## SELECTION OF POTASSIUM EFFICIENT AND RESPONSIVE WHEAT GENOTYPES FOR SUSTAINABLE LOW K-INPUT AGRICULTURE

## MUHAMMAD ALI KHAN\*, MUHAMMAD UBAIDULLAH SHIRAZI, AISHA SHEREEN, MAHBOOB ALI SIAL, MUHAMMAD ATHAR KHAN, ASMA AND SAIFULLAH BALOCH

Plant Physiology Division, Nuclear Institute of Agriculture, Tandojam, Pakistan \*Corresponding author's email: alipaec@hotmail.com

#### Abstract

The study was conducted at early seedling stage for the evaluation of K-efficient and K-responsive wheat genotypes using Johnson's solution adjusted to 0.3 mM (def.K) and 3.0 mM (adq.K) uses  $K_2SO_4$  as Potassium source. The experiment was arranged in completely randomized design (CRD) and each treatment was replicated thrice. It was found that usually K-deficiency resulted to decrease biomass production, K- contents and K- use efficiency. On the contrary potassium use efficiency was enhanced, almost four folds in the genotypes grown at low K (0.3 mM) and significantly correlated with total biomass (r=0.732). On the basis of growth parameters, i.e. Shoot dry weight(SDW), Root dry weight(RDW), Total biomass(TBM), Root shoot ratio(RSR) and Potassium Use efficiency(KUE) ) as well as K-allocations parameters, i.e. Shoot Potassium accumulation(TKA), nine genotypes, viz. MSH-14, NIA- Sundar, SD-4047, Khirman, 17-03, SD-222, NIA-MB-II, 54-03 and SD-621 were categorized as responsive & efficiently utilized for screening of wheat genotypes under deficient and adequate K conditions. It is further suggested that K-responsive and efficient wheat genotypes may be utilized in the breeding programme to develop K-efficiency for sustainable low K-input wheat production.

Key words: Potassium levels, Wheat, Potassium use efficiency (KUE).

## Introduction

Pakistan is an agriculture based country comprised population of 240 million. Wheat is the main agricultural crop among the cereals (Hussain *et al.*, 2012). The economy of 80% farming community is dependent on this crop. It engages approximately 70 percent of the Rabi crops and 40 percent (8.83 M ha.) of the total cropped area in the country while contribution of this crop to GDP is approximately 1.7 percent (Anon., 2020).The expansion of agricultural production of wheat is slow as compared to the population growth rate.

The population of the country for the year 2035 is estimated to be as high as 403 million and the food grain requirement for this population would be 51 million tons approximately which is almost double from the current production of 26 million tons (Anon., 2019). The potential yield of wheat is 8.0 tons/ha, while the average yield in the country is 2.87 tons/ha therefore the yield gap between potential and average yield is 64% (Anon., 2021) which is too high. Pakistan ranks 9<sup>th</sup> in area, 11<sup>th</sup>1in total production and 8<sup>th</sup> in average yield among the key wheat producing countries of the world (Anon., 2020).In spite of nearly 70 percent of area being rain-fed in the neighboring country (India), their average wheat yield is 2.640 tons ha<sup>-1</sup> in comparison with the highest yield of 2.491 tons ha<sup>-1</sup> ever achieved in Pakistan (Anon., 2014).

There are many reasons for low yields of wheat in the country including abiotic (water, salt, heat stresses and water logging) and biotic stresses (insect pest and diseases). Extensive research has been conducted for decades on these issues; however no efforts have been made for the development of nutrient efficient crops (Khan *et al.*, 2017). Nutrient efficient varieties have encouraging environmental impacts through reduced use of fertilizer in agriculture.

Potassium is among the main nutrients needed by the plants in higher quantities and necessary for plant processes (Wang et al., 2012).Crop metabolic productivity is directly influenced by its involvement in photosynthesis, enzyme activation, solute phloem transport, opening and closing of stomata, co-transport of sugars etc. (Marschner, 2012; Wang et al., 2013). Crop productivity may be enhanced either through increased or efficient use of Potassium (Pettigrew, 2008). This major element is usually neglected in the country due to elevated prices of fertilizers (Shah et al., 2011) and the common consent for the presence of enough amount of potash in the soil (Wakeel & Ishfaq, 2022). According to Wakeel (2015) and Saleem et al., (2011), potassium is employed in the country only @0.8 kg ha<sup>-1</sup> yr<sup>-1</sup> while world average for the use of this element is 15.1 kg ha<sup>-1</sup> (Khan et al., 2017). It is estimated an annual deficit of 0.265 million tons of K from Pakistani soils (Rafique et al., 2012 and Wakeel, 2015).

Presently 40% of soils are potassium deficient in the country while still 60% of the soils have adequate K. Therefore, there is a dire need to explore K-efficient (the genotype which perform well under K-deficient environment) & K-responsive (the genotype which perform well under K-sufficient environment) wheat genotypes. In future breeding programmes, wheat genotypes selected on the basis of K efficiency will be beneficial for low K-input agriculture (Wang & Chen, 2012), while K-responsive genotypes will yield higher in K-sufficient soil.

The objective of this study is to explore K-efficient and K-responsive wheat genotypes to discover potential candidate genotypes for sustainable low K-input wheat production in the country.

#### **Materials and Methods**

The present study consists of a series of experiments conducted at early seedling stage in growth cabinets programmed at  $25/25^{\circ}C \pm 5$  day/night temperature and 12 h photoperiod (irradiance: 22 Wm<sup>-2</sup>). Eighteen (18) wheat genotypes (Triticum aestivum L.) were screened out at two contrasting K levels i.e. adq. (3.0 mM) and def.-K (0.3mM). The diversified wheat germplasm was collected from plant breeding and genetics division (PBGD) of NIA, Tando Jam. The experiment was arranged factorially in completely randomized design (CRD) and replicated thrice. Seeds of each genotype were surface sterilized with sodium hypochlorite (NaOCl). Thirty seedlings in each treatment (i.e. adq. & def. K) were raised on plastic molded nets, placed in plastic bowls of 8.5 cm diameter (Anon., 1984-85), containing half (1/2)strength Johnson's modified solutions (Johnson et al., 1957) of respective K concentration. For smooth germination, the bowls were kept in dark for 72 hrs. The germinated seedlings were exposed to 12 h photoperiod for 11 days. The pH was adjustment regularly at  $5.5 \pm using$  either 1 N  $H_2SO_4$  or Ca (OH) 2

Plants were collected 14 days after sowing (DAS) and shoots & roots were separated gently and rinsed with distilled water. The SDW and RDW were taken on a digital weighing balance. RDW was divided with SDW for calculating root: shoot ratio (RSR). The roots and shoots were grinded in a wiley mill to pass through 1 mm (40 meshes) sieve. The finely grinded plant material (0.5 g) was digested in di-acid mixture of nitric acid (HNO<sub>3</sub>) and perchloric acid (HClO<sub>4</sub>) in a 3: 1 (Miller, 1998).

Potassium contents (mg g<sup>-1</sup>. dry weight) were determined with flame photometer (PFP-7) using standard curve while potassium relations were estimated with the help of formulae as suggested by various workers. K uptake or K accumulation (SKA & RKA) (in roots and shoots) = Dry weight x K concentration (Nawaz *et al.*, 2006), K utilization efficiency (KUE) = SDW  $\div$  Shoot K concentration (Glass, *et al.*, 1981), Potassium stress factor (KSF) = SDW<sub>adq.k</sub> - SDW<sub>def.k</sub> / SDW<sub>adq.k</sub> X 100 (Siddique & Glass. 1981).

Two methods were used for ranking the genotypes with respect to their response to K efficiency: 1) Gerloff (1977) and 2) Gill et al., (2004). According to Gerloff (1977) wheat genotypes were ranked into four groups, viz. 1) efficient 2) non-efficient 3) responsive and 4) nonresponsive on the basis of their shoot dry weight. The means of individual genotypes were compared with the population mean  $(\mu)$ . The genotypes were considered as efficient if they are yielding higher SDW at deficient K level in comparison with the population mean. Similarly non-efficient genotypes were those which were not yielding higher shoot dry weights at deficient K level in comparison with the population mean. In the same way the genotypes were considered as responsive if they yield 10% more SDW at adq.K as compared to its dry weight at deficient K level. Similarly the genotypes were categorized as non-responsive if the SDW at adq. K is less than 10% in comparison to its dry weight at def. K level.

Another widely used method for ranking the genotypes is of Gill *et al.*, 2004. In this study, this method was employed to group the genotypes into three categories on the basis of varietals means ( $\mu$ ) and STD (standard deviation).The contribution of a genotype was considered high if  $X > \mu$ +STD, low if  $X < \mu -$  STD, and the left over values were considered as having medium performance, where X is genotypic mean for specific parameter,  $\mu$  is a population mean and STD is standard deviation of population means. The index store value of 1, 2 and 3 were assigned to the genotypes having high, medium and low performance respectively.

#### **Statistical Analysis**

The software "Statistix ver. 8.1" (2006) was employed to carry out statistical analysis of data while varietal and treatment means were compared using Tukey's  $HSD_{0.05}$ .

## Results

The results of this study revealed existence of large genotypic differences among wheat genotypes and the differential reactions of biomass production (SDW& RDW), K accumulation and KUE at each K level. Tables 1, 2 & 3 shows the SDW, RDW, RSR and KSF of 18 wheat genotypes as affected by adq. and def. K levels. Data demonstrate a significant interaction between two K levels, genotypes and their interaction on these growth parameters.

At adq. K level, significantly ( $p \le 0.05$ ) higher SDW was recorded in genotype SD- 4047(0.558 g shoot<sup>-30</sup>), while lower in the genotype17-02 (0.398 g shoot<sup>-30</sup>). In the same way at def.K level, the genotype SD-502(0.519 g shoot<sup>-30</sup>), exhibited significantly ( $p \le 0.05$ ) higher SDW while two genotypes i.e. 5-02 and 17-02 depicted significantly lower SDW i.e. 0.310 g shoot<sup>-30</sup> (Table 1). The relative to adq.value for mean SDW of 18 genotypes at def. K level was 78 %, showing 22 % reduction because of K def. stress in comparison with adq. K level i.e., 100 (Fig. 1).

Wide genotypic variation for RDW was observed among wheatgenotypes at two K levels (Table 2). Maximum RDW was recorded in genotype SD-502  $(0.197 \text{ g root}^{-30})$  at adq.K. The values for RDW were statistically at par in genotype SD-222 (0.174 g root<sup>-30</sup>) and MSH-5 (0.170 g root<sup>-30</sup>). At def.K, the genotype SD-502 (0.213 g root<sup>-30</sup>) also maintained its superiority and increased RDW by10%, while other two genotypes i.e. SD-222 and MSH-5 exhibited comparatively less reduction of 4 and 5 %, respectively. The genotype MSH-5 and SD- 621 also showed their potential by exhibiting low reduction of 5 and 1% respectively at def.K level. In case of RDW, in contrast to SDW, 7 genotypes out of 18 increased their dry weight at def. k level, showing the capability of these genotypes to deal with def. K conditions. Un-expectedly, the genotypic mean of two K level i.e. adq. (0.148 g root<sup>-30</sup>) and def. (0.142 g root<sup>-30</sup>) showed non- significant interaction between two K level.

ť	inder adq.	and det. K	conditions	S.			
Construct		Sh	Inden	KSF			
Genotypes	Ad	q.K	Index	Def	.K	Index	(%)
MSH-14	0.542	ab	2	0.402	bc	2	26
NIA-Sarang	0.465	bcd	2	0.360	bc	2	23
22-03	0.495	abc	2	0.316	с	3	36
NIA-MB-I	0.468	abcd	2	0.386	bc	2	17
NIA-Sundar	0.494	abc	2	0.428	ab	2	14
SD-4047	0.558	а	1	0.449	ab	2	20
SD-502	0.533	ab	2	0.519	а	1	3
Chakwal-86	0.432	cd	3	0.365	bc	2	15
Khirman	0.510	abc	2	0.421	b	2	17
17-03	0.473	abcd	2	0.416	b	2	12
ESW-9525	0.482	abcd	2	0.314	с	3	35
SD-222	0.549	ab	1	0.438	ab	2	20
NIA-MB-II	0.533	ab	2	0.435	ab	2	18
MSH-5	0.514	abc	2	0.372	bc	2	28
54-03	0.552	ab	1	0.440	ab	2	20
SD-621	0.505	abc	2	0.413	b	2	18
5-02	0.538	ab	2	0.310	c	3	42
17-02	0.398	d	3	0.310	c	3	22
Population mea( $\mu$ )	0.502	А		0.394 B			
STD	0.044			0.057			
$\mu + STD$	0.546			0.451			
μ-STD	0.458			0.337			
Tukey HSD (0.05) for genotypic means	0.0	)92		0.0	94		
Tukey HSD (0.05) for Treatment mean			0.0213				

Table 1. Shoot dry weight (g shoot <sup>-30</sup> ) and potassium stress factor (KSF) of 18 wheat genotypes
under add and def K conditions

Genotypic means followed by similar alphabets in the column represents non- significant variation at  $p \le 0.05$ Genotypic means followed by similar numerical values in the column are alike in performance

Table 2. Root dry weights (g root <sup>-30</sup> )	) of 18 whe	at genoty	pes under	adq. and	def. K co	onditions.	
Constant		Rel.dec.					
Genotypes	Ad	q.K	Index	De	f.K	Index	(%)
MSH-14	0.159	bcd	2	0.132	bcd	2	17
NIA-Sarang	0.160	bcd	2	0.133	bcd	2	17
22-03	0.147	bcde	2	0.092	d	3	37
NIA-MB-I	0.128	Def	3	0.115	cd	3	10
NIA-Sundar	0.145	bcde	2	0.121	bcd	2	17
SD-4047	0.142	bcde	2	0.148	bc	2	(4)
SD-502	0.197	а	1	0.213	а	1	(10)
Chakwal-86	0.151	bcde	2	0.168	ab	2	(11)
Khirman	0.122	ef	3	0.157	bc	2	(29)
17-03	0.138	cdef	2	0.153	bc	2	(11)
ESW-9525	0.153	bcde	2	0.125	bcd	2	18
SD-222	0.174	ab	1	0.168	ab	2	4
NIA-MB-II	0.131	def	2	0.147	bc	2	(12)
MSH-5	0.170	abc	1	0.162	bc	2	5
54-03	0.138	cdef	2	0.121	bcd	2	12
SD-621	0.156	bcde	2	0.155	bc	2	1
5-02	0.146	bcde	2	0.119	bcd	2	18
17-02	0.105	f	3	0.131	bcd	3	(25)
Population mean(µ)	0.148	А		0.142	А		
STD	0.020			0.027			
$\mu$ +STD	0.168			0.170			
μ-STD	0.128			0.115			
Tukey HSD (0.05) for genotypic means	0.0	34		0.0	51		
Tukey HSD $(0.05)$ for treatment mean			0.0101				

Rel.dec. Relative decrease

		Rel.dec.					
Genotypes	Ad	q.K	Index	De	f.K	Index	(%)
MSH-14	0.294	cdef	2	0.328	defg	2	(11.56)
NIA-Sarang	0.338	abc	1	0.371	bcdef	2	(9.76)
22-03	0.296	cdef	2	0.291	fg	3	1.69
NIA-MB-I	0.274	defg	2	0.300	efg	3	(9.49)
NIA-Sundar	0.293	cdef	2	0.283	g	3	3.41
SD-4047	0.254	fg	3	0.330	cdefg	2	(29.92)
SD-502	0.363	а	1	0.411	abc	1	(13.22)
Chakwal-86	0.351	ab	1	0.459	а	1	(30.77)
Khirman	0.240	g	3	0.375	bcde	2	(56.25)
17-03	0.291	cdefg	2	0.368	bcdef	2	(26.46)
ESW-9525	0.319	abcd	2	0.396	abcd	2	(24.14)
SD-222	0.317	abcd	2	0.384	abcd	2	(21.14)
NIA-MB-II	0.247	fg	3	0.336	cdefg	2	(36.03)
MSH-5	0.329	abc	2	0.436	Ab	1	(32.52)
54-03	0.251	fg	3	0.275	g	3	(9.56)
SD-621	0.309	bcde	2	0.376	bcde	2	(21.68)
5-02	0.272	defg	2	0.386	abcd	2	(41.91)
17-02	0.264	efg	2	0.338	cdefg	2	(28.03)
Population mean( $\mu$ )	0.295	А		0.358	В		
STD	0.037			0.052			
$\mu$ +STD	0.331			0.410			
μ-STD	0.258			0.306			
Tukey HSD (0.05) forgenotypic means	0.053			0.082			
Tukey HSD $(0.05)$ for treatment mean							
Tukey HSD $(0.05)$ for treatment mean			0.0183				

Table 3. Root shoot ratio (RSR) of 18 wheat genotypes under adq. and def. K conditions.

Genotypic means followed by similar alphabets represent non- significant variation at  $p \le 0.05$ Genotypic means followed by similar numerical values in the column are alike in performance

Values in the parenthesis denote percentage (%) increase over adq.K

Table 4. Total Biomass (g plant <sup>-30</sup> )	) of 18 wheat genotypes	under adq. and def.	K conditions.

Genotypes	Ad	q.K	Index	De	f.K	Index	Rel. dec. (%)
MSH-14	0.701	abc	2	0.534	bcde	2	24
NIA-Sarang	0.625	abcd	2	0.494	bcde	2	21
22-03	0.641	abcd	2	0.408	e	3	36
NIA-MB-I	0.596	cde	2	0.501	bcde	2	16
NIA-Sundar	0.639	abcd	2	0.549	bcd	2	14
SD-4047	0.700	abc	2	0.597	b	2	15
SD-502	0.727	а	1	0.732	а	1	(1)
Chakwal-86	0.583	de	3	0.533	bcde	2	9
Khirman	0.632	abcd	2	0.578	b	2	9
17-03	0.611	bcde	2	0.569	b	2	7
ESW-9525	0.635	abcd	2	0.439	cde	3	31
SD-222	0.723	ab	1	0.606	ab	2	16
NIA-MB-II	0.664	abcd	2	0.582	b	2	12
MSH-5	0.683	abcd	2	0.534	bcde	2	22
54-03	0.689	abcd	2	0.562	bc	2	18
SD-621	0.661	abcd	2	0.568	b	2	14
.5-02	0.684	abcd	2	0.429	de	3	37
17-02	0.503	e	3	0.441	cde	3	12
Population mean( $\mu$ )	0.650	А		0.539	В		
STD	0.056			0.075			
μ+STD	0.706			0.614			
µ-STD	0.594			0.464			
Tukey HSD (0.05) for genotypic means	0.115			0.127			
Tukey HSD $(0.05)$ for treatment means			0.0414				

Genotypic means followed by similar alphabets represent non- significant variation at p≤0.05

Genotypic means followed by similar numerical values in the column are alike in performance (Values in the parenthesis denote percentage (%) increase over adq.K.

Rel. dec. Relative decrease

Data for RSR showed significant interaction between two K level and the mean value increased from 0. 295 (adq. K) to 0.358 (def. K). At adq.K level, the genotype SD-502 exhibited significantly higher (0.363) RSR followed by statistically at par values in Chackwal-86 (0.351), ESW-9525 (0.319), SD-222 (0.317), MSH-5 (0.329) and SD-621(0.309), (Table 3). Most of the genotype (16 out of 18) enhanced their RSR under def.K level.

The values for TBM under adq.and def.K environments were 0.650 and 0.539 g plant<sup>-30</sup> respectively and differed significantly ( $p \le 0.05$ ) (Table 4). Likewise, the genotypes SD-502, SD-222 and SD-4047 maintained their superiority under adq.K level and exhibited significantly ( $p \le 0.05$ ) higher TBM i.e. 0.727, 0.723 and 0.700 g plant<sup>-30</sup>, respectively. Among the tested genotypes, nine genotypes viz. MSH-14, SD-4047, SD-502, SD-222, NIA-MB-II, MSH-5, 54-03, SD-621and 5-02 showed TBM values higher the mean value i.e., 0.650 g plant<sup>-30</sup>at adq.K, showing the genotypic potential and/or responsiveness, under adq. K environment. Generally there was a gradual decrease in biomass of all the genotypes under K def. environment, except the genotype SD-502 (0.732 g plant<sup>-30</sup>) which coped with adverse K (def.K) conditions and maintained/increased its biomass. The other three genotypes viz. Chackwal-86,Khirman and 17-03 also showed encouraging performance and coped with adverse (def.K) K condition by exhibiting comparatively less reduction of only 9.0, 9.0 and 7.0% respectively as compared to TBM at adq.K level. The comparative to adq.value of mean TBM at def. K level was 82%, depicting a decrease of 18% due to low K (def.K) in comparison with adq. K level (Fig. 1).

The data for shoot and root potassium concentration (SKC, RKC) at both (adq. and def.) K levels are presented in Tables 5 and 6 respectively. Generally large reduction (50-69%) was observed due to K deficiency stress. The SKC varied significantly ( $p \le 0.05$ ) at both K regime with the mean value of 44.02 (adq.K) and 17.45 (def.K). However at adq.K level, the variation within the genotypes was non-significant. Comparatively higher SKC was recorded in four genotypes viz. SD-621 (48.87 mg g<sup>-1</sup> .dry wt.), MSH-5, NIA-Sundar and 5-02, ranged between 49 to 46.09 mg g<sup>-1</sup> .dry wt. while the genotype NIA-MB-II exhibited lowest SKC i.e.40.54 mg g<sup>-1</sup>.dry wt. The genotypes MSH-5, SD-621 and 5-02 also had significantly ( $p \le 0.05$ ) higher SKC at def.K level i.e.24.30, 23.05 and 23.03 mg g<sup>-1</sup> .dry wt. respectively. However maximum SKC was recorded in genotypes ESW-9525 (24.27 mg g<sup>-1</sup> .dry wt.). On the contrary the genotypes NIA-MB-I, NIA-MB-II and NIA-Sundar showed significantly lowest SKC (14.16 mg g<sup>-1</sup> .dry wt.).

The trend for RKC (mg g<sup>-1</sup> .dry wt.) is also varied significantly ( $p \le 0.05$ ) at both K levels with the mean values of 19.77 and 6.03 under adq.K and def.K environments, respectively. At adq.K, RKC exhibited non-significant variation among the genotypes. Three genotypes, viz. 17-03 (23.19 mg g<sup>-1</sup> .dry wt.), Chackwal-86(22.77 mg g<sup>-1</sup> .dry wt.) and 5-02 (22.50 mg g<sup>-1</sup> .dry wt.)

exhibited higher RKC at adq.K while the lowest RKC was found in the genotype 22-03 (15.41 mg g<sup>-1</sup> .dry wt.). At def. K. significant ( $p \le 0.05$ ) effects among the genotypes were observed. The genotype 5-02 (9.25 mg g<sup>-1</sup> .dry wt.) depicted significantly( $p \le 0.05$ ) higher RKC followed by statistically at par RKC in the genotype SD-222(7.71 mg g<sup>-1</sup> .dry wt.) while the genotype SD-502 (4.93 mg g<sup>-1</sup> .dry wt.) exhibited significantly lowest RKC. As in SKC, large reduction (59-74%) due to K-def. stress was also observed in case of RKC.

The shoot and root potassium accumulation (SKA and RKA)(mg plant<sup>-30</sup>) of 18 genotypes as affected by two K levels are presented in Tables 7 and 8 respectively. The SKA was statistically  $(p \le 0.05)$  affected by two contrasting K levels with the mean value of 22.07(adq.K) and 6.77(def.K). All 18 genotypes exhibited great decrease (range: 63-74%) due to low K (def.K). At adq.K, five genotypes, viz., 5-02 (24.90 mg shoot<sup>-30</sup>), SD-621(24.70 mg shoot<sup>-30</sup>), MSH-5(24.52 mg shoot<sup>-30</sup>), SD-222(24.06 mg shoot<sup>-30</sup>) and SD-502 (23.97 mg shoot<sup>-30</sup>) depicted significantly( $p \le 0.05$ ) higher SKA, while at def.K two genotypes, viz. SD- 621(9.47 mg shoot<sup>-30</sup>) and MSH-5(9.02 mg shoot<sup>-30</sup>) showed more SKA. The RKA was also statistically ( $p \le 0.05$ ) affected at both K levels with the mean value of 2.90 (adq.K) and 0.92 (def.K) (Table 8). Among the genotypes, surprisingly, non-significant variation in RKA was observed at both K level. At adq. K level, the genotype SD-502 (3.34 mg root<sup>-30</sup>), Chackwal-86 (3.45 mg root<sup>-30</sup>), 17-03 (3.19 mg root<sup>-30</sup>), ESW-9525 (3.39 mg root<sup>-30</sup>), SD-222 (3.31 mg root<sup>-30</sup>), MSH-5 (3.43 mg root<sup>-30</sup>), MSH-5 (3.43 g root<sup>-30</sup>) and 5-02  $(3.29 \text{ mg root}^{-30})$  showed comparatively higher RKA, while the genotype 17-02 (2.19 mg root<sup>-30</sup>) showed lowest RKA. Generally K deficiency stress showed large reduction (range: 61-77%) in RKC except the genotype 17-02, which showed less reduction (10%).

The results of KUE (g<sup>2</sup> SDW mg<sup>-1</sup> K) depicted a large increase in more or less all wheat genotypes because of low K(def.K) (Table 9). Out of 18, 11 genotypes, viz. MSH-14 (0.025g<sup>2</sup> SDW mg<sup>-1</sup> k), NIA-Sarang (0.025), NIA-MB-I (0.028), NIA-Sunder (0.031), SD-502 (0.032), Chackwal-86 (0.023), Khirman (0.028), 17-03 (0.028), SD-222 (0.029), NIA-MB-II (0.031), 54-03 (0.030), SD 621 (0.018) exhibited approx: 2 fold increases in KUE due to K deficiency stress. This is also indicated by the mean relative to adq. value of 208, revealing 108% increase in KUE due to K def. stress (Fig. 1). Significant differences ( $p \le 0.05$ ) amongst the genotypes at two Klevels (adq. and def.K) were observed. At adq .K, the genotype SD-4047 (0.014 g2 SDW mg<sup>-1</sup> K) exhibited significantly higher KUE, while the genotype 17-02  $(0.009 \text{ g}^2 \text{ SDW mg}^{-1} \text{ k})$  showed significantly lower KUE. At def.K, the genotype NIA-Sundar (0.031  $g^2$  SDW  $mg^{-1}$ k), SD-502(0.032  $g^2$  SDW mg<sup>-1</sup> k), SD-222(0.029  $g^2$ SDW mg<sup>-1</sup> k), NIA-MB- II (0.031 g<sup>2</sup> SDW mg<sup>-1</sup> K) and 54-03 (0.030  $g^2$  SDW  $mg^{-1}$  k) coped with the low K condition (def.K) and revealed statistically ( $p \le 0.05$ ) higher and similar KUE. The Two K level showed significant ( $p \le 0.05$ ) interaction with the mean value of 0.011(adq.K) and 0.024(def.K).

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Genotypes	Adq.K	Index	Def.I	K	Index	Rel. dec. (%)
MSH-14	43.32	2	16.38	bc	2	62.19
NIA-Sarang	41.93	2	14.70	bc	2	64.94
22-03	44.01	2	19.71	ab	2	55.21
NIA-MB-I	44.15	2	14.16	c	2	67.93
NIA-Sundar	46.09	2	14.16	c	2	69.28
SD-4047	40.82	2	17.22	bc	2	57.81
SD-502	44.98	2	16.10	bc	2	64.21
Chakwal-86	44.15	2	15.83	bc	2	64.14
Khirman	44.43	2	14.99	bc	2	66.26
17-03	41.65	3	14.72	bc	2	64.66
ESW-9525	44.71	2	24.27	а	1	45.72
SD-222	43.87	2	15.13	bc	2	65.51
NIA-MB-II	40.54	3	14.16	с	2	65.07
MSH-5	47.76	1	24.30	а	1	49.12
54-03	41.37	3	15.13	bc	2	63.43
SD-621	48.87	1	23.05	а	1	52.83
5-02	46.09	2	23.03	а	1	50.03
17-02	43.59	2	17.22	bc	2	60.50
Population mean(µ)	44.02 A		17.45 B			
STD	2.27		3.69			
$\mu$ +STD	46.29		21.15			
μ-STD	41.75		13.77			
Tukey HSD (0.05) for genotypic means	N.S		5.22			
Tukey HSD (0.05) for treatment means	1 4485					

Table 5. Shoot Potassium concentration (mg g<sup>-1</sup>. dry weight<sup>)</sup> of 18 wheat genotypes under adg. and def. K conditions.

 $\frac{\text{Tukey HSD (0.05) for treatment means}}{\text{Genotypic means followed by similar alphabets represent non- significant variation at p \leq 0.05} \\ \text{Genotypic means followed by similar numerical values in the column are alike in performance}}$ 

Rel. dec. Relative decrease

Table 6. Root Potassium concentration (mg g <sup>-1</sup> . dry weight) of 18 wheat genotypes
under adq. and def. K conditions.

Genotypes	Adg.K	Index	Def.	K	Index	Rel. dec. (%)
MSH-14	16.39	3	5.35	с	2	67.36
NIA-Sarang	16.66	3	5.14	с	2	69.15
22-03	15.41	3	5.99	с	2	61.13
NIA-MB-I	20.00	2	5.12	с	2	74.40
NIA-Sundar	20.00	2	5.64	с	2	71.80
SD-4047	20.41	2	6.32	с	2	69.03
SD-502	17.36	3	4.93	с	3	71.60
Chakwal-86	22.77	1	5.49	с	2	75.89
Khirman	21.52	2	6.53	с	2	69.66
17-03	23.19	1	5.35	с	2	76.93
ESW-9525	21.94	2	5.83	bc	2	73.43
SD-222	19.03	2	7.71	ab	1	59.49
NIA-MB-II	19.86	2	6.11	bc	2	69.23
MSH-5	20.69	2	6.46	bc	2	68.78
54-03	17.91	2	5.49	bc	2	69.35
SD-621	19.44	2	6.18	bc	2	68.21
.5-02	22.50	1	9.25	а	1	58.89
17-02	20.83	2	5.62	с	2	73.02
Population mean( $\mu$ )	19.77 A		6.03 B			
STD	2.28		1.04			
$\mu$ +STD	22.05		7.07			
μ-STD	17.49		4.99			
Tukey HSD (0.05) for genotypic means	N.S		2.26			
Tukey HSD (0.05) for treatment means		0.978	1			

Genotypic means followed by similar alphabets represent non- significant variation at  $p \leq 0.05$ 

Genotypic means followed by similar numerical values in the column are alike in performance

Rel. dec. Relative decrease

# Table 7. Shoot Potassium accumulation (mg shoot<sup>-30</sup>) of 18 wheat under adq. and def. K conditions.

Genotypes	Ado	<u>а.К</u>	Index	D	ef.K	Index	<b>Rel. dec. (%)</b>
MSH-14	23.46	ab	2	6.60	cde	2	72
NIA-Sarang	19.50	ab	2	5.29	e	3	73
22-03	21.78	ab	2	6.22	de	2	71
NIA-MB-I	20.65	ab	2	5.41	e	3	74
NIA-Sundar	22.79	ab	2	6.03	de	2	74
SD-4047	22.79	ab	2	7.70	abcd	2	66
SD-502	23.97	а	2	8.35	abc	1	65
Chakwal-86	18.98	ab	3	5.78	de	2	70
Khirman	22.67	ab	2	6.31	cde	2	72
17-03	19.74	ab	3	6.13	de	2	69
ESW-9525	21.10	ab	2	7.65	abcd	2	64
SD-222	24.06	а	2	6.61	cde	2	73
NIA-MB-II	21.58	ab	2	6.17	de	2	71
MSH-5	24.52	а	1	9.02	ab	1	63
54-03	22.78	ab	2	6.62	cde	2	71
SD-621	24.70	а	1	9.47	а	1	62
5-02	24.90	а	1	7.13	bcde	2	71
17-02	17.38	b	3	5.34	e	3	69
Population mean( $\mu$ )	22.07	А		6.77	В		
STD	2.16			1.23			
$\mu + STD$	24.23			8.00			
μ-STD	19.92			5.54			
Tukey HSD (0.05) for genotypic means	6.5	1		2	.07		
Tukey HSD (0.05) for treatment means				0.8	234		

Tukey HSD (0.05) for treatment means

Genotypic means followed by similar alphabet represent non- significant variation at  $p \le 0.05$ 

Genotypic means followed by similar numerical values in the column are alike in performance Rel. dec. Relative decrease

Table 8. Root Potassium accumulation (	mg root <sup>-30</sup> ) of 18	wheat genot	ypes under ad	q. and def.	K conditions.
Genotypes	Adq.K	Index	Def.K	Index	Rel. dec. (%)
MSH-14	2.63	2	0.71	2	73
NIA-Sarang	2.67	2	0.68	2	75
22-03	2.25	3	0.55	3	76
NIA-MB-I	2.56	2	0.59	3	77
NIA-Sundar	2.90	2	0.68	2	77
SD-4047	2.90	2	0.93	2	68
SD-502	3.34	1	1.05	2	69
Chakwal-86	3.45	1	0.92	2	73
Khirman	2.65	2	1.02	2	62
17-03	3.19	2	0.82	2	74
ESW-9525	3.39	1	0.72	2	79
SD-222	3.31	2	1.30	1	61
NIA-MB-II	2.63	2	0.90	2	66
MSH-5	3.43	1	1.05	2	69
54-03	2.48	3	0.67	2	73
SD-621	2.98	2	0.94	2	68
5-02	3.29	2	1.08	2	67
17-02	2.19	3	1.97	1	10
Population mean( $\mu$ )	2.90 A		0.92 B		
STD	0.41		0.33		
$\mu + STD$	3.32		1.25		
μ-STD	2.49		0.59		
Tukey HSD (0.05) for genotypic means	N.S		N.S		
Tukey $HSD(0.05)$ for treatment means		0 2140			

Tukey HSD (0.05) for treatment means 0.2149

Genotypic means followed by similar alphabet represent non- significant variation at  $p \le 0.05$ . Genotypic means followed by similar numerical values in the column are alike in performance

Rel. dec. Relative decrease

N.S= Non-significant

Table 9. 1 otassium use enficiency (g SDW mg	<b>K</b> ) UI 10 WI	icat genot	ypes unuer	auy. anu	uel. K con	luitions
Genotypes	Adq	. K	Index	De	f. K	Index
MSH-14	0.013	abc	1	0.025	abcd	2
NIA-Sarang	0.011	abc	2	0.025	abcd	2
22-03	0.011	abc	2	0.016	cde	3
NIA-MB-I	0.011	abc	2	0.028	ab	2
NIA-Sundar	0.011	abc	2	0.031	а	1
SD-4047	0.014	а	1	0.026	abc	2
SD-502	0.012	abc	2	0.032	а	1
Chakwal-86	0.010	bc	3	0.023	abcde	2
Khirman	0.011	abc	2	0.028	ab	2
17-03	0.011	abc	2	0.028	ab	2
ESW-9525	0.011	abc	2	0.013	e	3
SD-222	0.013	abc	1	0.029	а	2
NIA-MB-II	0.013	ab	1	0.031	а	1
MSH-5	0.011	abc	2	0.015	de	3
54-03	0.013	ab	1	0.030	а	2
SD-621	0.010	abc	3	0.018	bcde	2
.5-02	0.012	abc	2	0.014	de	3
17-02	0.009	c	3	0.018	bcde	2
Population mean(µ)	0.011	В		0.024	А	
STD	0.001			0.006		
$\mu + STD$	0.013			0.030		
μ-STD	0.010			0.017		
Tukey HSD (0.05) for genotypic means	0.00	03		0.	011	
Tukey HSD $(0.05)$ for `treatment means			0.0091			

Table 9. Potassium use efficiency (g<sup>2</sup> SDW mg<sup>-1</sup> K) of 18 wheat genotypes under adq. and def. K conditions

Genotypic means followed by similar alphabet represent non- significant variation at  $p \le 0.05$ .

Genotypic means followed by similar numerical values in the column are alike in performance

#### Discussion

Biomass production/growth response is a critical criterion for the evaluation of genotypes under nutrient study revealed deficiency stress. This wide genetic/genotypic variation in SDW, RDW, TBM and RSR at two K-levels. The variation in growth parameters pointed out differential adapting responses by wheat genotypes under low and highK regimes and legitimated earlier results, highlighting the significance of adq.K for wheat (Makhdum et al., 2007). The decline in wheat growth under K deficiency stress exhibited a critical role of potassium in various physiological process i.e., osmoregulation, membrane transport processes and activation of many enzymes (Marchner, 1995).

The data of SDW and RDW (Tables 1 & 2) exhibited hindered effects of low potassium (def. K) on shoot and root biomass of all the genotypes, however some genotypes (seven genotypes out of 18) showed increase in RDW under def. K environments. The increase in RDW of these genotypes may be associated with activation mechanisms under K-deficiency stress as reported earlier (Shin & Schachtman, 2004). Several workers recognized that transcription of the AtHAK5 transporter is activated in arabidopsis in response to K<sup>+</sup>deficiency (Yang *et al.*, 2020; Armengaud *et al.*, 2004; Hampton *et al.*, 2004; Gierth *et al.*, 2005). The increase in root growth of wheat genotypes is also corroborated with Nawaz *et al.*, (2006), who reported increased RDW at def.K-level in maize.

Wheat genotypes also exhibited major genetic/genotypic variation related to SDW production at two K-levels. The increase in SDW of all wheat genotypes at adq.K is attributed to higher photosynthetic activity, higher osmoregulatory effects and higher enzymatic activity under adq.K environment (Hasanuzzaman et al., 2018). Many researchers (Yang et al., 2003; Gao et al., 2005) found variation in SDW among several crops with different K level. This decreasing trend in dry weights (both shoot and root) in wheat genotypes at def.K is in line with the findings of Tahir (1999).Our study showed significant positive correlation (r = 0.646 \*\*) between SDW and RDW (Table 10) at def.K level. One of the mechanisms for increased root growth at def.K is the root growth at the cost of shoot to cope with K stress (Shah et al., 2011). Marschner (2012) pointed that plant responds preferably to biomass allocation into the root system to scavenge for nutrients from a larger volume of nutrient medium. This is also evident from increased RSR under nutrient deficiency (Table 3). Similar were the findings of Ruan et al., 2015 and Gill et al., 2004 in various field crops.

Potassium stress factor (%) is an assessment of comparative decline in SDW because of K deficiency (Table 1). It also furnishes the information about the responsiveness of the genotype to adq. K level. A high numerical value of KSF reflects elevated response of a genotype to adq. K supply, while a lower or negative value depicts little or no response to K supply (Khan *et* 

al., 2017). Wide genotypic variation for KSF (%) was observed among the tested wheat genotypes and it ranged from 3 to 42%. The lowest value of KSF (3%) for the genotype SD-502 shows the non-responsiveness of this genotype to adq. K supply, however at the same time it also explains the potential of this genotype under K stress as it maintained it's SDW under adverse K conditions. Similar results for wide genotypic variation in wheat genotype for KSF were reported by Chachar et al., (2015). The two genotypes NIA-Sunder and 17-03 also exhibited comparatively low KSF as compared to other genotypes i.e., 14 and 12%, respectively, depicting comparatively better responsiveness of these genotypes to adq. K supply as well as maintenance of SDW under low K environments. The genotype 5-02 exhibited highest KSF (42%), showing its high responsiveness to adq. K level and extremely low performance at def. K level (Table 1). The genotypic mean of two K level i.e. adq.  $(0.502 \text{ g plant}^{-30})$  and def.  $(0.394 \text{ g plant}^{-30})$  showed significant interaction between two K level.

Root shoot ratio (RSR) is an assessment of dry mass distribution between roots and shoots. The data regarding this attribute showed that SDW was affected more severely than the RDW under def.K environments, which resulted an enhanced RSR in most of the tested wheat genotypes except two (22-03 and NIA-Sunder) (Table 3). Enhanced RSR in our findings are in agreement with Peuke et al., (2002) whoreported inhibition of shoot development in Ricinnus communis at the cost of root development under low (def.) K level. Epstein and Bloom (2005) augmented that shoot acquired nutrition through roots, for this purpose energy is provided from photoassimilates, while K-deficiency results accumulation of sugars in wheat leaves. Another possibility for higher root growth under def. K environments is the enhanced N uptake, which may have possibly contributed in higher root growth (Osaki et al., 1995.) In contrast to these findings, incompatible behavior of RSR among wheat genotypes was observed by Tahir et al., (2008).

The results regarding TBM production under sufficient (adq.) K supply illustrated significantly higher values for TBM in three wheat genotypes i.e. SD-4047, SD-502 and SD-222, which is attributed to their better genetic potential i.e. high K response under sufficient (adq.) K supply (Table 4). Similar results were reported by Minjian et al., (2007) in maize genotypes for increased biomass at adq.K level. In contrast, various authors have reported genotypic variation for biomass production at two K levels (adq. and def.K) and a decrease in TBM production due to K deficiency in wheat (Zhang et al., 1999), sweet potato (George et al., 2002),rice (Yang et al., 2003),chickpea (Gill et al., 2005) and maize (Minjian et al., 2007). However the correlation study showed higher positive correlation of TBM with SDW(r=0.964 \*\*), RDW (r=0.826\*\*) and KUE (0.732 \*\*) at def. K level (Table 10).

It was noted that Potassium concentration in root (RKC) was decreased more severely when compared with shoot under K deficiency stress (3.28 fold decreases in root vs. 2.52 fold decrease in shoot). It is generally understood that under K deficiency stress wheat can translocate more K from root to shoot to cope with K deficiency stress (Rengel and Damon, 2008). Potassium

concentration in shoot had a significant negative correlation with KUE (r = -0.889) indicative of the fact that wheat genotypes with lower concentration of K in shoot had generally higher KUE. Ashley *et al.*, 2006 documented the need for selection of genotypes with high utilization efficiency at def. K level.

Shoot K accumulation (SKA) (mg shoot<sup>-30</sup>) is the quantity of K acquired by the plant for producing SDW at a specific growth stage (Marschner, 2012).Potassium accumulation in shoot and root is directly related to dry weights of shoot, root and total biomass. Significant positive correlations were recorded with SDW (r=0.838\*\*), RDW (r=0. 549\*) and TBM(r=0.860\*\*) under adq.K supply, similarly root K accumulation (RKA) also has significantly ( $p \le 0.05$ ) positive relations with RDW(r= 0.636) and RSR (r=0.588). This indicates the responsiveness of these genotypes under sufficient (def.) K environments (Table 11). These findings were also corroborated by Koebernick & Gwathmey (2007) and Sardans & Peñuelas (2021). At def.K level RKA has positive correlation with RSR (0.584\*\*) and SKA with SKC (0.697\*\*). Three genotypes i.e. SD-502(8.35 mg shoot<sup>-30</sup>), MSH-5(9.02 mg shoot<sup>-30</sup>) and SD-621(9.47 mg shoot<sup>-30</sup>) had more SKA than the mean value (6.77 mg shoot <sup>30</sup>) of 18 genotypes, indicating the efficiency of these genotypes under low K conditions. Similarly higher RKA of the genotypes viz., 5-02, MSH-5, SD-222 and SD-502 under low k condition also showed potential of these genotypes to be efficient under def.K level. According to Santa-Maria et al., (2015), under nutrient deficient environment plant develops efficient internal nutrient economy which results higher nutrient accumulation (in our case K). However, Hong & Guangzhou (2004) reported differential responses in terms of K accumulation. Although the genotype 17-02 had minimum RKA at adq.K, this is the only genotype, out of 18, that coped with the adverse K (def.K) condition and showed minimum reduction of 10 % than adq.K (Table 8). However significantly ( $p \le 0.05$ ) less SKA of this genotype (17-02) under def.K level depicts that accumulated K in root was not translocated to shoot.

As potassium use efficiency (KUE) is significantly correlated with SDW (r=0. 824\*\*) and TBM (r=0. 732\*\*) at low (def.K) K levels (Table 10) therefore KUE and SDW may be employed for selection of wheat genotypes under low K- condition. Sattelmacher *et al.*, (1994) and Ruan, *et al.*, (2015) in wheat and Arif (2009) in rice also advocated using these parameters (KUE and SDW) for the identification of nutrient efficient crops. An increase in KUE under K-deficiency stress is in line with the results of Arif (2009) in rice, Shah *et al.*, (2011) in cotton and Tahir (1999) in wheat. Howeverdifferential responses were reported for KUE by Hong & Guanghuo (2004) in rice, Ruan *et al.*, (2015) in wheat, George *et al.*, (2002) in sweet potato and Cassman *et al.*, (1989) in cotton.

Keeping in view the significance of shoot dry weight for screening the genotypes under def.K level, SDW of 18 wheat genotypes were correlated with variety of Parameters at adq. and def .K levels (Tables 12 and 13). At adq.K level SDW was significant positively associated with TBM (r=0. 943\*\*), SKA (r=0. 838\*\*) while at def.K level, itshowed high correlation with RDW (r=0. 646\*\*) and TBM (r=0. 964\*\*), again showing that this plant response parameter might be successfully applied for screening of wheat genotypes better adapted to low and high K condition. Similar results for the correlation of SDW with various parameters were found by Shah and Arshad (2008) in cotton and Arif (2009) in rice.

			8	1		1	
Parameters	KUE	RDW	RKC	RSR	RKA	SDW	SKC
RDW	0.351						
RKC	-0.371	-0.084					
RSR	-0.375	0.622**	0.152				
RKA	-0.169	0.338	0.292	0.584**			
SDW	0.824**	0.646**	-0.255	-0.188	-0.114		
SKC	-0.889**	-0.109	0.427	0.359	0.089	-0.505*	
SKA	-0.323	0.428	0.227	0.269	0.024	0.260	0.697**
TBM	0.732**	0.826**	-0.219	0.078	0.035	0.964**	0.412
TKA	-0.354	0.498*	0.294	0.410	0.281	0.220	0.692**

Table 10. Correlation coefficient among various parameter of wheat genotypes at def.K level.

\* Significant at  $p \leq 0.05$ 

\*\* Significant at p≤0.01

Table 11. Correlation coefficient among various parameter of wheat genotypes at adq.K level

Parameters	KUE	RDW	RKC	RSR	RKA	SDW	SKC
RDW	0.275						
RKC	1.000**	0.275					
RSR	-0.274	0.792**	-0.274				
RKA	0.055	0.363**	0.0554	0.588*			
SDW	0.877**	0.425	0.877**	-0.209	0.172		
SKC	-0.493*	0.324	-0.493*	0.374	0.384	-0.083	
SKA	0.503*	0.549*	0.503*	0.014	0.350	0.838**	0.471*
TBM	0.791**	0.702**	0.791**	0.128	0.371	0.943**	0.053
TKA	0.474*	0.623**	0.473*	0.121	0.509*	0.803**	0.505*
* Significant at p	≤0.05						

\*\* Significant at p≤0.01

 Table 12. Relationship of shoot dry weight of 18 wheat
 genotypes with various parameters at adq. and def. K levels.

Parameter	Adq.K	Def.k
RDW	0.425	0.646**
RSR	-0.209	-0.188
TBM	0.943**	0.964**
SKA	0.838**	0.260
RKA	0.172	-0.114
TKA	0.803**	0.220
SKC	-0.083	-0.505*
RKC	0.877**	-0.255
KUE	0.877**	0.824**

\* Significant at p≤0.05

\*\* Significant at p≤0.01

On the basis of this study, as per Gerloff (1977), the genotypes were ranked in tofour groups, i.e. 1) Efficient & Responsive (E&R) 2) Non-efficient & Responsive (NE &R) 3) Efficient & Non -responsive (E & NR) and 4) Non- efficient & non -responsive (NE & NR). Among these four groups, the highly desirable criterion is E & R, as the genotypes of this criterion can produce high yield under def. as well as under adq. K conditions. According to our study, most of the genotypes (9 out of 18) fell in the category of R & E. These findings are in good agreement with the finding of Shah *et al.*, (2011) who also ranked 11

cotton genotypes out of 26 as R&E. The Index scoring method of Gill *et al.*, 2004 also assigned # 2 (Medium performance) to most of the wheat genotypes However occurrence of different classes, i.e. high (1) medium (2) and low (3) in wheat genotypes reflect the genotypic variation for their response to K levels (Shah *et al.*, 2015).



Fig. 1. Contribution of various parameters of wheat genotypes at def.relative to adq. K level.

Construngs	Gill et a	<i>ul.</i> , 2004	Gerloff, 1977		
Genotypes	Adq.K	Def.K	Adq.K	Def.K	
MSH-14	Mr-Msdw	Me-Msdw	R	Е	
NIA-SARANG	Mr-Msdw	Me-Msdw	R	NE	
22-03	Mr-Msdw	Me-Lsdw	R	NE	
NIA-MB-I	Mr-Msdw	Me-Msdw	R	NE	
NIA-Sundar	Mr-Msdw	He-Msdw	R	Е	
SD-4047	Hr-Hsdw	Me-Msdw	R	Е	
SD-502	Mr-Msdw	He-Hsdw	NR	Е	
Chakwal-86	Mr-Lsdw	Me-Msdw	R	NE	
Khirman	Mr-Msdw	Me-Msdw	R	Е	
17-03	Mr-Msdw	Me-Msdw	R	Е	
ESW-9525	Mr-Msdw	Le-Lsdw	R	NE	
SD-222	Mr-Hsdw	He-Msdw	R	Е	
NIA-MB-II	Mr-Msdw	He-Msdw	R	Е	
MSH-5	Mr-Msdw	Le-Msdw	R	NE	
54-03	Hr-Hsdw	He-Msdw	R	Е	
SD-621	Mr-Msdw	Me-Msdw	R	Е	
5-02	Mr-Msdw	Me-Lsdw	R	NE	
17-02	Lr-Lsdw	Le-Lsdw	R	NE	

Table 13. Categorization of 18 wheat genotypes at adq. anddef. K level.

LE-LSDW: Low efficient-Low shoot dry weight, ME-LSDW: Medium efficient- Low shoot dry weight, HE-LSDW: Highly efficient- Low shoot dry weight, LE-MSDW: Low efficient- Medium shoot dry weight, ME-MSDW: Medium efficient- Medium shoot dry weight, HE-MSDW: Highly efficient- Medium shoot dry weight, LE-HSDW: Low efficient- High shoot dry weight, ME-LSDW: Medium efficient- High shoot dry weight, LR-LSDW: Low responsive- Low shoot dry weight, MR-LSDW: Medium responsive- Low shoot dry weight, HR-LSDW: Highly responsive- Low shoot dry weight, LR-MSDW: Low responsive- Medium shoot dry weight, MR-MSDW: Medium responsive- Medium shoot dry weight, HR-MSDW: Highly responsive- Medium shoot dry weight, LR-HSDW: Low responsive- Medium shoot dry weight, LR-HSDW: Low responsive- Medium shoot dry weight, LR-HSDW: Highly responsive- Medium shoot dry weight, LR-HSDW: Highly responsive- Medium shoot dry weight, LR-HSDW: Low responsive- Medium shoot dry weight, MR-HSDW: Medium responsive- Medium shoot dry weight, NE: non-efficient, R: responsive, NR: non-responsive

#### Conclusion

The identification of K-efficient and responsive wheat genotypes was the main objective of this study for sustainable low K-input wheat production. On the basis of growth and K-allocation parameters, it is concluded that shoot dry weight and Potassium use efficiency might be efficiently employed for screening of wheat genotypes under low (def.) and high (adq.) K conditions. Further the wheat breeders are recommended to include potassium responsive and efficient genotypes in their breeding programme for development of low K-input and sustainable wheat production in the country.

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