

Impact of irrigation water salinity on agronomical and quality attributes of *Cenchrus ciliaris* L. accessions



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ABSTRACT

Cultivation of salt tolerant perennial grasses using saline water irrigation is potentially an important strategy to save fresh water resources and maximize the forage yield of small-scale farms in the marginal environment. Field evaluation of 40 Buffel grass (*Cenchrus ciliaris* L.) genotypes was conducted at ICBA, Dubai, UAE over eight years (2006–2013) under three irrigation water salinities (EC: 5, 10 and 15 dS m⁻¹) to identify salinity tolerance potential based on plant growth, biomass yield and quality attributes. Total annual and average fresh (FW) and dry biomass (DW) varied significantly among genotypes under all salinity levels. Lower DW producing accessions were higher in nutritive value while higher DW producing accessions had lower nutritive value in terms of crude protein (CP) and neutral detergent fiber (NDF). From multivariate analysis, accessions 37, 2, 3, 12, and 15 were salt tolerant, high biomass and stable genotypes with adequate nutritive value at different salinities. In contrast, genotypes 21, 23, 24, 25, and 40 were salt sensitive and low yielding. Genotype 37 (Grif 1619) was the most stable and high yielder at all salinity levels. The local accession 38 (MAF 74) had higher yield comparable to 37 but declined sharply at the highest salinity that made it suitable for medium level salinity. It is concluded that wide genotypic diversity exists among a diverse collection of *C. ciliaris* accessions for salinity tolerance biomass production and multivariate analysis facilitate the grouping of stable and high yield accessions into different clusters. These salt-tolerant accessions can be grown to maximize forage production and desertification combat in the arid environment.

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1. Introduction

Salinity problems in crop production will become worse in areas with rapidly growing human population and limited water resources, which force growers to use poor quality water for irrigation. Soil salinity is a serious threat limiting crop production (Munns, 2002) as it adversely reduces the overall productivity of ecosystem. The plants face numerous abnormal, physio- morphological and biochemical changes under salinity stress and cause delayed germination, high seedling mortality, poor crop stand, stunted growth and reduce yields (Ahmad et al., 2010). The identification and development of salt tolerant fodder crops may help to address the scarcity of good quality water in many arid regions of the world where vast reserves of saline and brackish water exist. Many grasses and salt tolerant crops are able to produce high biomass under saline conditions. Buffel grass (*Cenchrus ciliaris* L.) is an important C₄ forage grass (family: Poaceae) being peren-

nial, sometimes produces rhizomes and is native to the Arabian Peninsula. It is drought tolerant plant that can be grown under the marginal soils and water scare conditions. It is very good pasture grass for hot and dry regions in the tropics and sub tropics and mainly cultivated for permanent pastures in Africa, Australia and Asia (Franklin et al., 2006; Arshadullah et al., 2011). Buffel grass has proved useful for pasture and soil retention in a wide range of environment due to its drought tolerance, deep roots, rapid response to summer rains, relative palatability and resistance to overgrazing. It produces viable seed so that stands can be self-replacing and pastures may not need to be reseeded. Buffel grass seed may survive for up to an estimated 4 years in the soil, but plants can live for many years (Winkworth, 1971). *C. ciliaris* plants are constantly confronted with various biotic and abiotic stress factors like high temperature, salt, drought, flooding, heat, oxidative stress and heavy metal toxicity (Ibarra-Flores et al., 1995; Ward et al., 2006).

Improved salinity tolerance permits the conservation of fresh water and its use for high 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

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Table 1
Buffel grass (*Cenchrus ciliaris* L.) germplasm collection with genebank entry numbers and country of origin during 2004–2005.

S.No.	Accessions	Entry numbers	Country of origin	S.No.	Accessions	Entry numbers	Country of origin
1	PI 153,671	2	Kenya	21	PI 409,267	393	South Africa
2	PI 161,633	6	South Africa	22	PI 409,295	417	South Africa
3	PI 161,637	9	South Africa	23	PI 409,429	507	South Africa
4	PI 185,564	18	South Africa	24	PI 409,556	565	South Africa
5	PI 225,012	48	Ghana	25	PI 409,585	576	South Africa
6	PI 225,583	49	South Africa	26	PI 409,669	600	South Africa
7	PI 271,206	88	India	27	PI 409,689	619	South Africa
8	PI 271,208	90	India	28	PI 409,704	632	South Africa
9	PI 271,209	91	India	29	PI 414,447	653	South Africa
10	PI 271,214	96	India	30	PI 414,452	658	South Africa
11	PI 271,219	101	India	31	PI 414,499	702	South Africa
12	PI 279,596	111	Philippines	32	PI 414,513	714	South Africa
13	PI 294,595	124	Australia	33	PI 442,096	750	Japan
14	PI 295,659	130	Zimbabwe	34	PI 443,507	754	Mexico
15	PI 365,650	220	Tanzania	35	PI 516,516	760	Morocco
16	PI 365,651	221	Tanzania	36	Grif 1619	764	Australia
17	PI 365,720	252	Tanzania	37	Grif 1639	784	Pakistan
18	PI 385,321	287	Tanzania	38	MAF 74		UAE
19	PI 409,174	315	South Africa	39	MAK 7		UAE
20	PI 409,216	349	South Africa	40	MAK 9		UAE

within the crop and, when available, within its wild relatives. These accessions should be characterized by high productivity under saline conditions, thereby extends agriculture to more marginal environments. Previously, no systematic effort has been undertaken to evaluate salinity tolerance in a wide range of *C. ciliaris* genotypes. Therefore, the present work was undertaken to evaluate and identify the salt-tolerant *C. ciliaris* from a large collection stored at ICBA's gene bank. The specific objectives of this study were to (a) identify genetic diversity among *C. ciliaris* genotypes for salt tolerance (b) evaluate genotypes for relative salt tolerance potential in terms of fresh biomass and dry matter yield under agro-ecological conditions of Dubai (U.A.E.) using multivariate analysis.

2. Materials and methods

2.1. Plant material

The organization of core collection of particular plant population and selection of top performing accessions under field offers better opportunities for specie screening and evaluating genetic diversity (Turi et al., 2012). We evaluated 40 *C. ciliaris* L. genotypes (selected from initial screening trial in germination bioassays out of 800 accessions from a global collection supplied by USDA) for salt tolerance potential under field condition (Table 1).

2.2. Field trial and experimental design

The experiments were conducted between 2006 and 2013 at International Center for Biosaline Agriculture (ICBA), Dubai, United Arab Emirates (25°13'N and 55°17'E). The experimental station is located in an arid desert climate where temperature is high and rainfall is negligible 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 d Sm⁻¹). 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 30 t ha⁻¹. Plots measuring 0.5 m × 4 m, (for a plot area of 2 m²) were established and planted manually with a row spacing of 0.5 m to enable manual weeding. An equal number of 16 plants per entry were used since the germination rate from prior tests did not differ between entries. The plots were sown in mid October to avoid high temperatures and desicating winds. N–P–K fertilizer (20–20–20%) was

applied at a rate of 100 kg ha⁻¹ (Growfert Solub™), corresponding to the recommended rate for the region.

2.3. Salinity treatments and agronomic measurements

Three salinity treatments were established, corresponding to irrigation water salinities of 5, 10 and 15 dS m⁻¹, denoted as S1, S2 and S3, respectively. The S1 level corresponds to the lowest salinity in irrigation water, while S2 is the prevailing level in the farmer's fields of the region and S3 is the maximum salinity level recommended by the extension services. The target saline irrigation water (5, 10, 15 dS m⁻¹) 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). A control treatment with lowest salinity, therefore, could not be established. The three salinity levels were maintained constantly throughout the cropping season during all the years. Each salinity level was monitored twice a week using a portable EC meter (TetraCon® 325Cond 197i, WTW, USA). Irrigation was applied at rates equivalent to ET₀ plus 10% for leaching requirements. After harvest, all plots were irrigated at ET₀ plus 25% for additional leaching. The plant samples were collected at heading stage from the middle 1 m of the two central rows to avoid edge effects and weighed to measure fresh biomass (t ha⁻¹), dried at 70 °C for three days and re-weighted to determine dry matter yield (t ha⁻¹). Every year, average five harvests were achieved and 120 samples of 0.5 m² were collected at each harvest.

2.4. Irrigation management system

The experimental field plots were supplied with high and low salinity water from two large reservoirs. Before delivery to the field, the water was mixed in a mixing unit inside a chamber and adjusted to achieve the target salinity and supplied to plants through drip irrigation system in the field plot area. The plots were laid out in strips where each genotype was grown on 1 row 4 m long with a planting density of 4 plants per linear meter. 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.

Table 2
Ranking of genotypes for their relative salt tolerance in terms of plant biomass (fresh and dry weight) in a cluster analysis. (Ward's minimum variance analysis).

Genotypes	Salt level (dS m ⁻¹)	Cluster group ranking ^a	Sum ^b	Genotype ranking ^c	Genotypes	Salt level (dS m ⁻¹)	Cluster group ranking ^a	Sum ^b	Genotype ranking ^c
37	5	1	3	1	17	5	2	9	6
	10	1				10	3		
	15	1				15	4		
2	5	1	4	2	18	5	3	9	6
	10	1				10	3		
	15	2				15	3		
3	5	2	5	3	6	5	4	10	7
	10	2				10	3		
	15	1				15	3		
12	5	3	5	3	28	5	3	10	7
	10	1				10	4		
	15	1				15	3		
15	5	2	5	3	10	5	4	11	8
	10	2				10	4		
	15	1				15	3		
30	5	1	5	3	33	5	3	11	8
	10	3				10	4		
	15	1				15	4		
8	5	2	6	4	35	5	4	11	8
	10	3				10	4		
	15	1				15	3		
11	5	2	6	4	13	5	3	12	9
	10	3				10	4		
	15	1				15	5		
16	5	2	6	4	22	5	4	12	9
	10	3				10	4		
	15	1				15	4		
38	5	1	6	4	26	5	4	12	9
	10	1				10	4		
	15	4				15	4		
5	5	2	7	5	27	5	5	13	10
	10	3				10	4		
	15	2				15	4		
9	5	2	7	5	36	5	5	13	10
	10	3				10	4		
	15	2				15	4		
29	5	2	7	5	39	5	5	14	11
	10	2				10	5		
	15	3				15	4		
31	5	3	7	5	4	5	5	15	12
	10	2				10	5		
	15	2				15	5		
32	5	1	7	5	20	5	5	15	12
	10	2				10	5		
	15	4				15	5		
34	5	1	7	5	21	5	5	15	12
	10	3				10	5		
	15	3				15	5		
19	5	3	8	6	23	5	5	15	12
	10	3				10	5		
	15	2				15	5		
1	5	3	9	6	24	5	5	15	12
	10	4				10	5		
	15	2				15	5		
7	5	5	9	6	25	5	5	15	12
	10	4				10	5		
	15	5				15	5		
14	5	3	9	6	40	5	5	15	12
	10	3				10	5		
	15	3				15	5		

^a Cluster groups were obtained from Ward's minimum-variance cluster analysis on the means of plant fresh and dry weight. Genotypes were divided into five cluster groups at 5, 10, and 15 dS m⁻¹ salinity level. Cluster group rankings were obtained from cluster means (data not shown) in the order from highest to the lowest cluster means.

^b Sums were obtained from the cluster group rankings by adding the ranking numbers at the three salt levels in each genotype.

^c Genotypes were finally ranked based on sums with the smallest sum being the most relatively tolerant.

2.5. Buffelgrass forage quality analysis

The dry ground plant samples were analyzed for crude protein (CP), neutral-detergent fibre (NDF), acid detergent fibre (ADF) and ash contents as described previously (AOAC, 1990; Van Soest et al., 1991) with slight modification (Kitcherside et al., 2000).

2.6. Statistical analysis

The experiment was laid out in a split-plot design and replicated thrice. Data of the 40 genotypes were analyzed using General Linear Model's (Multivariate analysis) with the statistical package SPSS (version 17.00) for Windows (SPSS Inc., Chicago, IL, USA). Principal component analysis (PCA) was performed on trait means (FW, DW),

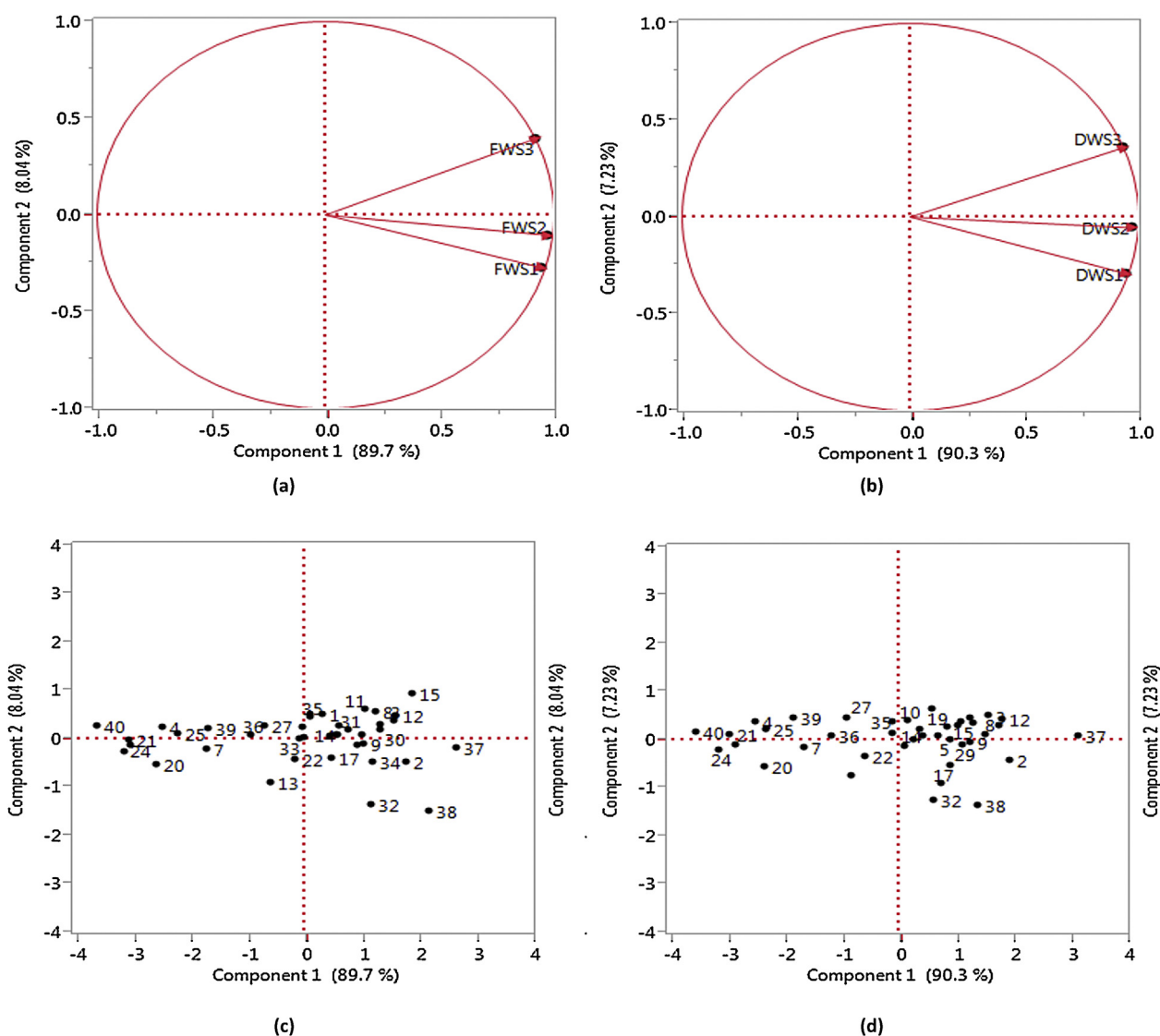


Fig. 1. (a,b) Principal component analysis of the variables: Fresh weight (FW) and dry weight (DW) at three irrigation water salinity levels (5, 10 and 15 dS m^{-1}). (c,d) Two dimensional scatter plot of genotypic relationship among 40 *Cenchrus ciliaris* accessions as revealed by first two principal components.

recorded at each salinity level. PCA helps the selection of entries, at 25% intensity, based on entries loadings on the first and the second components at each salinity level. Hierarchical cluster analysis of 40 *C. ciliaris* accessions were carried out using JMP 12.0 software. Cluster group rankings were obtained based on Ward's minimum variance on the means of the plant biomass at heading stage. The cluster group rankings were obtained from the averages of means in order from highest to lowest averages. A sum was obtained by adding the numbers of cluster group ranking at each salt level in each genotype. The genotypes were finally ranked based on the sums in order that those with the smallest sums were ranked as the most tolerant and those with the largest sums were ranked as the least tolerant in terms of relative salt tolerance.

3. Results and discussion

3.1. Impact of irrigation water salinity on total annual yield of *Cenchrus ciliaris* L. accessions

Average total annual yield in *C. ciliaris* genotypes ranged from 98.0 to 353.0 t ha^{-1} at low salinity (5 dS m^{-1}), 78.0–269.0 t ha^{-1} at medium (10 dS m^{-1}) and 73.5–225.5 t ha^{-1} at high salinity lev-

els (15 dS m^{-1}). Annual DW yield were in the range from 34.5 to 106 t ha^{-1} at 5 dS m^{-1} salinity level, 26.5–90.5 t ha^{-1} at medium salinity (10 dS m^{-1}) and from 24.5 to 73.0 t ha^{-1} at high salinity (15 dS m^{-1}) (data not shown). Genotypes were divided into five cluster groups at 5, 10, and 15 dS m^{-1} by simultaneous analysis on plant fresh and dry biomass using Ward's minimum-variance cluster analysis (Table 2). The accessions, which acquired lowest values in genotype ranking, were considered salt tolerant while others that had highest values were considered salt sensitive. The genotypes were finally ranked with accession 37 (Grif 1639 from Pakistan) as the most salt tolerant and accession 40 (MAK 9 from UAE) as the most salt sensitive in terms of plant biomass production. In the present study, wide genetic diversity was observed among the accessions from different part of the globe (Table 2). Previous screening of the different genotypes of *C. ciliaris* has also shown the genotypic differences for salt tolerance on seedling growth, plant fresh and dry biomass (Arshad et al., 2007; Jorge et al., 2008). The accessions 37, 2, 3, 12, 15 (corresponding to; Grif 1639, PI161633, PI161637, PI279596, and PI365650) had shown high salt tolerance potential whereas the others were less tolerant. These genotypes were originated from Pakistan, South Africa, Philippines and Tanzania, respectively. Moreover, it was revealed from the present

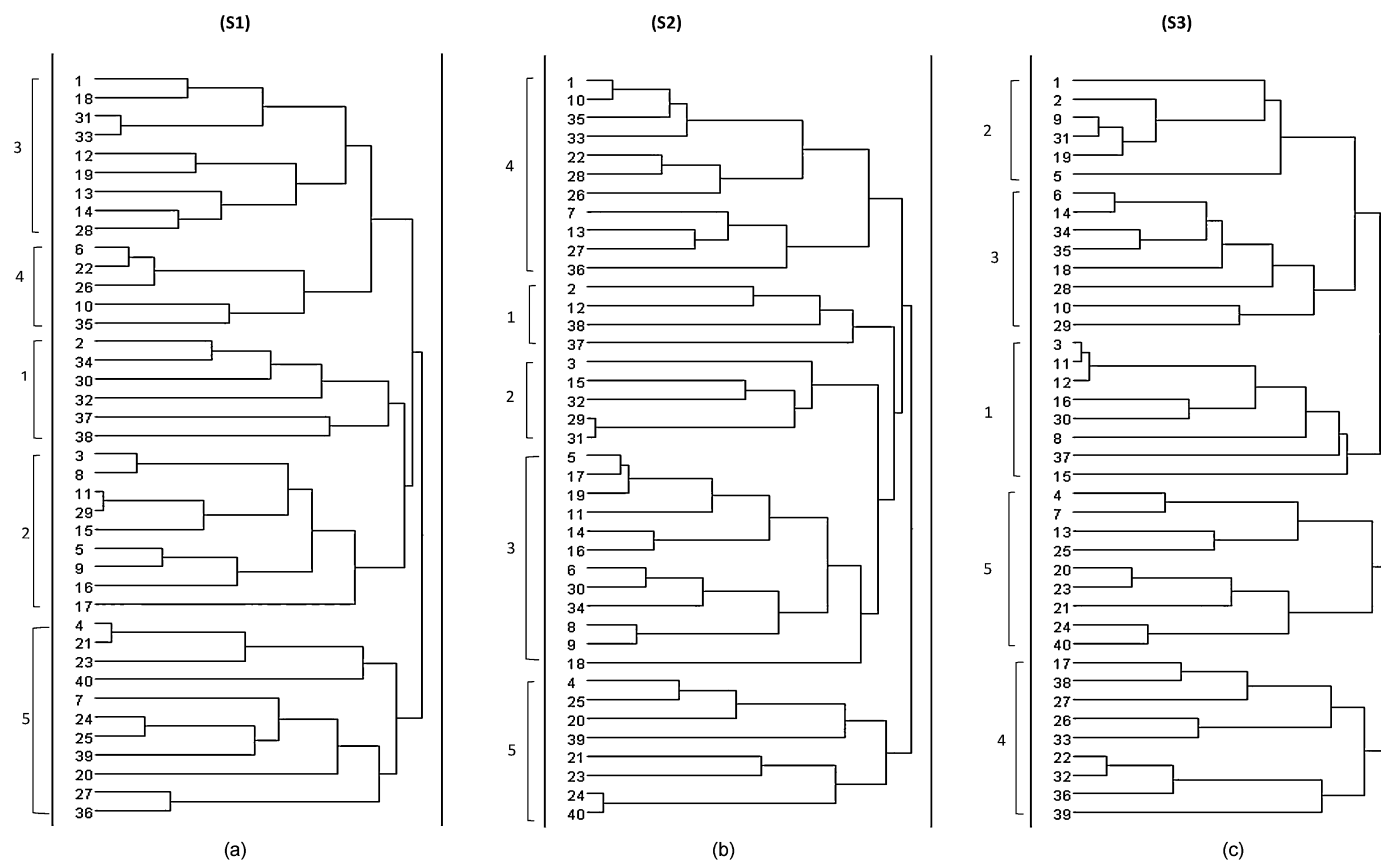


Fig. 2. (a,b,c) Dendrograms showing the relationship among 40 accessions of *Cenchrus ciliaris* L. based on plant biomass (fresh and dry weight) at three salinity levels (S1 = 5, S2 = 10, S3 = 15 dS m⁻¹) in a Hierarchical cluster analysis.

study, that several accessions like 20, 21, 23, 24, and 25 were produced less biomass and all were originated from South Africa. It was demonstrated that shoot dry weight was severely affected in the *C. ciliaris* ecotype from Faisalabad region, where it decreased from 29.83 to 8.02 g. The ecotype from the Salt Range region showed considerable increase in root fresh and dry weights accompanied by much less reduction in shoot fresh and dry weights as compared to that from the Faisalabad region (Nawazish et al., 2006). The decision to incorporate some genotypes in salt tolerance breeding programs depends on the combination of salt tolerance potential at different growth stages. When the development pattern of genotypes is different between growth stages, assessment of the actual salt tolerance of genotypes may be determined by comparisons of their biomass production over a long growth period (Leland et al., 1994; Munns et al., 2000).

3.2. Evaluation of *Cenchrus ciliaris* L. accessions based on multivariate analysis

3.2.1. Principal component analysis (PCA)

The *Cenchrus* accessions were further explored using PCA (Fig. 1). First principal component (PC1) depicted 89.7% of total variation among the fresh biomass trait. Fresh biomass at highest salinity (FWS3) contributed positively to PC1. The fresh biomass measured from all 40 accessions at salinity level (S1, S2) was included in the PCA, and illustrated primarily negative correlation with PC1 (Fig. 1a). The PC2 explained an additional 8.04% of the total variation among various traits and there was no correlation with any of traits measured at any salinity level. The DW measured from all 40 accessions showed 90.3% of the observed variation and could be explained by PC1. Dry weight at high salinity (S3) con-

tributed positively towards PC1. There was negative contribution towards PC1 by DW trait at lower and medium salinity (S1, S2) (Fig. 1b). Moreover, PC2 depicted 7.23% of the total variation among DW trait but there was no correlation with DW traits towards PC2 at any salinity. Salinity applies a gradual selection pressure on the entries (more variance captured when salinity increased), that was higher for dry biomass than fresh biomass. Each principal component (PC) accounted for a proportion of the variation and was correlated to different degrees to the measured parameters. Accessions 37, 2, 3, 12, 15, and 30 attained higher biomass while genotype 40 consistently produced minimum fresh/dry biomass than rest of the accessions. The first two principal components were plotted to observe the relationships between accessions and represented by two dimensional scatter plot of genetic relationship among genotypes. The separation on the basis of PC1 and PC2 revealed that the genotypes were scattered in all quarters, which show the high level of genetic diversity in evaluated genotypes. We might draw conclusions about the loading of factors (components) as follows: Factor 1 correlates well with the variables (accessions) 37, 2, 3, 12, 15, and 30 while Factor 2 is strongly correlated with variables (accessions) 21, 23, 24, 25 and 40 (Fig. 1c,d). Diversity of populations within a geographical origin and similarity of populations beyond geographical limits have also been reported in *C. ciliaris* genotypes (Arshad et al., 2007). The variability among the accessions from diverse origin could be related primarily to their morphological differences and secondly to agronomic use.

3.2.2. Hierarchical cluster analysis

Clustering based on plant biomass grouped the 40 genotypes into five clusters (Fig. 2). Cluster group "1" has salt-tolerant accessions followed by cluster "2" and produced highest biomass at

Table 3
Effect of three irrigation water salinity levels (5, 10, 15 dS m⁻¹) on nutrient composition of selected *Cenchrus ciliaris* L. accessions. Data were a percent (%) of dry biomass.

Accessions	Salinity levels	Crude protein			Acid detergent fiber (ADF)			Neutral detergent fiber (NDF)			Ash		
		5 dS m ⁻¹	10 dS m ⁻¹	15 dS m ⁻¹	5 dS m ⁻¹	10 dS m ⁻¹	15 dS m ⁻¹	5 dS m ⁻¹	10 dS m ⁻¹	15 dS m ⁻¹	5 dS m ⁻¹	10 dS m ⁻¹	15 dS m ⁻¹
2		4.70	6.50	4.90	42.6	40	43.4	75.5	75.3	77.6	10.6	9.4	11.3
5		7.40	7.90	7.70	37.1	39.6	36.8	69.7	71.3	70.7	12.5	14	12.8
6		7.40	7.40	7.20	39.2	36.6	37.9	70	67.7	69.7	14.8	16.7	13.6
8		5.00	5.50	6.00	41.1	43.9	42.2	75.3	76	73.2	12	11.2	10.1
13		5.70	5.60	4.00	39	43	46.10	67.2	71	75.5	14.2	11.9	11.6
15		6.50	7.40	6.40	39.2	40.3	40.4	70.8	71.4	71.6	13.9	15.1	12.6
21		5.40	7.60	5.90	46.5	40	42.2	74.6	75.8	72.7	11.9	10.8	13.7
37		4.80	6.40	5.50	40.9	38.9	44.8	72.8	75	75	12.5	9.9	11.3
38		4.70	6.00	6.20	44	47.7	43	73.7	73.5	66.5	12.3	14.3	15.2
40		6.00	7.40	5.60	43.4	41.8	40.7	72.3	72.1	73.9	13.9	13.1	12.5
Mean		5.76	6.77	5.94	41.30	41.18	41.75	72.19	72.91	72.64	12.86	12.64	12.47
S.E.		1.05	0.88	1.06	2.84	3.09	2.89	2.73	2.68	3.19	1.29	2.39	1.47

5 dS m⁻¹. Maximum number of accessions (11), were salt-sensitive and present in cluster group “5”, followed by group “4” (5 accessions) that produced lowest yield at low salinity (Fig. 2a). At medium salinity (10 dS m⁻¹), accessions were grouped into cluster group “1” (4), highly salt-tolerant; group “2” (5), moderately salt tolerant while group “3” (12), group “4” (11) and group “5” (8) represent sensitive accessions (Fig. 2b). Hierarchical cluster analysis showed that some of accessions collected from various regions were grouped into the same cluster, while many others fell into different clusters. The application of cluster analysis in multivariate observations has been suggested for comparisons of cultivar means (Zeng et al., 2002; Juan et al., 2005). The Fig. 2c showed that cluster “1” consisted of highly salt tolerant genotypes (8) that acquired maximum biomass yield at high salinity (15 dS m⁻¹) while 6 accessions were pooled into group “2” and were moderately salt-tolerant. It was concluded that all accessions having same origin would always have low diversity among themselves. For example, in Australia where *C. ciliaris* is grown extensively, rainfall can occur during the cooler months and most cultivars of *C. ciliaris* respond poorly to these rains owing to the cold temperature. Accessions originating from cool, dry environment could be promising for these areas through improved performance in spring, owing to a better response to rains during the cooler seasons (Hacker and Waite, 2001). A good starting point in selecting suitable accessions for dry areas is to test accessions with good agro-morphological attributes and which originate from areas with very low rainfall.

3.3. Effect of irrigation water salinity on nutrient composition of selected *Cenchrus ciliaris* L. accessions

The grasses are the cheapest form of animal feed available in term of quantity and quality. Feeding value of forages is mainly dependent on the crude protein, fiber and ash contents. Crude protein content (CP) was higher in low biomass yielding *C. ciliaris* genotypes (6 and 40) that produced 7.4% CP following treatment at 10 dS m⁻¹ (Table 3). The highest crude protein content (7.9%) was obtained in genotype 5 at medium salinity (10 dS m⁻¹) while lowest CP (4.0%) was analyzed in genotype 13. The low DW producing accessions were higher in nutritive value and higher DW producing accessions had lower nutritive value in terms of CP. Overall crude protein is medium level in all genotypes, fiber is comparable to good quality grasses and ash is within the acceptable levels even at 15 dS m⁻¹. The present results are in agreement with Suyama et al. (2006), whom reported the lower crude protein content at non saline and higher CP values at higher salinity in *Paspalum*, creeping wildrye and Bermudagrass. Moreover, NDF (neutral detergent fiber) also increased as salinity in irrigation water increased from lower to medium level (5–10 dS m⁻¹) and forage quality increases as CP increase and as NDF decreases. Crude protein is very use-

ful in the diet of ruminants to keep up their milk and maintaining livestock meat quality (Afzal and Ullah, 2007). Differences in NDF among the Buffelgrass accessions were similar to that for CP those having lower CP tended to have higher NDF and accession 2 had highest NDF values (75.5–77.6%) while accession 5 and 6 had lowest NDF values (69–71%) among the genotypes. Accession 37 (Grif 1619) and 38 (MAF 74) had less than 47% NDF (38–47%), but accession 5 and 6 had ADF ranging from 36 to 39% (Table 3). Genotypic differences in the nutritional parameters among the cultivars of *C. ciliaris* and other grasses have also been reported by Arshadullah et al. (2011).

In conclusion, it showed the existence of wide genetic diversity among the *Cenchrus* genotypes. The accessions (37, 2, 3, 12, and 15) were identified as salt tolerant, high yielder and stable genotypes under various salinity levels. Accession 37 (Grif 1619) was found the best genotype in terms of biomass yield at all salinity levels during all cropping seasons under UAE conditions and had adequate nutritional value. These genotypes hold good salt tolerance potential and can be grown to enhance farm productivity and stability in hot and arid environments

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