 dS $m^{-1}$) in field experiment during 2003/2004, 2004/2005 and 2005/2006.

| Variable | Source | DF | Sum of Squares | F Value | Pr > F |
|---|---|---|---|---|---|
| SY | Salinity | 2 | 160.614 | 269.77 | $10^{-4}$ |
| | Year | 2 | 2548.144 | 4279.89 | $10^{-4}$ |
| | Entry | 24 | 234.155 | 32.77 | $10^{-4}$ |
| | Replication (Year) | 6 | 9.145 | 5.12 | $10^{-4}$ |
| | Salinity × Year | 4 | 100.075 | 84.04 | $10^{-4}$ |
| | Salinity × Replication (Year) | 12 | 10.544 | 2.95 | $7\ 10^{-4}$ |
| | Year × Entry | 48 | 302.400 | 21.16 | $10^{-4}$ |
| | Replication × Entry (Year) | 144 | 80.686 | 1.88 | $10^{-4}$ |
| | Salinity × Entry | 48 | 209.160 | 14.64 | $10^{-4}$ |
| | Salinity × Year × Entry | 96 | 540.72 | 18.92 | $10^{-4}$ |
| | Residual | 288 | 85.734 | | |
| BY | Salinity | 2 | 612.907 | 639.52 | $10^{-4}$ |
| | Year | 2 | 1745.789 | 1821.59 | $10^{-4}$ |
| | Entry | 24 | 324.622 | 28.23 | $10^{-4}$ |
| | Replication (Year) | 6 | 6.951 | 2.42 | $2.7\ 10^{-2}$ |
| | Salinity × Year | 4 | 364.323 | 190.07 | $10^{-4}$ |
| | Salinity × Replication (Year) | 12 | 22.528 | 3.92 | $10^{-4}$ |
| | Year × Entry | 48 | 325.058 | 14.13 | $10^{-4}$ |
| | Replication × Entry (Year) | 144 | 126.921 | 1.84 | $10^{-4}$ |
| | Salinity × Entry | 48 | 254.785 | 11.08 | $10^{-4}$ |
| | Salinity × Year × Entry | 96 | 688.497 | 14.97 | $10^{-4}$ |
| | Residual | 288 | 138.008 | | |
| GY | Salinity | 2 | 199.562 | 1845.38 | $10^{-4}$ |
| | Year | 2 | 69.682 | 644.36 | $10^{-4}$ |
| | Entry | 24 | 40.264 | 31.03 | $10^{-4}$ |
| | Replication (Year) | 6 | 0.337 | 1.04 | 0.40 |
| | Salinity × Year | 4 | 107.941 | 499.07 | $10^{-4}$ |
| | Salinity × Replication (Year) | 12 | 2.007 | 3.09 | $4\ 10^{-4}$ |
| | Year × Entry | 48 | 75.735 | 29.18 | $10^{-4}$ |
| | Replication × Entry (Year) | 144 | 10.585 | 1.36 | $1.5\ 10^{-2}$ |
| | Salinity × Entry | 48 | 35.519 | 13.69 | $10^{-4}$ |
| | Salinity × Year × Entry | 96 | 63.513 | 12.24 | $10^{-4}$ |
| | Residual | 288 | 15.572 | | |

(an 'environment' indicates any salinity level in a given year). The more stable an entry is, the lower will be its yield variation with environment. Stability was estimated using genotype regression coefficients and computed for each entry. Regression coefficients were estimated for the interaction term between entries and environments. The more stable an entry was across the environments, the closer its regression coefficient $\rho_g$ approached zero. Clustering entries according to their regression coefficients and mean yields was possible since the threshold values corresponding to the ANOVA model mean were used.

All analyses were performed with SAS Software System Version 6.1 (SAS Institute 1990, Cary, NC, USA) using the GLM procedure.

## RESULTS AND DISCUSSION

Averaged across all salinity levels, years (cropping seasons) and entries, SY, BY, and GY were 3.37, 6.06 and 1.99 tons $ha^{-1}$, respectively. The ANOVA revealed significant effects of year, salinity and entry for all variables (Table 2). Under the lowest salinity, SY, BY and GY were high (maximum recorded values of 13, 16.8 and 5.2 t $ha^{-1}$, respectively). In contrast, the minimum values

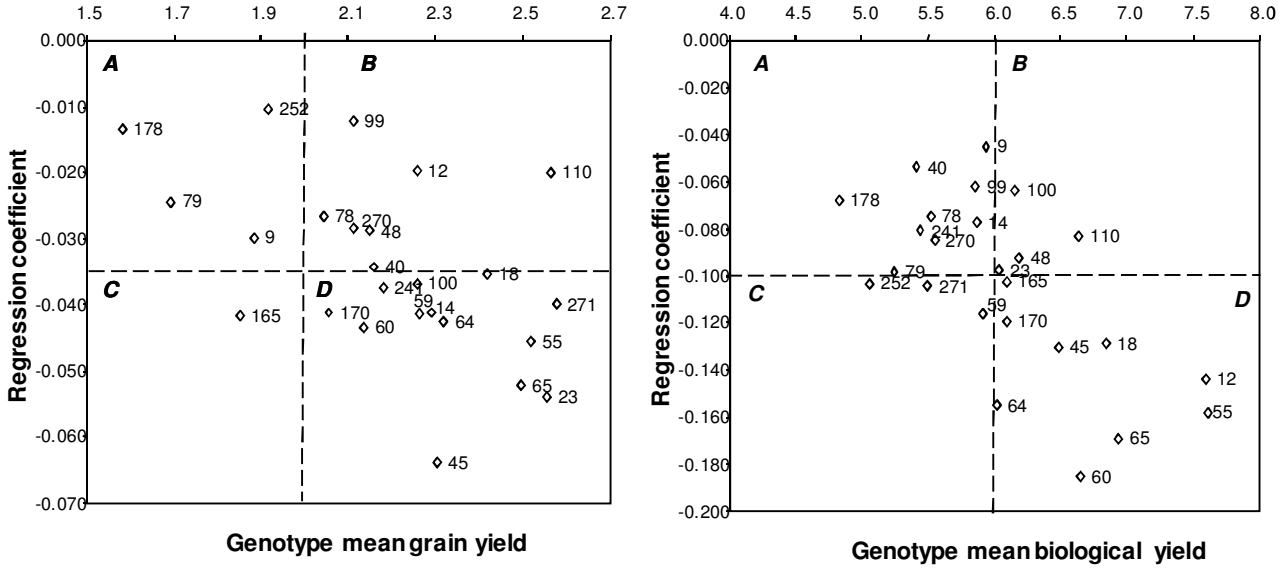


**Figure. 1.** Clustering of the collection of 25 barley entries using regression coefficients and means of grain and biological yields recorded in the three salinity levels (2, 8 and 14 dS $m^{-1}$) across three cropping seasons.
A, entries specifically adapted to unfavorable environments (specific adaptation).
B, entries generally adapted to all environments (wide adaptation).
C, entries not adapted to all environments.
D, entries specifically adapted to favorable environments (specific adaptation).
For entries codes see Table 1.
Vertical and horizontal dashed lines correspond to threshold values for mean yields and regression coefficients, respectively.

were 0.2, 1.4 and 0.14 t $ha^{-1}$ for the three variables, respectively. Salinity reduced SY and BY by about 30% at the highest level of 14 dS $m^{-1}$ compared with values at the lowest salinity of 2 dS $m^{-1}$. The reduction was higher for GY (equal to 37%) suggesting a continuous salinity impact on yield building during the entire growth cycle. The results showed a high response variation in the entries tested. The values of all response variables decreased as the salinity increased. The reduction of yield was accentuated when irrigation water salinity exceeded 8 dS $m^{-1}$. The results obtained here are consistent with those reported in the literature (Richards et al., 1987; Al-Maskri et al., 2006; Jaradat et al., 2004a,b; Munns et al., 2006; Royo and Aragüés, 1999).

Inter-entry variation was large, with the top-yielding entries at the highest salinity level displaying GY and BY values higher than 2 and 5 t $ha^{-1}$, respectively (Figure 1). Inter-entry variation in the regression coefficient for the interaction with year and salinity effects was about 70%. Year and salinity factors contributed 30-65% to the mean squares. For all variables, the top ten ranking differed between salinity levels, with a high entry × salinity interaction. Stability varied over the three years where the three salinity levels were applied.

Entry regression coefficients ranged between -0.01 and -0.2. Entries showing the highest regression coefficient in absolute terms contributed the most to the entry × salinity interaction. As the range of variation for entry stability was more than twice as high for BY as for GY, different thresholds for the regression coefficient were used. These threshold values were equal to -0.1 and -0.035 for BY and GY corresponding to averages, respectively. Mean GY and BY predicted by the model was equal to 1.99 and 6.06 t $ha^{-1}$, respectively. These values were close to the target GY of 2 t $ha^{-1}$ and BY of 6 t $ha^{-1}$. Thus, these target values were used as yield thresholds for clustering entries as either high yielding or low yielding.

Four entry clusters were identified for each end-use purpose. Simultaneous use of both thresholds allowed the entries to be clustered into four groups (denoted by A-D, Figure 1). Low yielding entries having low regression coefficients (cluster A) were specifically adapted to unfavorable environments, while those displaying high regression coefficients (cluster C) were not adapted to the production environment. In contrast, high yielding entries displaying low regression coefficients (cluster B) were characterized by wide adaptation while those having high regression coefficients (cluster D) were specifically adapted to favorable environments. The most interesting entries were those belonging to cluster A and B. For cluster A, there were four and nine entries, while in cluster B there were seven and four entries for GY and BY, respectively. Entries 110 and 48 were widely adapted across all environments for dual-purpose end-use, and entries 18, 55, 60, 64, 65 and 170 performed well for dual-purpose

end-use under favorable environments. Less than 15% of the entries tested were not adapted to all environments. Entry 9 displayed yields close to the threshold value for cluster A, and so could be suitable in extremely harsh environments.

For GY, 16% of the entries were adapted to unfavorable environments while 28% were widely adapted to all environments. However, when forage production rather than grain production was considered, the proportion of well adapted entries was higher, with 36% adapted to unfavorable environments. The collection evaluated for yield was mainly constituted of the Batini landrace resulting from neutral selection as well as entropic action within subsistence farming systems (Jaradat et al., 2004a,b). This specific adaptation to salinity stress is illustrated by the proportion of entries adapted to favorable environments being 16% higher for GY compared to BY. Also, the proportion of entries not adapted to all environments was lower than 15%.

The findings here illustrate the high genetic potential of the Batini landrace collection (primarily originating in the harsh environment of Batinah, Jaradat et al. 2004a b), where the growing factors favor forage production, and contrast with the ICARDA entries which were originally selected for grain production in semi-arid environments. Reference entries from each stability cluster can be used for future studies concerning the mechanisms involved in salinity tolerance. In addition, a further study in wider multisite experiments covering WANA countries would be valuable to confirm the stability of the entries and to eventually bring suitable genetic material to farmers.

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**References**

Al-Dakheel, AJ, Peacock, JM, Al-Hadrami, G (2001). Salinity tolerance and chemical composition of selected barley and pearl millet genotypes grown in the UAE. In: Proceedings on: “Prospects for biosaline agriculture in the Arabian Peninsula”, March 2001. Dubai, UAE.

Al-Maskri, AY, Shahid, M, Jaradat, AA (2006). Multivariate phenotypic structures in the Batini barley landrace from Oman. J. Food, Agric. and Env., (4)2: 208-212.

Jaradat AA, Shahid M, Al-Maskri AY (2004a). Genetic diversity in the Batini barley landrace from Oman: I. Spike and seed quantitative and qualitative traits. Crop Sci. 44: 304–315.

Jaradat, AA, Shahid, M, Al-Maskri, A (2004b). Genetic diversity in the Batini barley landrace from Oman: II. Response to salinity stress. Crop Sci. 44: 997–1007.

Karim, FM, Al-Dakheel, AJ (2006). Salt tolerant plants of the United Arab Emirates. International Center for Biosaline Agriculture, Dubai, UAE.

Munns, R, James, RA, Läuchli, A (2006). Approaches to increasing the salt tolerance of wheat and other cereals. J. Expt. Botany (57)5 : 1025–1043.

Richards, RA, Dennett, CW, Qualset, CO, Epstein, E, Norlyn, JD, Winslow, MD (1987). Variation in yield of grain and biomass in wheat, barley, and triticale in a salt-affected field. Field Crops Res., (15) 3–4: 277–287.

Royo, A, Aragüés, R (1999). Salinity-yield response functions of barley genotypes assessed with a triple line source sprinkler system. Plant Soil, 209: 9–20.

SAS Institute (1990). SAS/STAT User’s guide, SAS Institute Cary, NC, USA, 1(2):6,4.

Shannon, MC (1997). Adaptation of plants to salinity. Advances Agron., 60: 87–120.