Multivariate analysis in wheat (*Triticum aestivum* L.) for yield and attributing traits under soil salinity and alkalinity in Haryana, India

Abstract:

Salt-affected soils could be used by improving and developing salt-tolerant genotypes depending upon the amount of genetic variation and salt stress response of adapted and donor sources of wheat. Salt stress affects 20% of global cultivable land and is increasing continuously owing to the change in climate and anthropogenic activities. Globally, Saline soils cover 3.1% i.e. 397 million ha of the total land area and around 6.74 million ha area of India is affected due to salinity. Salinity stress negatively affects the growth and development of wheat leading to low grain yield and quality. A station varietal trial was conducted to identify salt-tolerant genotypes, wherein 24 genotypes including 4 checks- KRL 19, WH 157, KRL 210 & KRL 283 were evaluated in 6 replications in 4.0 m x 1.20 m in RBD under natural saline patch at Research area of Department of Genetics & Plant Breeding (pH 8.5, EC_e 4.2 dsm^{-1}) and Dept. of Soil Science (EC_e 8.5 dsm^{-1}), CCSHAU, Hisar during *Rabi* 2021-22. Data was recorded for germination (%), days to heading, days to maturity, plant height (cm), tillers per meter row, 1000-grain weight (g), grain yield per plot (g/plot) and hectoliter weight (kg/hl). High positive correlation has been observed for 1000-GW (g) and GY/P (g/plot), PH (cm) and hectoliter weight (kg/hl). No correlation was observed between days to heading and germination (%) with plant height (cm) and hectoliter weight (kg/hl). Clustering of genotypes based on Ward Euclidean method done so that identical genotypes grouped together; 24 genotypes were divided into three distinct clusters. Hectolitre weight (kg/hl) expressed as point of dissection of studied traits as GY/P (g/plot), 1000-GW (g), DM and PH (cm) falls at one side and germination (%), DH and T/meter row lies at another side. Identification of wheat genotypes based on simultaneous selection among contributing traits will improve grain yield of wheat and promising and stable genotypes may be included in breeding program aimed to develop saline alkaline tolerant varieties for state and national level to ensure nutrition-food security.

Key words: Abiotic stress, G x t biplot, multivariate, yield and attributing traits, salinity and alkalinity, wheat

Introduction:

At global level, vast area is in grip of one or more of abiotic stresses. Among various abiotic stresses which affect the crop yield substantially, soil salinity and alkalinity are a global challenge to agricultural production. The total area of salt affected soils is 954.83 mha which is more than 7% of the world's total surface area. It has been estimated that more than 50% of the arable land would be salinized by the year 2050 [1]. "Saline soils cover 3.1% i.e. 397 million ha of the total land area of the world and around 6.74 million ha area of India. Saline soils occupy 44% area covering 12 states and one Union Territory, while sodic soils occupy 47% area in 11 states. Estimates suggest that every year nearly 10% additional area is getting salinized, and by 2050, around 50% of the arable land would be salt-affected" [2]. "Soil salinity results in lower crop growth and yields and highest production losses were observed in wheat (31.2%). India would be in need of around 311 million tons of food grains (cereals & pulses) during 2030 to provide meal to around 1.43 billion people and the requirement unsurprisingly would further increase to 350 million tons by 2050 when country's population would be around 1.8 billion" [3].

At global level, it is estimated that soil salinity range from 340-950 x10^6 ha while in India various authors mentioned the area ranging from 7-12 x 10^6 ha estimates of the area of salt affected soils vary widely, ranging from 6% to 10% earth's land area and 77 million ha of irrigated lands . Salt tolerance is a complex trait and reported to be polygenic in nature that's why only few successful attempts have been made to develop salt tolerant crop varieties like KRL 1-4, KRL 19, KRL 283 by CSSRI, Karnal. Existence of genetic variability determines the success of any breeding program and fortunately many crops like rice, wheat, barley and mustard have exhibited a good spectrum of variability towards salinity and alkalinity stresses. Salinity is a soil condition characterized by a high concentration of soluble salts. Soils are classified as saline when the electrical conductivity (EC) of the saturation extract (EC_e) in the root zone exceeds 4 dS m^{-1} which is equivalent to approximately 40 mM NaCl at 25 °C and has exchangeable sodium of 15%and generates an osmotic pressure of approximately 0.2 MPa. This definition of salinity derives from the EC_e that significantly reduces the yield of most crops. Saline soil contains sufficient soluble salts to adversely affect the growth of most of lower plant with the lower limit of electrical conductivity of the saturated extract (EC_e)=4 desi Siemens per meter or 4mmhos/cm.

For all important crops, losses in production are mostly due to drought and high soil salinity, environmental conditions which will worsen in many regions because of global climate change. The reduction in yield normally ranges from 10% to 90% for wheat, 30% to 50% for rice, 50% to 75% for cotton and 30% to 90% for sugarcane; herewith gradually increasing pressure on land, there is urgent need to overcome these stresses for meeting the demand of food production targets. "In developing countries, 1.2 billion people rely on wheat to survive. The stress response varies with developmental stages of the genotypes, amount of adaptation potential of genotypes chosen for study and the ability to survive under stress conditions. Salt-tolerance consists of complex responses at the molecular, metabolic, cellular, and physiological levels and many other responses, e.g., mechanisms controlling ion uptake, osmotic regulation, transport, balance, antioxidant metabolism, and hormone metabolism. Adding to basic mechanism, stress signals or secondary messengers play significant roles in increasing a plant's resilience against salinity stress" [4]. "Wheat (*Triticum aestivum* L.) is an important food crop of the world fulfilling the energy, protein, and dietary fiber need of majority of humans. It is the second most important crop in India after rice with an annual production of 106.41 million tons from 30.54 mha with 34.84 q/ha productivity" [5]. Among various field crops, generally, wheat is more sensitive to salinity that hampers the growth and development of plant, leads to low productivity or even complete crop failure under extreme severity of salinity.

"The most common effects of salinity on plants are suppression of growth. Three major hazards are associated with such situations: (i) osmotic stress arising from the more negative water potential (elevated osmotic pressure) of the rooting medium, (ii) specific ion toxicity usually associated with excessive intake of sodium, chloride, sulphate or other ions, and (iii) nutrient imbalance, when the excess of these ions leads to a diminished uptake of potassium, nitrate or phosphate or impaired internal distribution of one or another of these elements. Salinity is the most adversely affecting factor on productivity and quality of wheat by causing hinderance in smooth functioning of physiological as well as biochemical activities in plants. Generation of ROS due to Na^+ toxicity, which damage biomolecules (e.g., lipids, proteins, and nucleic acids) on the cellular level and alters redox homeostasis, is a common phenomenon under salt stress" [6]. "The reduction in the capability of roots for water uptake owing to osmotic stress contributes to growth inhibition, declined crop productivity, and inferior grain quality" [7]. Thus, grain quality is drastically affected by the devastating effects of osmotic stress, while the subsequent slower ion toxicity phase is even more detrimental.

Keeping above points in mind, the present study was conducted to characterize wheat genotypes for tolerance towards salinity and alkalinity stresses and study of effects of these stresses on yield and its attributing traits.

- To assess the genetic variability for grain yield and its attributing traits based on morphological and quality traits among genotypes for salinity and alkalinity
- To study the character association, path coefficient analysis, genetic divergence morphological and quality traits among yield and yield attributes under different salinity and alkalinity conditions

Materials and methods:

Experimental material and site:

To identify salt-tolerant genotypes, two station varietal trials- SVT (Sal./Alk.) were conducted wherein 24 genotypes including 4 standard Checks- KRL 19, WH 157, KRL 210 & KRL 283 were evaluated in Randomized Block Design under natural saline patch (pH 8.5, EC_e 4.2 dsm^{-1}) at Research area of Wheat and Barley Section, Department of Genetics & Plant Breeding and Department of Soil Science (ECe 8.5 dsm^{-1}) during *Rabi* season 2021-22. Department of Genetics & Plant Breeding and Department of Soil Science, Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana, India is situated at the latitude of $29^0 10'$N, the longitude of $75^0 46'$E and altitude of 215.2 m amsl in the semi-tropical region of NWPZ. The genotypes were grown in plot size 4.0 m x 1.2 m with 6 replications keeping row to row spacing 20 cm and plant to plant spacing 10 cm. The experiment was conducted in 2022 cropping season. Evaluation of wheat genotypes grown on two sites (>1 km) was done and data was recorded for various metric traits, namely, days to heading, days to maturity, plant height (cm), tiller per meter row length, 1000-grain weight (g), grain yield per plot (g per plot) and 1 quality trait, hectoliter weight (kg/hl). Disease reaction (under natural condition) for susceptibility towards yellow rust and brown rust was also recorded. The pedigree details of all genotypes with checks presented in Table 1. Recommended tillage and plant protection practices were followed to raise good crop.

Soil Sampling and Analysis:

From the experimental areas, a minimum of five locations were selected for soil sampling. Samples were collected from each selected location to a depth of 15 cm, 25 cm and 40 cm. Soil samples were extruded onto a plastic liner and then sectioned at 0.0–0.1 m, then successively at 0.2 m intervals to 40 cm. Sectioned soil samples from the five locations were composited for each corresponding depth. Samples were dried at 40 °C, then ground to pass through < 2 mm sieve for analysis. Soil pH and EC were determined in a 1:5 soil: water suspension. Electrical conductivity of saturated extract was calculated from $EC_{1:5}$ and clay content relationship [8].

SAS 9.3 statistical software was used for data analysis.

Table 1: Pedigree details of genotypes undertaken for study under salinity and alkalinity conditions

Sr. No.	Entry	Parentage
1	WH 1301	W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1/5
2	WH 1302	UP2338*2/VIVITSI/3/FRET2/TUKURU//FRET2/4/MISR1/5/TUKURU//BAV

		92/RAYON*2/3/PVN
3	WH 1303	WH542/P13352
4	WH 1304	BOKOTA/5/UP2338*2/VIVITSI/3/FRET2/TUKURU//FRET2/4/MISR1/6/BABAX/LR42//BABAX*2/3/KUKUNA/4/CROSBILL#1/5/BECARD
5	WH 1305	WH1184/P12864//WH1194/P13020
6	WH 1306	CROC1/AE.SQUARROSA(205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/5/ CIRO16
7	WH 1307	SOKOLL/WBLL1/4/D67.2/PARANA66.270//AEGILOPSSQUARROSA(320)/3/CUNNINGHAM
8	WH 1308	P12959/P12963//P12971/P12954
9	WH 1309	P13416/P13485
10	WH 1310	P13496/P13350
11	WH 1311	QUAIU/FRNCLN
12	WH 1312	PRL/2*PASTOR*2/5/CROC1/AE.SQUARROSA(205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2
13	WH 1313	NELOKI//SOKOLL/EXCALIBUR
14	WH 1314	SAUAL/YANAC//SAUAL/3/2*KUTZ
15	P 13582	SNB//CMH79A.955/3*CN079/3/ATTILA/4/CHEN/AEGILOPSSQUARROSA (TAUS)//BCN/3/2*KAUZ/5/KINGBIRD#1
16	P 13650	MISR1
17	WH 1402	SHORTENEDSR26TRANSLOCATION//2*WBLL1*2/KKTS/3/BECARD
18	WH 1403	PAURAQ/4/HUW234+LR34/PRINIA//PBW343*2/KUKUNA/3/ROLF07
19	WH 1404	CROC_1/AE.SQUARROSA(205)//BORL95/3/PRL/SARA//TSI
20	WH 1405	CHIPAK
21	KRL 19(C)	PBW255/KRL1-4
22	WH 157(C)	NP876/S308//CNO/8156
23	KRL 210(C)	PBW65/2*PASTOR
24	KRL 283(C)	CPAN3004/KHARCHIA65//PBW343

Results and Discussion:

The identification of genotypes tolerant to salinity and alkalinity soils may be an alternative to maintain and improve productivity on these soils. ANOVA suggests significant variations among the genotypes for studied traits. Entries, namely, WH 1313 (59.6 q/ha), WH 1306 (54.9 q/ha) and WH 1309 (52.9 q/ha) performed better and found significantly superior to the best check WH 157 (43.5+8.2 q/ha). P 13582 (61.6 q/ha), P 13650 (62.1 q/ha) performed better and found significantly superior to best check KRL 283 (46.4±13.7 q/ha) in Research area of Dept. of Soil Science. WH 1403 (81.05 kg/hl) followed by WH 1402 (80.93 kg/hl) reported highest value for hectoliter weight. P13650 and WH1305 had highest sedimentation value (46.5 ml). 1000-GW positively correlated with Grain yield per plot. High positive correlation observed for 1000-GW (g) and GY/P-2 (g/plot), PH (cm) and hectoliter weight (kg/hl) (Figure 1 and 2). These traits were important yield contributing traits. No correlation was observed between days to heading and germination (%) with plant height (cm) and hectoliter weight (kg/hl). Nearly similar type of relationship was exhibited by tillers per meter row length with plant height. The difference between the biplot origin and genotype position in the biplot was the vector length of the genotype and it is a measure of the distinctiveness of the genotype from other genotypes as reviewed by [9]. Similar results reported by other workers while studying genotypes x traits biplot for multivariate analysis in wheat [10 and 11].

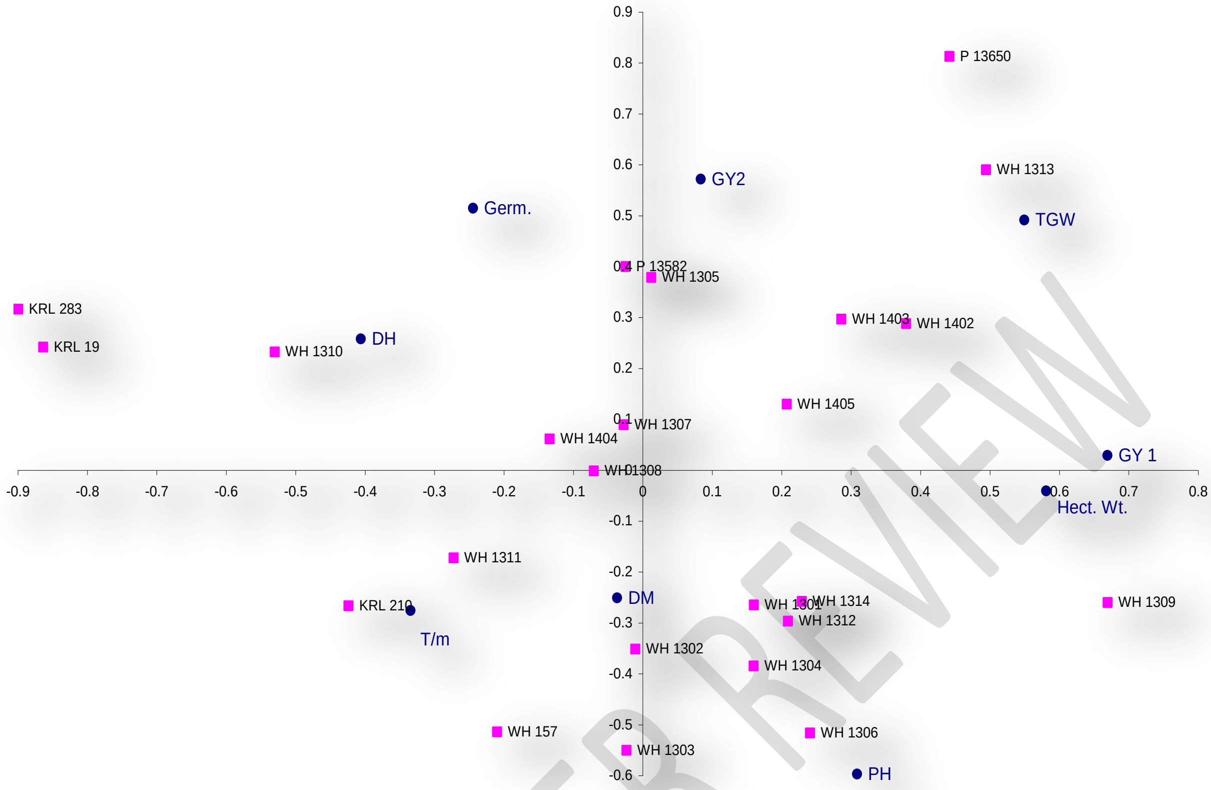

Fig 1. Genotype and traits under biplot analysis

P 13650, WH 1309, WH 1313, KRL 283 and KRL 19 lies far from other genotypes. Mainly three clusters of small and moderate sizes were observed in biplot analysis. Tiller per meter row lies in first quadrant. Second cluster comprised of plant height(cm) and hectoliter weight (kg/hl). Third cluster contains grain yield 1 (obtained at Department of Genetics and Plant Breeding), grain yield 2 (obtained at Research area Department of Soil Sciences) and 1000 grain weight (g).

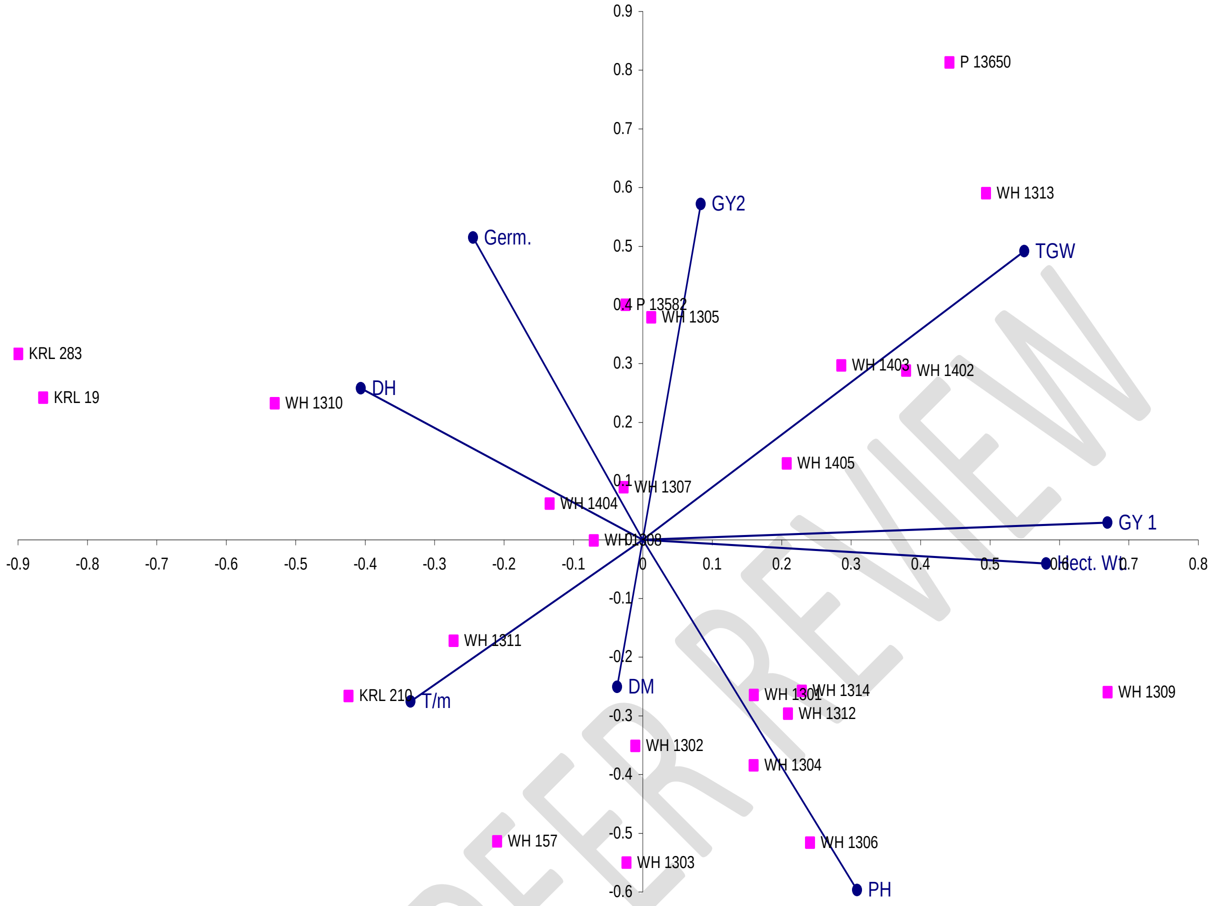

Fig 2. Association analysis among traits

Multivariate hierarchical clustering: Based on multivariate hierarchical clustering, the classification of diverse genotypes based on set of traits led to grouping of genotypes so as to keep alike genotypes in the similar group. The cluster analysis has no mechanism for distinguishing irrelevant and relevant variables. Clustering of genotypes based on Ward Euclidean method had been exploited under multivariate clustering of genotypes so that identical genotypes grouped together. Multivariate hierarchical clustering grouped 24 genotypes into 3 major clusters, where, 10 genotypes + WH 157 and KRL 210 falls in Cluster I while remaining 10 genotypes falls in Cluster II and KRL 19 and KRL 283 lies in cluster III (Figure 3). Multivariate hierarchical clustering of genotypes vis-à-vis traits demonstrates that hectolitre weight (kg/hl) expressed as point of dissection of studied traits as GY/P (g/plot), 1000-GW (g), DM and PH (cm) falls at one side and germination (%), DH and T/meter row lies at another side (Figure 4).

Information on genetic diversity in wheat under soil salinity and alkalinity condition is scanty; therefore this experiment was conducted to identify genetically divergent genotypes as donors with desirable traits for hybridization particularly for sodic soils coupled with high yield and its attributing traits. Similar results obtained by [12]. “It is well recognized that more is the distance between clusters, wider the genetic diversity would be between the genotypes. Therefore, highly divergent genotypes would produce a broad spectrum of segregation in the subsequent generations so that transgressive segregants can be obtained enabling further selection and improvement. The hybrids developed from the selected genotypes within the limit of compatibility of these clusters may produce desirable transgressive segregants of high magnitude of heterosis. This would be useful in a wheat breeding programme particularly for targeting hostile conditions of soil salinity and alkalinity" [12].

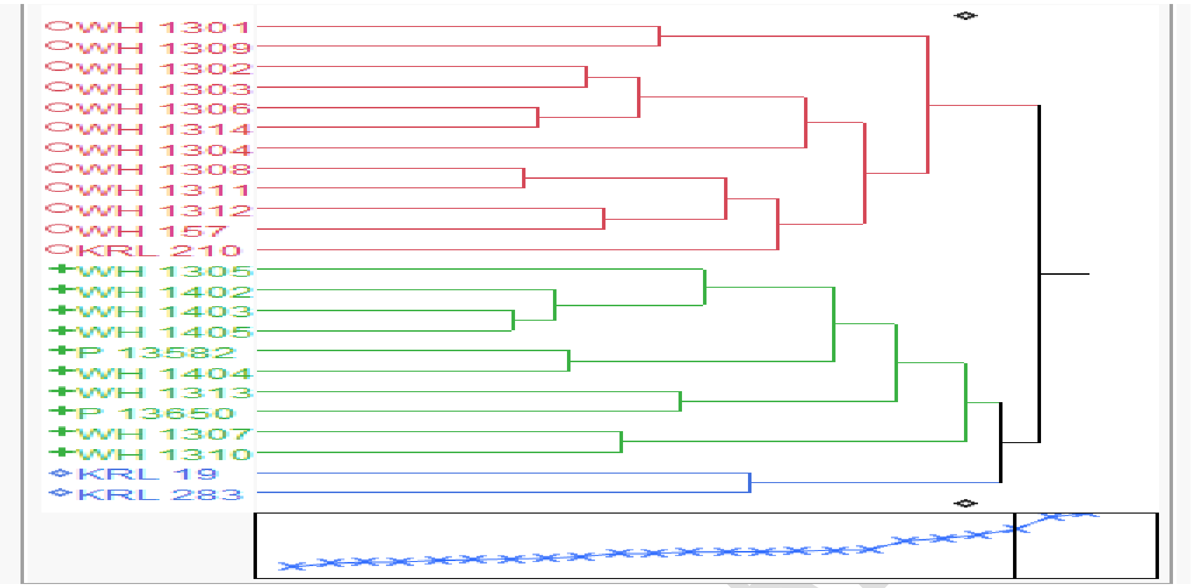

Fig 3. Multivariate hierarchical clustering of genotypes based on Ward's method

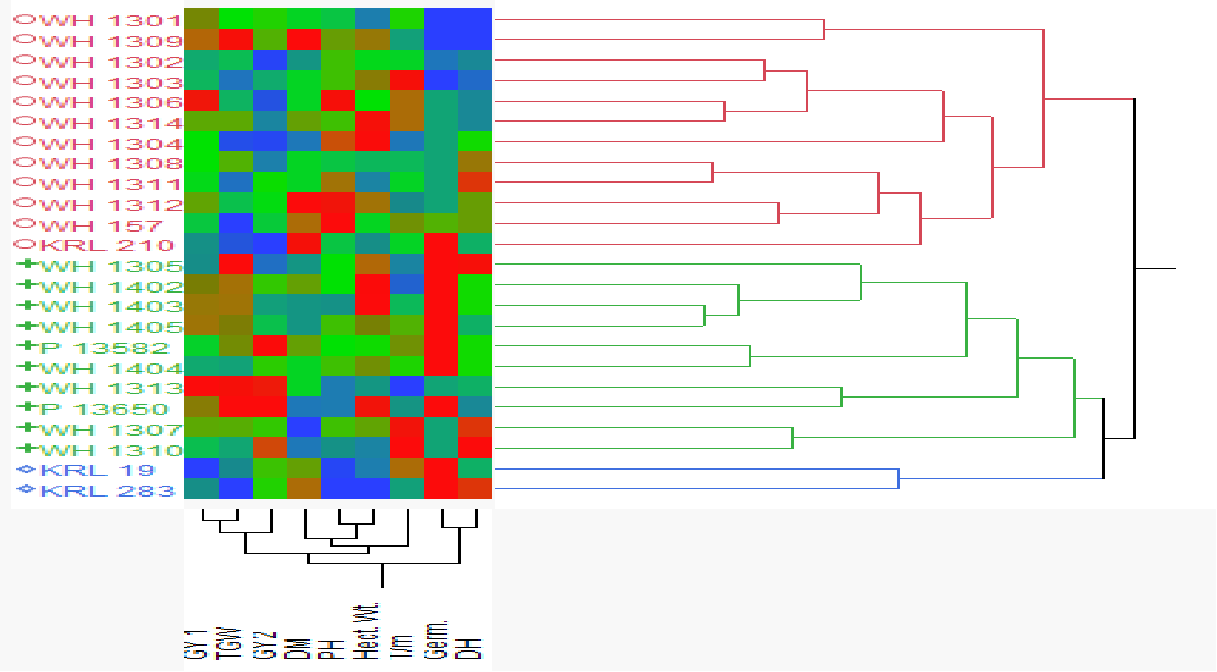

Fig 4. Multivariate hierarchical clustering of genotypes vis-à-vis traits

Conclusion:

Identification of potential wheat genotypes based on simultaneous selection among contributing traits will improve the grain yield of wheat. Promising and stable genotypes can be included in breeding programme aimed to develop tolerant varieties for soil salinity and alkalinity for state and national level to ensure food and nutritional security.

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