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Genetic variability for root traits and its role in adaptation under conservation agriculture in spring wheat

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Abstract

Breeding wheat for improved root traits and suitability under conservation agriculture (CA) practices has the potential to boost and sustain grain yield in different parts of the world. Difficulties in scoring for root phenes under field conditions, considered a major hurdle to breed for root traits, can be surmounted by scoring under hydroponic conditions. Significant variability was found for rooting depth (RD), shoot dry weight (SDW) and root dry weight (RDW) when 175 genotypes were screened for root traits under hydroponic conditions. Further evaluation of a subset of 19 genotypes under field conditions showed that four root traits - total root length (TRL), root volume (RV), root surface area (RSA) and root tip numbers (RN) are integrated with RDW because of their positive correlation with this trait. Both RDW and SDW could be combined favorably to obtain the most appropriate (higher) biomass and greater yield under a set of crop growth durations. Significant correlation and strong direct effect of RDW on crop yield under CA appeared to justify its selection in the breeding programme. A derivative of the cross EGPSN-36/ PBW343 showed maximum value for all root traits including RDW and therefore can be used in future breeding programmes.

Key words: Root traits, grain yield, conservation agriculture, spring wheat, hydroponic

Introduction

Plant root systems have played a major role in the evolution and adaptation of crop plants for different ecologies of crop production (White et al. 2013; Vadez 2014). Wheat is a major contributor for calorie intake throughout the world and is crucial for food security in India. Wheat is adapted to very diverse ecologies and hence grown from tropical to temperate regions, from near sea level to high mountainous regions and with almost negligible rainfall to very high rainfall area. Stabilization of yield through better varieties and improved production system is essential for a country like India, especially in its North Western Plains Zone (NWPZ) which provides 90% of the buffer stock of a country (Yadav et al. 2010). Conservation agriculture (CA) practices encompassing zero or minimum tillage with residue retention on the surface and crop rotation along with adapted varieties or hybrids have been advocated as a mean for yield stabilization at a higher level (Yadav et al. 2017). Root besides enabling crop plants to explore different strata of the soil for meeting its nutrient need also keeps the plant standing for better capturing of sunlight. Wheat is grown in a highly diverse soil environment and its root traits are in continuous flux for optimized growth except for carbon and oxygen. As plants meet their nutrient requirements mainly through roots and therefore distribution and functioning of the root system are the major component deciding crop yield (Den Herder et al. 2010).

Wheat yield is being continuously improved through selection among observable traits. However, the root being hidden underground is rarely selected for or against directly for improving adaptation *vis-a-vis* crop yield. Declining genetic gain and/or stagnating wheat yield can be surmounted by tapping unexplored variation in root traits (Vadez 2014). Roots like many

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other growth traits are highly plastic, however, the extent of plasticity is genetically governed and search for its QTLs is the center point of research in investigating the genetic variation for root system architecture traits in plants (De et al. 2007; Ranjan and Yadav 2019). The majority of the traits leading to local adaption are generally governed by multiple genes with small effect and root traits are no exception to this. Root length density plays a major role in water deficiency tolerance both under irrigated and rainfed conditions (Fang et al. 2017). Root development and its pattern of distribution are largely determined by the soil environment (Mosaddeghi et al. 2009), genotype (Naryanan et al. 2014) and their interaction (Acuna and Wade 2013). Conservation agriculture (CA) in contrast to conventional tillage (CT) agriculture is a totally different but favorable production environment for crop growth, its interactive role with different types of root phenes can provide important clues about the genetic adaptation of wheat under CA. Integrating root traits in wheat breeding programme adapted to conventional as well as conservation agriculture, though essentially required but was largely lacking because of difficulty in its phenotyping (Ranjan et al. 2019a; Ranjan and Yadav 2020). However, hydroponic screening (growing plants in nutrient solution) can facilitate large scale screening for root phenes by minimizing the confounding resulted from environment variations (Ranjan et al. 2019 b). In the present investigations, we have tried to test the hypothesis that root traits data generated under hydroponic conditions can provide important clues for their role in adaption to conservation agriculture.

Materials and methods

Experiment I

Plant materials and growth conditions

The study consists of 175 spring wheat genotypes (Table 1). The list of genotypes include 34 commercially released wheat cultivars of India, 24 elite germplasm lines from CIMMYT, Mexico and 117 advanced breeding lines bred through systematic selection for CA adaptation at Indian Agricultural Research Institute (IARI), New Delhi. All of the commercially released varieties and international materials have been bred through selection under CT conditions only.

Hydroponic screening

The experimental material was grown under 10/14 hours of light and dark timing using an automatic timer having 25/22 °C day/night temperature with light intensity of 300 µmol m^{-2} s^{-1} using cool fluorescent lamps and relative humidity of 65-70 % was maintained (Ayalew et al. 2014). Surface sterilized the seeds of each genotype by 1% sodium hypochlorite for 2 minutes followed by thoroughly washing with distilled water and transferred to towel paper for germination in seed incubator. A week seedlings, each of 175 genotypes were placed to the hydroponic system. A hydroponic system devised with 18 litres capacity plastic boxes having ceramic lid. Lids were drilled with 8mm diameters holes. Cotton plug wrapped two seedlings and were transferred to each hole of the lid in such a way that the roots of seedling remain immersed in hydroponic solutions of the plastic box. The experiment was repeated in three replicas. The pH around6-6.5of the hydroponic solution was maintained by using 1M HCl or 1M KOH. The solution was continuously aerated through the aquarium air pump. The nutrient solution used in hydroponic system contained 2 mM $CaNO_3$, 10 mM KNO_3, 0.4mM NH_4NO_3, 0.1 mM KH_2PO_4, 2mM $MgSO_4$, 0.1 mM Fe-EDTA, 1.5mM $Cacl_2$, 2 µM $MnCl_2$, 3 µM $ZnSO_4$, 12.5µM H_3BO_3, 0.1 µM Na_2MoO_3, 0.5 µM $CuSO_4$, 25 µM KCland 0.1 µM $NiSO_4$. To maintain the normal status of the nutrients the solution was replaced every week. After 8 weeks of growth under hydroponic conditions, plants along with root were removed carefully to record the data on plant height (PH), rooting depth (RD), shoot dry weight (SDW) and root dry weight (RDW) for each independent plant. For RD, at harvest, shoot was separated from the root by cutting at the base of a shoot of each plant. The root was laid in a flat surface, stretched and measured their length estimate the RD. Whereas, for SDW and RDW; dry weights were taken after oven drying at 60ºC for 4 days.

Experiment II

Evaluation of subset of 19 genotypes for root biomass component traits

On the basis of mean values for different traits (SDW, RDW and gN), a subset of 19 genotypes from 175 genotypes was constituted. Extreme seven (four highest ranked and three lowest-ranked) genotypes for SDW, six (three highest and three lowest-ranked) for RDW and six (three highest and three lowest-ranked) for gram nitrogen in shoot (gN) were selected to constitute the subset. Gram nitrogen in shoots (gN) was calculated by multiplying shoot dry weight (g) with

Table 1. A list of genotypes studied

S.N.	Pedigree/ Genotypes	S.N.	Pedigree/ Genotypes	S.N.	Pedigree/ Genotypes	S.N.	Pedigree/ Genotypes
1	CL1449/HUW585	45	PS755/PBW502	89	HD2967/DBW56	133	K 9107
2	DL672/PS6270//DE8	46	CL1705/HD2894	90	HD2967/K-07-08	134	43IBWSN-1201
3	HW5015/UP2538	47	CL1705/HD2894	91	HD2967/WH1073	135	28SAWSN-3012
4	HD2898/HD29	48	HD2851/HD2329	92	HD2967/WH1073	136	43-IBWSN-1054
5	HD2953/HS365	49	HD2851/HD2329	93	HD2967/PBW 617	137	43-IBWSN-1187
6	CL1449/PBW343	50	VL610/KUNDAN	94	HD2967/PBW 596	138	28-SAWSN-3028
7	HD2878/HD29	51	PBW343/PICCI LOCAL//RL6080	95	HD2967/DT2756	139	CL1705/HD2894
8	CL2636	52	HW3083/HD2639	96	HD2967/HD3024	140	HW3083/HD2873
9	PBW343/HD2877	53	HW3083/HD2639	97	HD2967/HD3034	141	HD3117
10	18-HRWYT-214	54	HW3083/HD2639	98	HD2967/HD3034	142	CSW16
11	18-SAWYT-303	55	HW3083/HD2639	99	HD2967/HD3035	143	DL849/YSCN-08
12	HD2448/HW1305	56	DWG107/RAJ 3765	100	HD2967/HD3035	144	DL672/P66.270//DE894/3/CUMYN
13	HW4023/HW5028//HD2932/DW1309	57	DWG107/RAJ 3765	101	HD2967/DT2761	145	HD2329/WR544//PBW343/NW2041
14	HD2833/DW538	58	WH542/UP290//DBW72	102	HD2967/DT2761	146	18SAWYT-311
15	39th IBWSN-23	59	CL 2596/K9451//Cl882/HD2329	103	HD2967/DT2761	147	18HRWYT-214
16	29th SAWSN-3145	60	DWG107/HDK-10//C306	104	HI 1544	148	18th SAWYT 36
17	CSW 43	61	DWG107/HDK-10//C306	105	HI1563	149	HD2733/PBW343/HD2733/PBW343
18	HD2932/UP2425	62	DWG107/HDK-10//C306	106	HI 1500	150	WH542/YSCN-10
19	WL462/VCC/KOCL/3/Pes/Me-11	63	HD3239/WR562	107	HI1531	151	HD2687/HP1896//WH542
20	UP2425/CL146	64	DL5/PBW343//DEEPALI	108	RAJ 4120	152	CSW44
21	JOSHI 3	65	DL5/PBW343//DEEPALI	109	RAJ 3765	153	PBW12/HW2078
22	HD2967/DW1350	66	DL5/PBW343//HD2891	110	RAJ 4083	154	HD2824/VL796
23	HD2448/HW1305	67	DL5/PBW343//DEEPALI	111	DBW-14	155	HD2402/CPAN4067/HW4022/DW5247
24	HD2878/HD29	68	DL5/PBW343//HD2891	112	DBW17	156	UP2425/UP2626
25	CL1705/PBW12	69	DL5/PBW343//HD2891	113	WH 542	157	HD2733/HD2329
26	CL1705/HD2894	70	DL5/PBW343//HD2891	114	PBW 621-50	158	VL849/UP2571
27	HD2824/VL796	71	DL5/PBW343//HD2891	115	PBW 596	159	HD2733/PBW343/HD2733/PBW343
28	VL610/KUNDAN	72	CL2596/K9451//CL882/HD2009	116	PBW 590	160	IBWSN-06-07 KARNAL
29	31-ESWYT-132	73	G-9/ MC-10	117	PBW 502	161	HD2877/HS451
30	5-EBWYT-519	74	G-9/MC-10	118	PBW 443	162	CL1591/CL1475
31	43-IBWSN-1006	75	CL22596/K9451//CL882/HD2329	119	PBW 373	163	31 ESWYT121
32	43-IBWSN-1077	76	CP264/CL1633//CNO 63/Well.	120	PBW 343	164	6th EBYT-503
33	43-IBWSN-1090	77	CL 2596/K9451//Cl882/HD2329	121	HD 2285	165	CL1705/HD2687
34	43-IBWSN-1102	78	CL2596/K9451/CL882//HD2009	122	HD 2894	166	CL1705/HD2687
35	43-IBWSN-1106	79	CL2596/K9451/CL882//HD2009	123	HD 2932	167	CL1705/HD2687
36	43-IBWSN-1153	80	HD2669/HD3016	124	HD 2985	168	CL264//CL1633/CNO-601
37	43-IBWSN-1182	81	HD2669/HD3016	125	HD 2987	169	CL264//CL1633/CNO-601
38	43-IBWSN-1187	82	HD2967/HUW631	126	HD 3043	170	CL264//CL1633/CNO-601
39	29-SAWN-3028	83	HD2967/DBW17	127	HD 2329	171	EGPSN-36/PBW 343
40	HW5028/HD2250	84	HD2967/DBW17	128	HD 3090	172	EGPSN-36/PBW 343
41	HW2930/DW1309	85	HD2967/HD3024	129	HD 3059	173	EGPSN-36/PBW343
42	HD2948/HD2894	86	HD2967/HD3024	130	HD 3086	174	CL2596/K9451/CL882//HD2009
43	HD2948/HD2894	87	HD2967/HD3024	131	GW 366	175	CL2596/K9451/CL882//HD2009
44	PS755/HD29	88	HD2967/DBW54	132	WL 711		

N % in shoot. The Kjeldahl method was followed for the estimation of N% in shoot (Jackson 1967).

These 19 genotypes (Table 2) were grown twice under hydroponic conditions for 4 weeks to generate root biomass component traits. The period of 4 weeks in contrast to 8 weeks was chosen to facilitate better measurement for root traits. At 4 weeks duration, the root overlap is minimum and root separation is maximum with other genotypes than 8 weeks (Narayanan and Prasad, 2014). The RD-cm was measured manually, whereas other root traits like total root length (TRL-cm), root volume (RV-cm^3), root surface area (RSA-cm^2), average root diameter (AD-mm) and tip numbers in root (RN) were generated by scanning the roots in root scanner with winRHIZO pro image analyzer(Narayanan et al. 2014) for each plant. Subsequently, RDW and SDW were recorded after oven drying at 60ºC for 4 days.

Experiment III

Generation of yield and phenological data on 175 genotypes under conservation agriculture and conventionally tilled conditions of the field

The same set of 175 genotypes were planted in the field during cropping season of 2014-15 and 2015-16 under conventional tillage (CT) as well as CA conditions maintained at the farm of IARI, New Delhi. The CA field has been maintained at this farm for the last nine years. The genotypes were grown in randomized complete block design in two replicas. Each genotype comprised six rows with row-row of 20 cm and row length of 4.0 meter each. The material was sown during the first fortnight of November and to raise healthy crop recommended fertilizer dose of 120 Kg N, 60 Kg P_2O_5 and 60Kg K_2Oha^{-1} were used. The experimental area was irrigated five times at an interval of 20-25 days, the first being at 21 days after sowing. Data were recorded for days to flowering (DTF) and plot yield.

Statistical analysis

Analysis of variance (ANOVA) was analysed, as complete randomized design for hydroponic experiment and as randomized block design for field experiments with OPSTAT software (Sheoran et al. 1998). Path coefficient and Karl Pearson correlation coefficient analyses were also carried out with the same software. MS excel was used to regress among different parameters. Cluster analysis was done by using Euclidean distance with average linkage by STAR-nebula, IRRI, Philippines.

Results

Genetic variability for the root and yield traits

The ANOVA revealed statistically significant differences among the genotypes for root traits, days to flowering and grain yield (Table 3). The range for rooting depth (RD) and root dry weight

Table 2. A list of 19 sub-set of genotypes

No.	Pedigree/Genotypes	Weight (gm)	No.	Pedigree/Genotypes	Weight (gm)	No.	Pedigree/Genotypes	Weight (gm)
On the basis of mean shoot dry weight		**On the basis of mean Nitrogen efficient**			**On the basis of mean root dry weight**			
154	HD2824/VL796	1.88	86	HD2967/HD3024	0.775	173	EGPSN-36/PBW 343-1	0.1875
144	DL672/P66.270//DE894/3/CUMYN	1.12	78	CL2596/K9451/CL882//HD2009	0.615	171	EGPSN-36/PBW 343-2	0.1435
151	HD2687/HP1896//WH542	1.51	101	HD2967/DT2761	0.595	143	DL849/YSCN-08	0.186
152	CSW44	1.195	114	PBW 621-50	0.08	89	HD2967/DBW56	0.0165
84	HD2967/DBW17	0.195	51	PBW343/PICCI LOCAL//RL6080	0.11	71	DL5/PBW343//HD2891	0.019
128	HD 3090	0.31	92	HD2967/WH1073	0.11	99	HD2967/HD3035	0.0235
5	HD2953/HS365	0.265						

No. = Sl. No. of the genotype from Table 1

Table 3. Variability parameters for characters under study of 175 genotypes under hydroponics

Characters	Mean square	Mean ± SE	Range	GCV	PCV	h^2	GA@1%	GAM@1%
SDW (g)	**	0.62 ± 0.019	0.195-1.889	41.3	42.2	0.96	0.66	107
RDW (g)	**	0.064 ± 0.003	0.016- 0.246	57.2	57.2	0.98	0.095	149
RD (cm)	**	32.18 ± 0.909	17.167- 72.077	36	36	0.99	30.3	94.7
R:S	**	0.109± 0.034	0.026-0.327	48	71	0.45	0.095	85.5
DTF	**	95 ± 0.40	82-104	8.64	10.54	0.56	14.80	15.58
Yield (ZT) (kg/ha)	**	4967 ± 52.02	2708-6708	12.22	16.56	0.54	1186	23.81
Yield (CT) (kg/ha)	**	4595 ± 51.03	2770-6646	12.07	17.05	0.49	1023	22.29

**Significant at 1% level of significance

SDW: Shoot dry weight, RDW: Root dry weight, RD: Rooting depth, R:S: Root : Shoot, DTF: Days to flower

Table 4. Mean of selected 19 genotypes of various root parameters

Characters	Mean square	Mean ± SE	Range
Shoot Dry Weight (SDW)	**	0.071 ± 0.001	0.034-0.137
Root Dry Weight (RDW)	**	0.017 ± 0.000	0.01-0.033
Root : Shoot (R:S)	**	0.247 ± 0.017	0.139-0.438
Rooting Depth (RD)	**	20.82 ± 0.53	16.5-25.5
Total root length (TRL)	**	425 ± 29.137	166-630
Root surface area (RSA)	**	41.5 ± 2.849	20-64
Root Volume (RV)	**	0.329 ± 0.024	0.145-0.55
Average root diameter (AD)	**	0.326 ± 0.009	0.277-0.474
Number of root tips (RN)	**	1607 ±156.73	520-2898

**Significant at 1% level of significance

(RDW) under hydroponic conditions among the studied genotypes was 17.2-72.1 cm and 0.016- 0.246 g, whereas, for shoot dry weight (SDW), it was 0.195-1.889 g respectively. The range for grain yield in the field experiment was 2770–6646 kg/ha under CT and 2708-6708 kg/ha under CA respectively. The distribution of genotypes for RDW (g), RD (cm) and SDW (g) are presented in Fig. 1. The majority of the genotypes (68 per cent) fell in a single class for *i.e.*< 0.075 g for RDW; 0.46-0.9 g for SDW and 20-40 cm for RD (Fig. 1). The elaborative data on root biomass component traits generated by repeating the hydroponic experiments for the subset genotypes again showed highly significant differences among genotypes for all the root characters under study (Table 4).Under hydroponic condition genotypes 173 (EGPSN-36/PBW343-1), 171(EGPSN-36/PBW343-2) and 143 (DL849/YSCN-08) recorded the highest RDW (Table S2).The same entries *i.e.,* EGPSN-36/PBW343-1repeated in subset experiment showed maximum value for TRL, RSA, RV, RN and RDW.

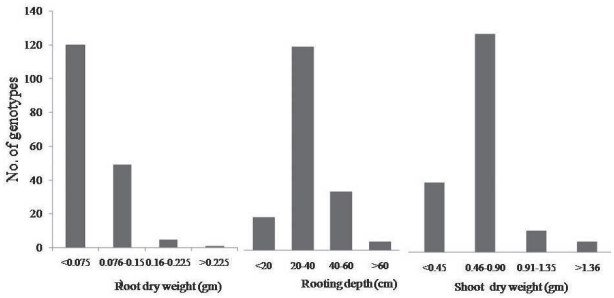

Fig. 1. Distribution of root dry weight, rooting depth and shoot dry weight among 175 spring wheat genotypes

The relationship among root traits under hydroponic condition and extrapolation with grain yield of a field experiment

Correlation worked out among the different root traits studied under experiment I is presented and their extrapolation with grain yield is presented in Table 5. The result clearly shows the positive correlations between grain yield of experiment III under both sets of environmental conditions with RDW and SDW of

Table 5. Correlation among root and yield traits

Traits	SDW	RDW	R:S	RD	DTF	Yield (ZT)	Yield (CT)
SDW	1						
RDW	0.502**	1					
R:S	-0.246**	0.653**	1				
RD	0.266**	0.577**	0.425**	1			
DTF	0.027NS	0.175*	0.176*	0.204**	1		
Yield (ZT)	0.178*	0.275**	0.123NS	0.039NS	0.195**	1	
Yield (CT)	0.229**	0.261**	0.080NS	0.215**	0.271**	0.407**	1

** Significant at 1 % and * significant at 5%

SDW = Shoot dry weight (g), RDW = Root dry weight (g), RD = Rooting depth (cm), R:S = Root : Shoot, DTF = Days to flower

Table 6. Direct (diagonal) and indirect (off diagonal) effects of yield (ZT)

SDW	RDW	R:S	RD	DTF	Correlating yield (ZT)
-0.066	0.251	0.041	-0.052	0.005	0.178
-0.033	0.500	-0.109	-0.114	0.031	0.275
0.016	0.327	-0.167	-0.084	0.031	0.124
-0.018	0.288	-0.071	-0.197	0.036	0.039
-0.002	0.087	-0.029	-0.040	0.179	0.195

SDW = Shoot dry weight (g), RDW = Root dry weight (g), RD = Rooting depth (cm), R:S = Root : Shoot, DTF = Days to flower

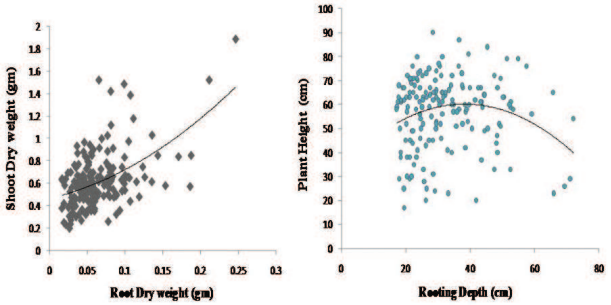

Fig. 2. Relationship between root and shoot traits of 175 spring wheat genotypes

hydroponic data. RDW was found to have a positive and significant correlation with RD and SDW. The coefficient of determination (R^2) was 0.261 at P=0.005 for RDW and SDW whereas a non-significant regression line was obtained between plant height (PH) and RD (Fig. 2).To further understand the yield formation process, it becomes imperative to partition such association into direct and indirect effects of component character through path analysis. Path analysis (Table 6) showed a maximum direct effect of RDW on grain yield under CA followed by DTF. RD showed a significant negative direct contribution to grain yield under CA conditions. To elucidate root

Table 7. Correlation between the root traits of selected 19 genotypes

Traits	RSA	RV	AD	RN	RD	TRL	SDW	RDW	R:S
RSA	1								
RV	0.941**	1							
AD	-0.270^{NS}	-0.044^{NS}	1						
RN	0.474*	0.384^{NS}	0.220^{NS}	1					
RD	0.112^{NS}	0.068^{NS}	0.136^{NS}	0.307^{NS}	1				
TRL	0.921**	0.859**	-0.071^{NS}	0.643**	0.095^{NS}	1			
SDW	0.569*	0.620**	0.189^{NS}	0.172^{NS}	-0.052^{NS}	0.669**	1		
RDW	0.603**	0.519*	0.001NS	0.443^{NS}	0.096^{NS}	0.741**	0.514*	1	
R:S	-0.001^{NS}	-0.100^{NS}	-0.151^{NS}	0.205^{NS}	0.027^{NS}	-0.018^{NS}	-0.559*	0.340^{NS}	1

** Significant at 1 % and * significant at 5%

Units of RD= cm TRL= cm, RSA=cm^2, RV= cm^3, AD= mm, SDW= gram (gm), RDW= gram (gm)

Table 8. Cluster mean of different traits of 175 genotypes

Clusters	RDW	RD	SDW	S:R	DTF	Yield (CT)	Yield (ZT)	Total score	Rank
I	0.06(4)	28.79(4)	0.54(5)	10.45(3)	94(3)	4434(4)	4886(4)	27	V
II	0.09(3)	44.51(3)	1.47(2)	17.11(2)	93(4)	4066(5)	4392(5)	24	III
III	0.03(5)	22.46(5)	0.67(4)	22.79(1)	92(5)	4730(3)	5100(3)	26	IV
IV	0.10(2)	49.74(2)	0.77(3)	9.19(4)	97(2)	5136(2)	5322(2)	17	II
V	0.23(1)	54.53(1)	1.71(1)	7.44 (5)	99(1)	5807(1)	5689(1)	11	I

*Values in parentheses indicate relative score for each character across 5 clusters

Table 9. Cluster mean of different traits of subset

Cluster	RSA	RV	AD	RN	RD	TRL	SDW	RDW	R:S	Yield (ZT)	Yield (CT)	Score	Rank
I	40.60(3)	0.33(1)	0.34(1)	1663(2)	21.6(2)	423(2)	0.07(2)	0.02(1)	0.25(2)	5828(1)	5691(1)	18.00	I
II	41.94(2)	0.33(1)	0.31(3)	1413(3)	19.3(3)	427(1)	0.08(1)	0.02(1)	0.24(3)	5128(3)	4411(2)	23.00	III
III	46.00(1)	0.30(2)	0.32(2)	2589(1)	24.0(1)	423(2)	0.06(3)	0.02(1)	0.28(1)	5528(2)	3270(3)	19.00	II

*Values in parentheses indicate relative score for each character across 3 clusters

biomass formation in the subset genotypes, the data on the number of root component traits were analysed (Table 7). RDW showed a positive and significant correlation between TRL, SA, RV and SDW. Also, TRL too was influenced by RSA, RV and RN significantly in a positive direction. The regression line of RDW with RSA, SDW, RV showed a linear trend line with R^2 of 0.446, 0.286 and 0.392 respectively (Fig. 3). The correlation between root traits in natural conditions (pipe) and hydroponic under no input limiting in the subset genotypes display good accord under two conditions. Observation for RDW under pipe and hydroponic evidenced a significant positive relationship with a correlation coefficient of 0.537.

Classification of genotypes

To analyse the pattern in the data, mean Euclidean distance grouped 175 genotypes into five major clusters with cluster I accommodating maximum (123) genotypes followed by Cluster IV (29), cluster III (18), Cluster II (3) and cluster V (2), respectively. Cluster V comprising the genotype No. 151 (HD2687/HP1896// WH542) and 154 (HD2824/VL796) showed maximum mean value for most of the root characters under study. Most of the promising lines including the released varieties and advanced breeding genotypes for the North-Western plain zone of India where the experimental location of this study is situated also fell in cluster IV (Table 8) and ranked second for cluster mean (Table 8). Genotypes grouped under cluster I (last rank) were having poor score (3-5 scores) for the

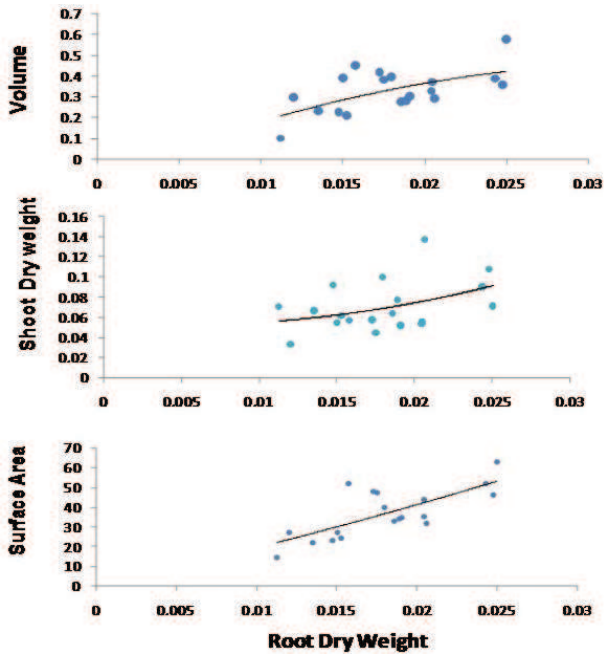

Fig. 3. Association of root dry weight to root surface area, shoot dry weight and root volume among 19 subset wheat genotypes

majority of root and other adaptive traits and comprised released varieties for other geographic areas or genotypes with comparatively shorter duration. Among the subset genotypes, cluster 1 comprising ten genotypes (1, 2,16, 7, 8, 18, 3, 12, 4 and 14), ranked first on the basis mean of five different traits (Table 9)

and was followed by cluster III comprising only one genotype (a derivative of HD2967/DBW56) with mean value highest for five characters. Cluster II having eight genotypes (5, 6, 9, 15, 13, 10, 11 and 19) ranked last on the basis of cumulative rank value. Cluster I comprised the most promising genotypes with desirable root traits and yield.

Discussion

To meet the food security needs of the growing population, stabilizing wheat yield at a higher level under different production systems is very essential for developing economies (Yadav et al. 2017; Gupta and Yadav 2014). Root plasticity along with appropriate management practices like conservation agriculture (CA) can be an important means to counter the stresses (Joshi et al. 2007) induced by changing climatic conditions and depleting natural resources mainly irrigation water and soil health (Yadav et al. 2019). Large scale screening of the genotypes under field conditions for root traits either by destructive method or root image analysis is challenging (Narayanan and Prasad 2014; Ranjan et al. 2019b). Further, because of strong soil heterogeneity and poor heritability for the root traits, breeders are usually hesitant to integrate these traits in their breeding programme (Malamy 2005; Lynch 2007). Therefore low-cost techniques having no confounding effect of the environment, such as hydroponic screening, can be very effective in quantifying the genetic basis for differences in root traits (Petrarulo et al. 2015; Ranjan and Yadav 2020).

A number of root traits like root hairs, root tip diameter, number and length of lateral root, root cortical parenchyma have been reported to be important for evaluating genetic differences (Paez-Garcia et al. 2015). However, the generation of these data on a large number of genotypes is not feasible. Therefore, while screening initially; we concentrated on two important root and shoot traits only. Significant genetic variability and a wide range for these traits in the elite breeding material and released varieties indicated the absence of any directed selection for them and corroborate the earlier findings (Ranjan et al. 2019a; Ahmadhi et al. 2018; Narayanan et al. 2014). The presence of such a strong variability in the elite background with resistance to all major diseases and high yield provides a good opportunity for further yield consolidation in wheat (Yadav et al. 2017). Significant correlations of root and shoot weight under the hydroponic condition with yield realised in the field under two production environments viz., CA and CT suggest that selection for root and shoot weight under hydroponic conditions can be equally effective for yield improvement (Ranjan et al. 2019b). Under conventionally tilled irrigated condition in many wheat-growing areas of South Asia where bore wells go dry before the end of the wheat season. Shallow-rooted genotypes with lesser root proliferation suffer heavily from simultaneous heat and water stress. However, path analysis under CA shows the direct effect of the only RDW on grain yield and therefore, further yield consolidation can happen only by paying more attention to below-ground root parts. Elaborative analysis on a subset of genotypes of 19 that were selected based on SDW, gN, and RDW, also confirmed the presence of significant variability for the most root traits that was investigated in the present study. The component traits for RDW have no conflict among them and can be selected for improving the heritability of RDW under varying field environment. The significant correlation between RDW with most of the traits like RV, TRL, and RSA in the subset indicates that probably all these traits are combined into RDW. The selection on the basis of RDW, which is comparatively measured easily for a large number of plants in the early segregating generations under hydroponic condition, can give the desired result. The impact of RSA on RDW has also been reported earlier by Caassen and Barber (1976). As the contact area between the root surface and the soil is quite large, the greater amount of nutrients (Fageria and Moreira 2011) and water is taken up by plants having larger root biomass that can lead to much higher biomass production. Another major finding of this experiment is a significant correlation between RDW and SDW which supports many earlier works (Seeraj et al. 2004; McPhee 2005; Narayanan and Prasad 2014; Ranjan et al. 2019a). No conflict between RDW and SDW indicates that both can be selected simultaneously for furthering the yield gain in wheat. Lack of correlation between plant height (PH) and rooting depth (RD) in the present experiment supports the earlier finding of Seeraj et al. (2004). It has been suggested that introducing of dwarfing genes had no impact on RDW (Bush and Evans 1988). Therefore, higher plant height may not necessarily result in higher RDW as also explained by Miralles et al. (1997).

The cluster analysis among the original set of 175 genotypes, on the basis of root and yield traits, revealed that around 68% of the genotypes including released varieties were clubbed into a single cluster. Therefore, a significant genetic variation observed in

ANOVA appears to be because of a few selected genotypes. It was interesting to find two advance breeding lines (HD2687/HP1896//WH542 and D2824/VL796) of cluster V ranked first for most of the root and shoot traits. However, these two were not among the top-yielding genotypes under CA. Comparatively lesser yield in these genotypes under CA indicates that for achieving higher yield; root traits have to be synergistically combined with above-ground traits. Interestingly there seems to be no conflict between roots and shoot traits for resource allocation since genotypes with high RDW also had high SDW. The results of this study suggest that root traits can be integrated into the wheat breeding program for higher yield realization through improved sink capacity.

Authors' Contribution

Conceptualization of research (RR, RY); Designing of the experiments (RR, RY, KG); Contribution of experimental materials (RY, KG); Execution of field/lab experiments and data collection (RR, KG, NK, RP); Analysis of data and interpretation (RR, RY, MK); Preparation of the manuscript (RR, RY, AKJ, PB).

Conflict of interest

The authors declare no conflict of interest.

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