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Full Length Research Paper

Evaluation of Batini barley landraces from Oman and breeding lines under various irrigation salinity levels

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Abstract

The objective of this study was to conduct a field evaluation of a large collection of barley (*Hordeum vulgare* L.) landraces from the Batinah coastal region of Oman (Batini), together with international elite germplasm, under different irrigation water salinities. This study was conducted on a subset of 234 (out of 2308 landraces) Omani landraces, together with an international elite germplasm composed of 43 breeding lines. Field experiments were conducted over two cropping seasons using three replications of irrigation water salinities corresponding to electrical conductivities of 2, 8 and 14 dS m^{-1}. The total yield variation was estimated to be higher than 80%. During 2003/2004, 277 entries were evaluated and only 70 entries were selected for a second year assessment. Averaged across all salinity levels, biomass yield and grain yield were 6 and 2 t ha^{-1}, respectively. Salinity reduced biomass yield and grain yield by 35% and 55% respectively, particularly at the highest level of 14 dS m^{-1}. However, some entries maintained 7-9.5 and 2-2.6 t ha^{-1} of biomass yield and grain yield, respectively. Genetic variation in salinity tolerance in the Omani landraces embeds the whole range of variance of the breeding lines. Salt-tolerant entries were identified for cultivation for biomass, grain and dual-purpose end-uses (grain plus straw).

Keywords: Genetic resources, *Hordeum vulgare* L., Salt-tolerance, Dual-purpose end-use

INTRODUCTION

Salinity is a major abiotic stress affecting agricultural production in arid and saline environments. Salinity generally slows the rate of crop growth, resulting in plants with smaller leaves, shorter stature and reduced economic yield (Shannon, 1997). The degree to which crop growth is curtailed by salinity differs with crop species and cultivars (Shannon and Grieve, 1999). Barley (*Hordeum vulgare* L.) is among the most salinity tolerant glycophytes and is the most tolerant cereal crop (Maas, 1986; Steppuhn et *al.*, 2005). Barley's tolerance is due both to its rapid growth and fast phenological development which enable it to avoid long exposure to salinity stress and to genetic factors controlled by many loci (Gorham et *al.*, 1987, Munns et *al.*, 2006). Several previous studies have shown that large genetic variation in salinity tolerance exists within the barley species (Jaradat *et al.*, 2004a,b).

Agriculture is a major sector in the economies of developing countries in the West Asia and North Africa (WANA) region. In WANA countries where dry land cropping systems dominate agriculture, barley is an important crop due to its resilience and its role in integrated crop-livestock systems and as a source of stable farm income. A strategically major objective is to improve barley yield in harsh environments where irrigation water and soil salinities are increasing. WANA has been primarily targeting screening and breeding research to improve drought tolerance. Nevertheless, there is an increasing need for improving salinity tolerance as is the case for other dry environments such as India and Pakistan (Munns *et al.*, 2006). Moreover, in the WANA region, barley production under salinity stress is often variable because the actual cultivars used are not sufficiently tolerant (Steven, 2011). One of the means by which barley grain and forage yields may be increased and stabilized is selection of genotypes with high yield

potential under high salinity levels. Improved salinity tolerance permits the conservation of fresh water and its use for higher value purposes, providing both ecological and economic benefits essential for sustainable agriculture in dry lands (Keating *et al.*, 2010).

The initial step in the development of salt-tolerant cultivars is to identify sources of salinity tolerance within the crop and, when available, within its wild relatives. International Center for Biosaline Agriculture (ICBA) program aims to identify superior genotypes for both forage and grain production under arid conditions. These genotypes should be characterized by high productivity under saline conditions, thereby improving agricultural production in saline regions and extend agriculture to more marginal environments. The present work is a part of an extensive program targeting the identification of salt-tolerant barley from a large collection stored at ICBA's gene bank. Previously, no systematic effort has been undertaken to evaluate salinity tolerance in a wide range of barley genotypes. The genetic potential for salinity tolerance exists in the regions where local landraces are cultivated and ICARDA (International Center for Agricultural Research in the Dry Areas) has developed material representing the vast genetic diversity in the WANA region. Previously, 2308 barley landraces were collected from Oman and more than 1100 breeding lines were provided by ICARDA to ICBA.

Batini landraces usually grown in saline environments were chosen because of their expected specific adaptation to salinity. The landraces were collected from farmers' fields in the costal Batinah region, and were mainly grown in the context of subsistence farming for forage and dual-purpose (grain and straw). Batini landraces were collected and identified based on their characterization under controlled conditions, prior to the present study. Most of the research on these landraces has focused on the quantification of genetic variation during early seedling growth (Jaradat *et al.*, 2004a,b; Al-Maskri *et al.*, 2006). These previous studies showed that Batini landraces are variable for several morphological traits. It would seem that the long history of in situ conservation of this landrace in a multitude of subsistence farming systems of Oman contributed to this high level of diversity. There were significant differences among the Batini landraces for susceptibility indices (SSI) estimated for shoot length and number of roots, (Jaradat *et al*., 2004b). On average, 66% of the total Batini landrace was considered tolerant to salinity.

The present study focused on the assessment of the grain and forage yields of the collection in order to identify entries with high yield under saline conditions. The experiments were conducted in field trials to record yield performance in desert conditions. The most valuable selection criteria used were biomass, straw and grain yield under both low and high irrigation water salinity. Our study aims to complement information collected under controlled conditions with field measurements under extreme aridity. We report here a field experiment in which 277 landraces and breeding lines were grown under three salinity levels.

MATERIALS AND METHODS

Barley collection

The collection consists of two types of genetic material:

(1) Batini landrace material including 234 entries selected from the 2308 entries that ICBA has collected from Oman. Seven subpopulations (Batini 1-7 according to Jaradat *et al.* 2004a) have been previously identified within the Batini landraces (Jaradat *et al.*, 2004a,b). The entries screened in the present study belong to subpopulations (Batini 1-5) that are known to carry salinity tolerance (Jaradat *et al.*, 2004a, b), with 80, 72, 20, 56 and 6 entries from the five subpopulations, respectively.

(2) International breeding material from ICARDA composed of: 27 barley entries from the Barley Observation Nursery (selected from 328 entries); 5 entries from the Heat Nursery Q2-4 (selected from 458 entries) and 11 entries from the Special Heat Nursery (selected from 320 entries). The breeding lines were selected based on screening for salinity tolerance from 1999-2003 at the UAE University Research Station in Al-Ain under the same salinity levels as the present study (Al-Dakheel *et al.*, 2001).

Field experiments

Field experiments were conducted during 2003/2004 and 2004/2005 cropping seasons at the Experiment Station of the International Center for Biosaline Agriculture (ICBA), Dubai, United Arab Emirates (25°13'N and 55°17'E). In the first cropping season, all the 277 entries were evaluated while in the second cropping season 70 entries (25% of the total) were evaluated. The experimental station is located in an arid desert climate where temperatures are high and rainfall is negligible from April to November (Karim and Al-Dakheel, 2006). The soil is a Carbonatic, Hyperthermic Typic Torripsamment having a negligible level of inherent soil salinity (0.2 dS m^{-1}). Three salinity treatments were established, corresponding to irrigation water salinities of 2, 8 and 14 dS m^{-1}, denoted as S1, S2 and S3 respectively. The S1 level correspond to the lowest available in water irrigation, while S2 is the prevailing level in the farmers fields of the region and S3 is the maximum level recommended by the extension services for growing cereals. The 8 and 14 dS m^{-1} irrigation salinities were accomplished by mixing highly saline groundwater (with EC_w up to 25 dS m^{-1}, SAR>26

mmol/l with Na and Cl concentrations higher than 190 meq/l and pH=7.6) with the 2 dS m^{-1} water, which was the lowest saline water available (SAR=4 mmol/l with Na and Cl concentrations lower than 11 meq/l and pH=8.5). Because of this, a control treatment with low salinity could not be established. The three salinity levels were maintained constant throughout each season. Each salinity level was monitored twice a week using a portable EC meter (TetraCon® 325 Cond 197i, WTW, USA). Typical salinities in the Arabian Penisula are of the order of 8 dS m^{-1} (Hussain, 1997). 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. All plot data were collected from the middle 1 m of the two central rows so as to avoid edge effects.

The experimental design was split-plot with three replicates. The main-plot factor was the salinity level and the subplot factor was the entry tested, with the entries randomized within each main-plot.

Prior to planting, the site was harrowed to ensure an even seedbed. Organic compost from cow manure (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) was spread and incorporated at the rate of 10 tons ha^{-1}. Plot measuring 2 m x 4 m, (for a plot area of 8 m^2) were established and seeded manually with a row spacing of 0.5 m to enable manual weeding. An equal number of 1600 seeds per entry were used since the germination rate from prior tests did not differ between entries. The plots were sown around mid November to avoid high temperatures and desiccating winds. N-P-K fertilizer (20-20-20%) was applied at a rate of 100 kg/ha (Growfert Solub™), corresponding to the recommended rate for the region. A drip irrigation system was used with a dripline for each row and an emitter spacing of 0.25 m.

Physiological maturity extended from late March to late April. The plots were harvested at maturity to measure yields of biomass (BY) and straw (SY) at 0% moisture. Grain yield (GY) was measured at 15% moisture. Harvest index (HI) was calculated as GY/BY. All yields are expressed in units of tons per hectare.

Statistical Analyses

Statistical analyses were performed on SY, BY, GY and HI in three stages:

(1) Analysis of variance (ANOVA) was done according to split-plot design. The 277 total entries for the first cropping season and 70 total entries for the second cropping season (Batini and ICARDA) were compared using Fisher's protected LSD test at the $P < 0.05$ level.

(2) Principal component analysis (PCA) was performed on trait means recorded at each salinity level in order to cluster the tested entries from the Batini landrace and ICARDA's germplasm according to their end-uses purposes, either grain, forage, or both (dual use), for each salinity level. Note that 'variate' stands for any response variable and 'individual' stands for any entry in this analysis. PCA helps the selection of a nursery, at 25% intensity of selection, based on entries loadings on the first and the second components at each salinity level. Selection was done at each salinity level independently. Firstly, we selected entries having simultaneous high values for both BY and GY. These entries will serve dual-purpose end-use. Secondly, we selected entries having high BY will serve for forage production. Thirdly, we selected entries having high GY to benefit the purpose of grain production. The intensity of selection of 25% was as balanced as possible for all end-uses. Note that end-use ability of an entry was determined using its loadings on the two components of PCA at each salinity level. During the second cropping seasons, there were 25 entries selected out of the 70 entries (36% intensity of selection) according to the same procedure.

(3) In the third step, the stability of the selected genotypes was analyzed. Stability assessment aims at characterization of the observed yield variation for each entry under different salinity levels. The more stable an entry is, the lower will be its yield variation with salinity. Stability was estimated using genotype ecovalences (von Wricke, 1962) and computed for each entry of the 70 selected entries. Ecovalence describes stability type 2 (Lin et al., 1986) in which stable genotypes respond as a parallel line to the mean of all tested genotypes. This parameter quantifies genotype x environment interaction. Higher values of ecovalence mean lower stability.

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

RESULTS

Evaluation of the entire collection of 277 entries

Average SY, GY, BY and HI were 4.2, 1.99, 6.2 t ha^{-1} and 31.2%, respectively, as shown in table 1. Salinity reduced SY, GY, BY, and HI, particularly at the higher level of 14 dS m^{-1} under which the reductions were 33%, 68%, 47%, and 33%, respectively. At the intermediate salinity level of 8 dS m^{-1} the decreases were less than 22%. The analysis of the entire collection reveals significant effects of salinity and salinity × entry ($P = 10^{-4}$) as shown in table 2. The salinity factor contributed the most towards sum of squares of the ANOVA (higher than 94%) followed by the effect of the entry and the interaction term. For all traits, the models were parsimonious with no more than 33% of

Table 1. Comparison of Batini landraces (Batini 1-5) to breeding lines (HN, ON and SHN), in the collection of 277 entries, for straw yield (SY, t ha^{-1}), grain yield (GY, t ha^{-1}), biomass yield (BY, t ha^{-1}) and harvest index (HI, %) at three salinity levels (S1=2 dS m^{-1}, S2=8 dS m^{-1} and S3=14 dS m^{-1}).

Traits	SY (t ha^{-1})			GY (t ha^{-1})			BY (t ha^{-1})			HI (t ha^{-1})		
salinity level	**S1**	**S2**	**S3**	**S1**	**S2**	**S3**	**S1**	**S2**	**S3**	**S1**	**S2**	**S3**
Batini landraces												
Batini1	6.379	5.365	4.425	3.131	2.405	1.014	9.51	7.77	5.439	34.028	32.162	20.409
Batini2	5.626	5.519	3.462	2.496	2.049	0.897	8.123	7.568	4.359	31.866	27.807	22.071
Batini3	5.505	4.684	2.935	2.253	2.021	1.134	7.758	6.705	4.069	30.269	30.916	26.883
Batini4	5.232	5.269	3.21	2.931	2.171	0.884	8.163	7.44	4.094	35.668	30.417	23.463
Batini5	5.262	5.364	5.069	2.684	2.295	0.978	7.946	7.659	6.047	33.975	31.114	16.939
Breeding lines												
HN	4.371	3.283	2.497	3.59	1.503	1.098	7.961	4.787	3.595	39.861	28.289	30.78
ON	3.774	4.166	2.377	2.556	2.367	0.778	6.33	6.533	3.155	40.164	36.63	27.198
SHN	3.679	4.147	3.138	3.258	2.222	0.987	6.937	6.368	4.125	46.164	34.615	26.812

HN, heat nursery; ON, observation nursery; SHN, special heat nursery.
S1–3, mean of all salinity levels.

the degrees of freedom used. Note that the error term of the interaction between replication and salinity was not significant for the integrative trait HI. A comparison of the means of SY, GY, BY, and HI for the 277 entries for each salinity level showed least significant differences of 0.2, 0.1, 0.25, t ha^{-1} and 0.9%, respectively (T tests LSD). Therefore, the entries can be clustered into different groups according to their end-use purposes.

Correlation between the traits related to forage and grain yields were analyzed using a PCA (Figures 1 and 2) representing more than 97% of the variation and clustering the entries into significantly different groups according to their end-uses. Note that the loadings of all variates were equal to 1. Axis 1 (first component) accounted for more than 54% of the variation. This component was influenced by forage production parameters BY and SY. Whereas, Axis 2 (second component), accounting for more than 40% of the variation and influenced by grain production parameters: GY and HI. Plots of the entries orders the best yielding entries with positive coordinates for both principal components (Figure 2).

For all salinity levels, Batini landrace variability subsume the breeding lines for forage yield parameters, whereas breeding lines displayed the highest variability for grain yield parameters. Twelve percent, 32% and 4% of the collection was suitable for grain, forage and dual purpose uses respectively regardless of the salinity level. Most of the entries that are suitable for all uses belong to the Batini landrace. For grain use, 21% of the breeding material (SHN and HN nurseries) and 11% of the Batini landraces displayed high yield at all salinity levels tested. Breeding lines SHN and HN were the most adapted since they displayed the highest harvest index. However, for forage use, there were no breeding lines with a stable response. In contrast, 26 Batini landraces (particularly Batini 1) displayed a stable yield over the range of salinity. Indeed, regardless of yield reduction due to salinity, the Batini landraces displayed the lowest reduction in forage yield (a maximum reduction of 38%) as compared to the breeding lines (a maximum reduction of 45%). For grain use, the breeding lines belonging to nurseries selected for heat tolerance (HN and SHN) were the most adapted.

Note that at the lowest salinity (2 dS m^{-1}) the Batini landrace a34 (Batini 1) was ranked among the top ten for both BY and GY, whereas at highest salinity (14 dS m^{-1}) Batini landraces a52, b37 and a31 were ranked among the top yielding for all yield components. These entries maintained BY and GY yields of 10-12 t ha^{-1} and 2-2.5 t ha^{-1}, respectively. The average yield reduction compared to the potential was intermediate (50%) compared to the lowest yielding entries for which the reduction was 90%. Over all the salinities, there were only three entries that were suitable for dual purpose use (a17, a22 and a71 from Batini 1). The most interesting entries for forage and grain yield were a12 and a73 (from Batini 1), respectively. There were variations in the coordinates of the entries in the three PCAs, showing a high G × E interaction. Based on entry coordinates a selection of a subset of 70 entries was achieved. Selected entries capture all the variation for forage and grain yields and yield stability. Only one genotype among the bottom ten entries was selected (b26 from Batini 2) as a control.

Table 2. Analyses of variance for straw yield (SY, t ha^{-1}), grain yield (GY, t ha^{-1}), biomass yield (BY, t ha^{-1}) and harvest index (HI, %) in the collection of 277 entries.

Traits	Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
SY (t ha^{-1})	Replication	2	42.403	21.202	36.44	10^{-4}
	Salinity	2	1756.315	878.158	1509.32	10^{-4}
	Replication x Salinity	4	27.241	6.81	11.7	10^{-4}
	Entry	276	4480.173	16.233	27.9	10^{-4}
	Salinity x Entry	552	4995.136	9.049	15.55	10^{-4}
	Residual	1656	963.496	0.582		
GY (t ha^{-1})	Replication	2	0.014	0.007	0.11	0.89
	Salinity	2	1511.392	755.696	11752.62	10^{-4}
	Replication x Salinity	4	1.026	0.256	3.99	$3.2\ 10^{-3}$
	Entry	276	883.856	3.202	49.8	10^{-4}
	Salinity x Entry	552	984.958	1.784	27.75	10^{-4}
	Residual	1656	106.481	0.064		
BY (t ha^{-1})	Replication	2	40.884	20.442	30.63	10^{-4}
	Salinity	2	6484.982	3242.491	4858.77	10^{-4}
	Replication x Salinity	4	37.197	9.299	13.93	10^{-4}
	Entry	276	6167.753	22.347	33.49	10^{-4}
	Salinity x Entry	552	6012.152	10.892	16.32	10^{-4}
	Residual	1656	1105.127	0.667		
HI (%)	Replication	2	654.828	327.414	14.35	10^{-4}
	Salinity	2	59885.738	29942.869	1311.93	10^{-4}
	Replication x Salinity	4	135.172	33.793	1.48	0.20
	Entry	276	135446.416	490.748	21.5	10^{-4}
	Salinity x Entry	552	198433.478	359.481	15.75	10^{-4}
	Residual	1656	37795.871	22.824		

DF, Degree of freedom.

Evaluation of the selected collection of 70 entries in 2003-2005

Analyses of variance for all traits in the 70 entries tested revealed significant effects for year, salinity, and entry factors. Interaction terms of entry with year and salinity showed high genotypic interaction with the environment. The salinity level tested on salinity x year interaction (error A pooled over years) was significant ($P=10^{-4}$, Table 3). The term of replication x salinity (year) was not significant (error B pooled over years) for the integrative trait HI. These ANOVAs explained 94-98% of the variance using only 56% of the degrees of freedom (Table 3). Averaged across all factors, SY, GY, BY, and HI were equal to the values obtained for the whole collection of 277 entries, but the Batini and Breeding lines differed significantly ($P=3\ 10^{-2}$). The correlation between the traits related to forage and grain yields were analyzed using a PCA resuming more than 95% of the variation enabling the entries to be clustered into significantly different groups according to their end-uses (Figure 3). Salinity applies a gradual selection pressure on the entries (more variance captured when salinity increased), that was higher for forage than for grain production. Batini landraces had more well performing entries for forage and dual purpose end than breeding lines.

Over all salinity levels, there were three entries suitable for dual purpose end-use (a12, a18 and a55 from Batini 1). For forage purpose end-use, the most stable genotypes were a15-16, a60, d24 and e3. However, for grain purpose end-uses there were 17 entries displaying high yield over all salinity levels. There were 2-3 genotypes from the Batini landrace that were the most variable for each trait and percent contribution to

Table 3. Analyses of variance for straw yield (SY, t ha^{-1}), grain yield (GY, t ha^{-1}), biomass yield (BY, t ha^{-1}) and harvest index (HI, %) in the collection of 70 entries.

Variable	Source	DF	Sum of squares	Mean square	F Value	Pr > F
SY (t ha^{-1})	Year	1	1480.772	1480.77	2970.19	10^{-4}
	Replication (Year)	4	7.853	1.96	3.94	$3.7\ 10^{-3}$
	Salinity	2	356.034	178.02	357.07	10^{-4}
	Year x Salinity	2	67.063	33.53	67.26	10^{-4}
	Replication x Salinity (Year)	8	10.274	1.28	2.58	$9.1\ 10^{-3}$
	Entry	69	1038.361	15.05	30.19	10^{-4}
	Year x Entry	69	647.398	9.38	18.82	10^{-4}
	Replication x Entry (Year)	276	204.390	0.74	1.49	10^{-4}
	Year x Salinity x Entry	138	1045.761	7.57	15.2	10^{-4}
	Salinity x Entry	138	976.779	7.078	14.2	10^{-4}
	Residual	552	275.197	0.50		
GY (t ha^{-1})	Year	1	216.466	216.47	3473.47	10^{-4}
	Replication (Year)	4	0.085	0.02	0.34	0.85
	Salinity	2	354.047	177.02	2840.56	10^{-4}
	Year x Salinity	2	136.256	68.13	1093.2	10^{-4}
	Replication x Salinity (Year)	8	0.982	0.12	1.97	$4.8\ 10^{-2}$
	Entry	69	218.366	3.16	50.78	10^{-4}
	Year x Entry	69	138.794	2.01	32.28	10^{-4}
	Replication x Entry (Year)	276	21.622	0.08	1.26	$1.3\ 10^{-2}$
	Year x Salinity x Entry	138	171.138	1.24	19.9	10^{-4}
	Salinity x Entry	138	181.943	1.318	2.16	10^{-4}
	Residual	552	34.401	0.06		
BY (t ha^{-1})	Year	1	1860.787	1860.79	2756.87	10^{-4}
	Replication (Year)	4	6.635	1.66	2.46	$1.5\ 10^{-2}$
	Salinity	2	1458.903	729.45	1080.72	10^{-4}
	Year x Salinity	2	371.430	185.72	275.15	10^{-4}
	Replication x Salinity (Year)	8	16.619	2.08	3.08	$2.1\ 10^{-3}$
	Entry	69	1292.069	18.73	27.74	10^{-4}
	Year x Entry	69	719.226	10.42	15.44	10^{-4}
	Replication x Entry (Year)	276	261.626	0.95	1.4	$4\ 10^{-4}$
	Year x Salinity x Entry	138	1330.59	9.64	14.29	10^{-4}
	Salinity x Entry	138	1209.615	8.76	12.99	10^{-4}
	Residual	552	372.581	0.67		
HI (%)	Year	1	2095.294	2095.29	123.39	10^{-4}
	Replication (Year)	4	266.735	66.68	3.93	$3.7\ 10^{-3}$
	Salinity	2	10641.657	5320.83	313.34	10^{-4}
	Year x Salinity	2	4825.614	2412.81	142.09	10^{-4}
	Replication x Salinity (Year)	8	177.296	22.16	1.31	0.24
	Entry	69	33699.458	488.40	28.76	10^{-4}
	Year x Entry	69	23541.223	341.18	20.09	10^{-4}
	Replication x Entry (Year)	276	6160.995	22.32	1.31	$3.8\ 10^{-3}$
	Year x Salinity x Entry	138	27908.408	202.23	11.91	10^{-4}
	Salinity x Entry	138	27614.970	200.11	11.78	10^{-4}
	Residual	552	9373.448	16.98		

DF, Degree of freedom.

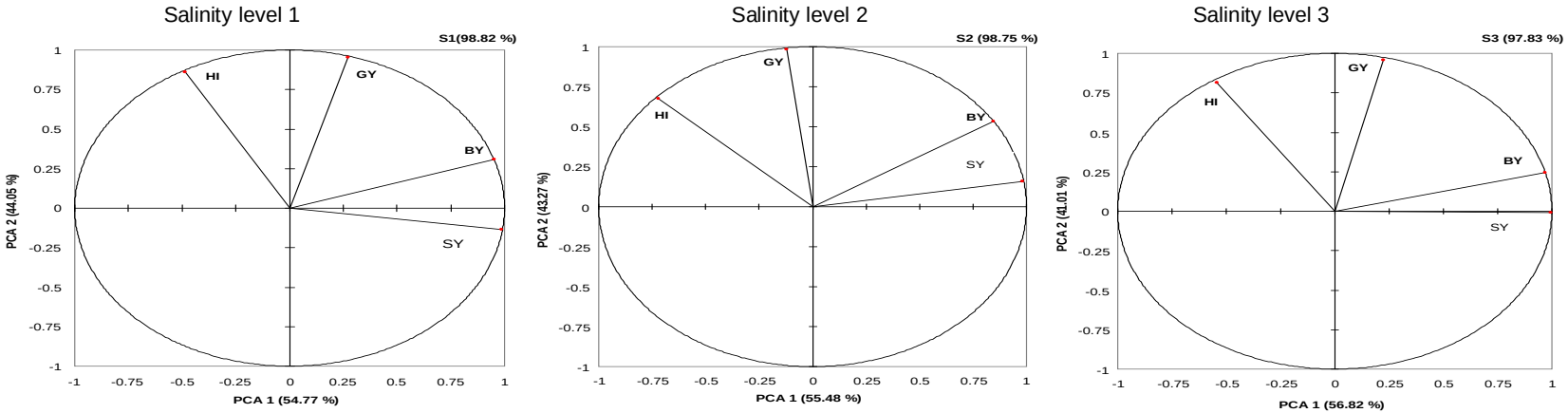

Figure 1. Principal component analyses of the variates: straw yield (SY, t ha^{-1}), grain yield (GY, t ha^{-1}), biomass yield (BY, t ha^{-1}), and harvest index (HI, %), and the 277 entries tested in 2003/2004, at three salinity levels S1 (2 dS m^{-1}), S2 (8 dS m^{-1}) and S3 (14 dS m^{-1}).

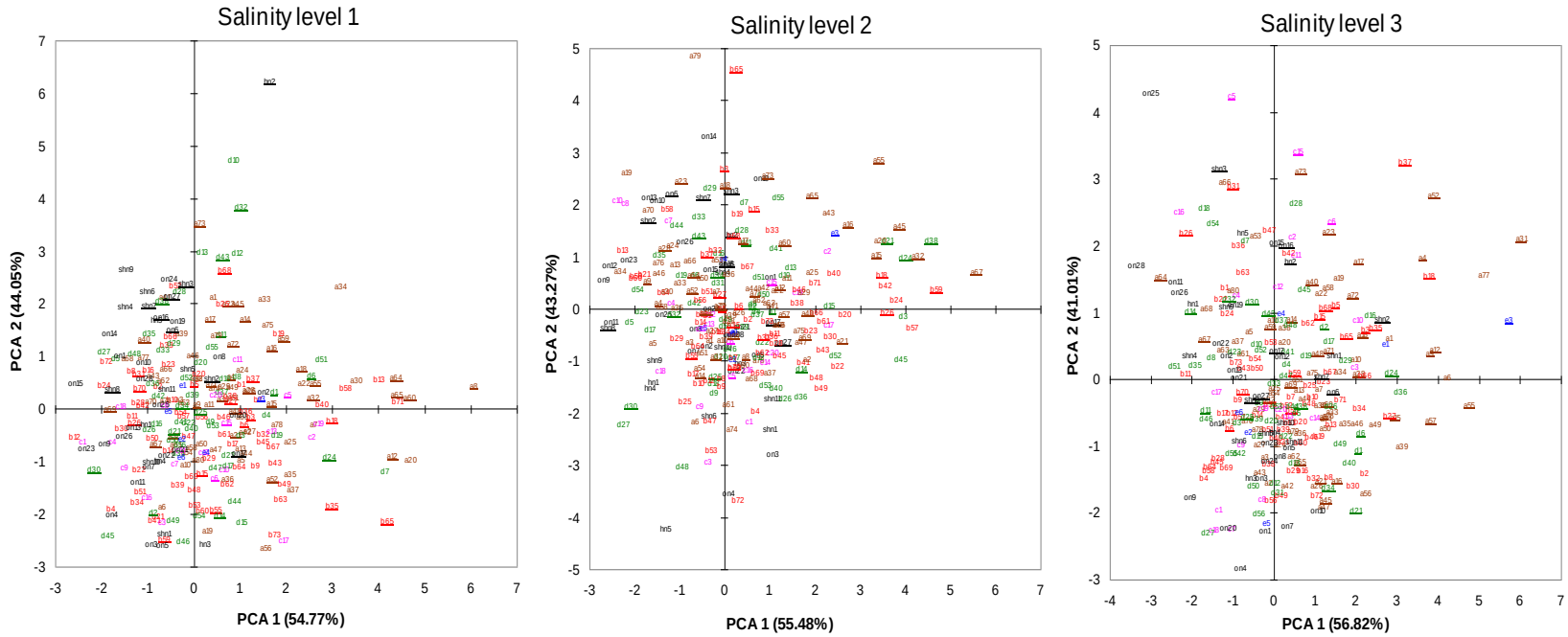

Figure 2. Projection of 277 entries, grown in 2003/2004, on two axes: first component (axis 1) and second component (axis 2) at three salinity levels S1 (2 dS m^{-1}), S2 (8 dS m^{-1}) and S3 (14 dS m^{-1}).

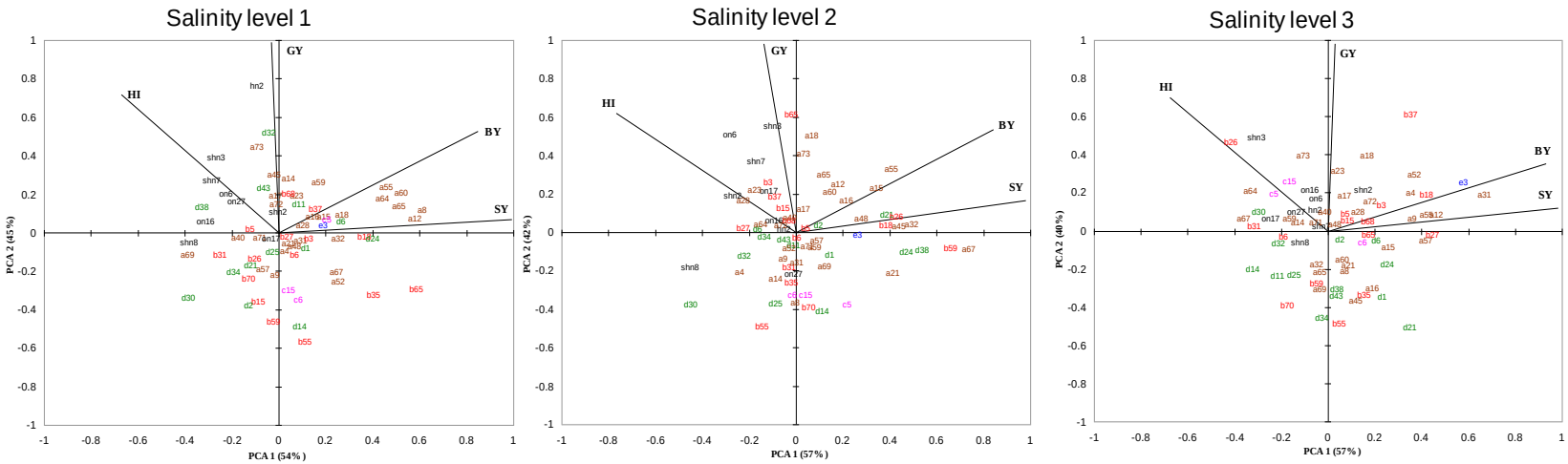

Figure 3. Biplots of principal component analyses of the variates: straw yield (SY, t ha^{-1}), biological yield (BY, t ha^{-1}), grain yield (GY, t ha^{-1}) and harvest index (HI, %), and the entries tested during 2003/2004 and 2004/2005 cropping seasons. Projection of 70 entries on two axes: first component (PCA 1) and second component (PCA 2) at three salinity levels S1 (2 dS m^{-1}), S2 (8 dS m^{-1}) and S3 (14 dS m^{-1}).

genotype × environment interaction was higher than 5% (Figure 4). The entries that were most variable for biomass yield were a32, a69 and b27, and those responsible for grain yield interactions with year were entries b68 and shn2. Entries b18 and a55 were among the best forage yielding and the less variable over the two cropping seasons. There were entries a18, a73, c15, on16 and shn3 having simultaneous grain yield stability and top performance. However, only entry a4 was slightly interactive for both yields and ranked among the best. A representative nursery composed of 25 entries was selected, in order to capture all the variation in genotype stability. Comparison of means, variances and yield correlations showed that the subset of the 25 entries selected out of the 70 assessed was representative and could be evaluated extensively for further agronomic traits in future studies. Among the 25 selected entries, there were 21 entries from the Batini landrace and four from ICARDA's breeding lines (see underlined entries in Figure 3). The selected Batini entries included 13, 5 and 3 from Batini 1, Batini 2 and Batini 4, respectively. The ICARDA's selected breeding lines included two entries from the Observation Nursery and two entries from the Special Heat Nursery.

DISCUSSION

The present paper reports results of evaluation of a large panel of barley composed of Batini landrace and breeding lines under various irrigation water salinity. The salinity factor applied here seems to create a high selection pressure on entries for single-purpose as well as for dual-purpose uses, but in higher magnitude for forage production. Genotypic differences in reaction to similar salinity stresses were reported for barley cultivars differing in salt tolerance (Munns *et al.*, 2006). Tolerant and sensitive cultivars experienced 40 to 55% and 65 to 70% reduction in biomass yield, respectively. These results were recorded after a 30-d exposure to 17 dS m^{-1}. In another experiment reported by Royo and Aragüés (1999), reductions in grain and straw yields were up to 80% and 46%, respectively. High forage yields under salinity were attributed to either longer crop growth duration before harvest, higher leaf and tiller numbers per plant, or higher plant density. Otherwise, forage yield reductions of 40% and 85% were reported for barley as salinity increased to medium (9 dS m^{-1}) and high (16 dS m^{-1}) levels, respectively (Royo and Aragüés, 1999). The reduction of yield observed in the present experiments was accentuated when irrigation

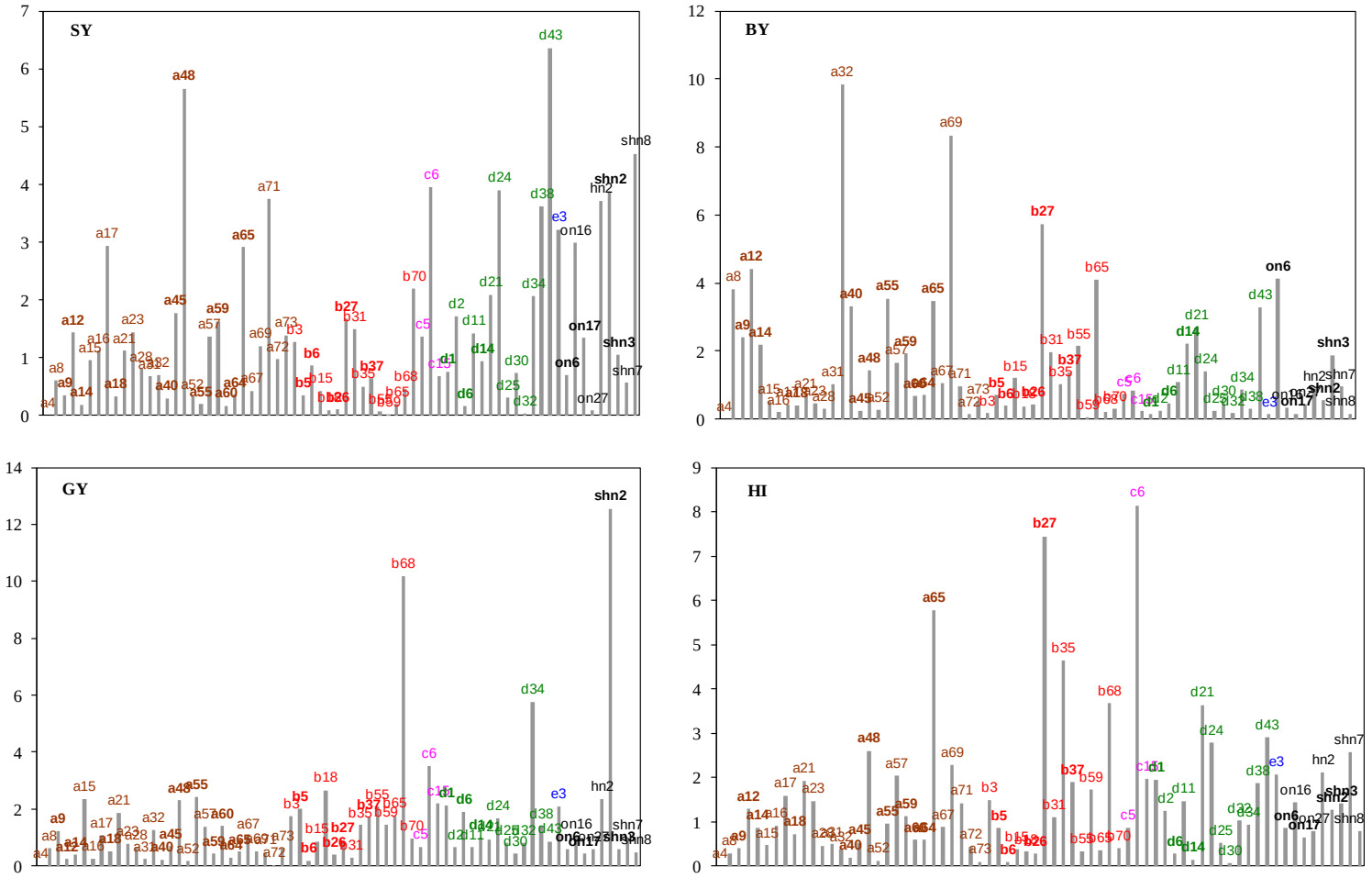

Figure 4. Relative contribution of each entry (in percent), of the collection composed of 70 entries, to entry x year interaction estimated by use of von Wricke's ecovalence method for straw yield (SY, t ha^{-1}), biomass yield (BY, t ha^{-1}), grain yield (GY, t ha^{-1}) and harvest index (HI, %) during 2003/2004 and 2004/2005 cropping seasons

water salinity exceeded 8 dSm^{-1}. These results are consistent with others reported in the literature (Richards *et al.*, 1987; Al-Miskri *et al.*, 2006; Jaradat *et al.*, 2004a,b; Royo and Aragüés, 1999). Jaradat *et al.* (2004a) estimated genetic variation for salinity tolerance in the Batini landrace at 73%. This landrace is a genetically heterogeneous population and is considered a potential reserve of useful genes for adaptation to biotic and abiotic stresses. The Batini landraces originate from harsh environments where growing factors favor forage production compared to ICARDA's

breeding lines which were originally selected for grain production in arid and semi-arid environments. The Batini landrace displayed the highest forage ability whatever salinity level was imposed in the present experiment. However, ICARDA's entries were more adapted to grain purpose end-use. The gap between the distributions of the two collections particularly increased at 14 dS m^{-1}. The selected entries would constitute a reference collection composed of genetically diversified material representing the whole range of variation as well as high yielding and stable entries to be further evaluated in on-farm trials. Salt tolerant entries selected from this work could outperform exotic barley cultivars under subsistence farming systems characterized by low inputs and high irrigation water salinity. Our results showed that Batini 1, Batini 2 and only entry e3 from Batini 5 were the most adapted to salinity. Batini 1-2 landraces are known to have an intermediate gene diversity (Jaradat *et al.*, 2004a). Salinity tolerance was associated with longer seedling roots than the average of the entries in Batini 2. The most salt tolerant subpopulation was Batini 4 (having short rachilla hair which is characteristic of high tolerance) as suggested by Jaradat *et al.* (2004b) and in this study exhibited a low contribution to genotype x year interaction. Reductions of 10-72% were estimated for Batini 4, which is a highly salt tolerant subpopulation of the Batini landrace (Jaradat *et al.*, 2004a, b).

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