Indian J. Genet., 76(3): 266-273 (2016)
DOI: 10.5958/0975-6906.2016.00041.9

Exploring indicator scoring as a selection tool in plant breeding: A study under conservation *vs* conventional tillage systems

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(Received: February 2016; Revised: August 2016; Accepted: August 2016)

Abstract

Indian agriculture is on an edge of transition from conventional to conservation agriculture, the only limiting constrant is avaliblity of cultivars adapted to conservation agriculture. This study explores possibility of indicator scoring system for identification of genotypes suitable for different tillage management system namely, conventional tillage flat bed (CTFB) and conservation agriculture (CA). Minimum data set (MDS) was constructed by selecting the traits from each of five principal components (PC) accounting for 71.26% of total variation. Multiple linear regression between MDS as independent variable and yield and biomass as dependent variable showed R^2 value of 0.661 and 0.605. Indicator score identified through nonlinear scoring of the MDS found out CA as a superior environemt to conventional agriculture in both years. Indicator score identified HD3117 and HDCSW 18 for CA which support the use of indicator scoring as a selection tool in plant breeding as both of these lines are the product of systematic breeding under CA condition and have revealed significant superiority over other in multilocational yield trials for CA.

Key words: Wheat, principal component, minimum data set, indicator scoring, selection

Introduction

Wheat is the staple nourishment harvest of the globe, serving the calorie need of more than 40% of the world population. Global wheat production touched 721 mt in 2014, however, with simultaneous increase in demand (~2%) (http://www.igc.int/en/grainsupdate). The world population is projected to reach 9.1 billion by 2050 and to meet the energy requirement of such a large population and animal feed, cereal production has to be increased by atleast 0.9 b tons (FAO 2009). India is the second largest wheat producer after China, with a record harvest of 95.88 m tons during 2013-14. By 2020, India will need 109 m tons of wheat to meet indigenous demand (Kumar 1998). Wheat is grown under several management practices; of these the conservation agriculture (CA) was found to be the best tillage management practice for wheat production (Erenstein et al. 2008; Zamir 2010; Yadav et al. 2012; Sagar, et al. 2014b; Gupta and Yadav, 2014). The CA supports crops with more water (Hassan et al. 2005), nutrient (Martinez et al. 2008), better anchorage, organic matter, healthy crop rotation and a permanent soil cover (Trethwon et al. 2005). To exploit the better production environment under CA, it is essential to develop the variety responsive to such environment. Traits for emergence, establishment and phenology with regard to adaptation under contrasting production condition including tillage were well studied by several authors (Trethwon et al. 2005; Rebetzke et al. 2007; Joshi et al. 2007; Kharub et al. 2008; Liang et al. 2012; Sagar et al. 2014a). Selection for these traits, for adaptation to CA from a segregating population under CA highlights the importance of parental selection for adaptation to different growing conditions. Significant genotype × tillage (G × T) interactions for wheat crop under CA was reported not only from India (Joshi et al. 2007; Kharub et al. 2008; Yadav et al. 2012; Sagar et al. 2014b) but from several other researchers across the globe (Carr et al. 2003b; Trethwon et. al. 2005). Yield gain can be realized through improved agronomy, better and adapted cultivars and positive interaction between genotype × management (G × M) interaction. According to Fischer (2009), annual gain of 1.1 percent in wheat yield in Australia has been realized through all these factors. Therefore genetic gain without exploiting genotype × production environment (G × E)

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interaction will be highly restricted, as the effectiveness of plant breeding strategiesis strongly influenced by these interactions. Knowledge about the amount and pattern of G× E can help us in designing breeding programme to develop production environment specific varieties. However before harping on breeding programme, it is very important to develop overall growth index under CA to identify the traits for adaptation to such environment. Genotypic health under different management can also be worked out to identify specific adaptation similar to soil physical quality index (Bhardwaj et al. 2011; Shahid et al. 2013; Sinha et al. 2014; Liu et al. 2014). An attempt has been made in this paper to evolve genotypic growth/ performance indexes for CA and CTFB.

Materials and methods

Materials and experimental site

Experimental materials for the study comprised of 42 differentially adapted genotypes selected from on going breeding programme on wheat improvement for CA adaptation and also includes three recently released varieties of north western plain zone. A long-term experiment on breeding for conservation agriculture and cropping system was initiated during 2006 and is at place since then, in the experimental farm of Indian Agricultural Research Institute, New Delhi, located at 28^o 35 N latitude, 77^o 12 E longitude and at an altitude of 228.16 m above mean sea level. Maize and wheat crops were grown each year with no tillage and full residue retained on the surface. To explore the effect of production environment, same set of wheat material was raised on adjacent field in flat bed with full tillage operation and no residue retention (CTFB). The genotype included in the present study were product of this breeding programme. The soil at the experimental site belongs to the major group of Indo-Gangetic alluvium. The soil is non-calcareous and slightly alkaline in reaction. Surface and subsoil texture ranges from sandy loam to loam, with medium to weak angular blocky structure.

Experimental design and agronomic management

The experiment was laid out in a randomized block design (RBD) with two replications for all the 42 entries in two environments *viz*., CA and CTFB for two years. Overall area of each plot in each tillage management was maintained at 5.60 m^2. The plot under conventional tillage comprised six rows of 4 meter each and 23 cm apart. The plot under CA (maintained since 2006) comprised two ridges of 4m each with 70 cm. Seeding rate was 100 kg/ha for conventional tillage and 80 kg/ha for permanent bed CA. Under conventional tillage condition, full dose of DAP and 50% of urea along with Zinc sulphate were broadcasted and mixed in soil with last tillage operation. The remaining urea was broadcasted in two split doses i.e. at CRI stage in mid-December after 1^{st} irrigation and after third irrigation. Under permanent bed condition, full dose of DAP along with 50% of urea and zinc sulphate were broadcasted before seeding. Remaining dose of urea was applied as in case of conventional tillage condition. Under permanent bed condition, glyphosate was sprayed evenly on all experimental area, two days before seeding to control all emerged weeds. Subsequently weeds were controlled through application of selective herbicide and manual weeding.

Data recording and statistical analysis

Data were recorded on morpho-physiological and yield attributing traits during the Rabi season of 2011-12 and 2012-13 for 42 genotypes under different management regime. A proper scale was followed for the data recording and at specific crop growth stage (Zadoks et al. 1974). Yield and total biomass of each entry was recorded on middle rows of eachplot. Canopy temperature (CT) and normalized difference vegetation index (NDVI) was recorded on sunny and bright days. Data analysis was done using software IBM SPSS statistics 20.0, SAS version 9.2.

Computation of genotypic performance index (GPI)

Principal component analysis was done using the software IBM SPSS 20.0. To develop minimum dataset (MDS), PC with eigen values e”1 and explaining at least 5% of the variation in the data (Wander and Bollero 1999; Brejda et al. 2000) were considered. Highly weighted factors with absolute values in the range of 10% of the highest factor loading were retained for developing minimum data set (MDS). If any single principle component has more than one selected factor/trait, multivariate correlation coefficient analysis was used to identify the redundant trait and was disposed off from the MDS (Andrews et al. 2002a). On the off chance that the highly weighted variables were not correlated, each was viewed as critical and was held in the MDS. As a check of how well the MDS represented the tillage management system, and to identify the key indicators, multiple linear regressions (MLR) were performed using the indicators retained in the MDS as independent variables and the endpoint measures, such as mean yields and total biomass as dependent variable.

Every observation of each MDS indicator was transformed using a non-linear scoring (Bastida et al. 2006) method. Scores were assigned to each indicator, keeping 'more is better'. Non-linear scoring function:

$$y = a/(1 + (x/x_0)b)) \tag{1}$$

where 'a' is the maximum value reached by the function (in present case, a = 1) x is the unknown of the equation, corresponding to the value of the parameter in question in each case, x_0 is the mean value of each parameter of the study. The use of the mean value in the equation is important because it centres the curve in a normalised value of 0.5. b is the value of the slope of the equation. Using b = –12.5, we obtain curves that fit a sigmoidal tending to 1 for all the proposed parameters. The above value provides curves that vary between 0 and 1 in a suitable way.

Genotypic performance index was calculated by summing, the weighted MDS indicator score for each observation.

$$GPI = \sum_{i=1}^{n}(Wi \times Si) \tag{2}$$

Where, *Si* is the score for the subscripted variable and *Wi* is the weighing factor obtained from PCA. Weighted factor for these PC were calculated by dividing the individual PC score with the cumulative total of the all PCs. The GPI obtained was normalised by dividing the obtained GPI with maximum value so that best treatment gets maximum score of 1. Steps and concept followed to determine the genotypic performance intex has been detailed out in Fig. 1.

Results and discussion

Analysis of variance (ANOVA) for various traits under study showed significant differences among the genotypes in all environments. It indicate that material in the study are highly diversre and therefore scoring developed by using these genotypes would be equally applicable in other breeding material. To improve the breeding efficiency, it is very important to identify the trait which indicate the adaptaion to a particular production system/environment (Probability values are not presented). The attribute which best represent the system can be selected on the basis of eigen values of principle componets and factor loading. The loading is correlation of each character with PC factor. Principle component analysis identified five significant PC accounting for 30.360, 15.431, 11.574, 7.902 and 5.995 percent of variance, respectively. Total variance explained by these PC was 71.262 % (Table 1).

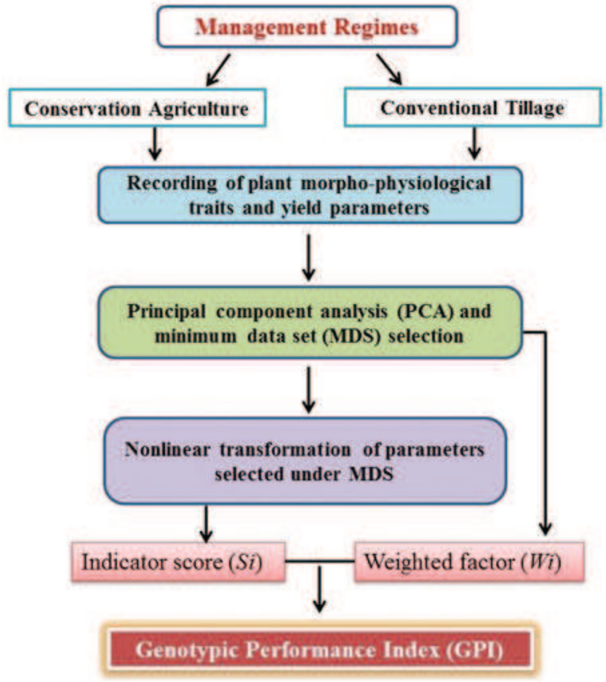

Fig. 1. **Steps and concept for determining genotypic performance index**

Table 1. Performance of growth parameters indicators in term of factor loading/eigen vector values in principal component analysis

PCs	PC1	PC2	PC3	PC4	PC5
Eigenvalue	5.465	2.778	2.083	1.422	1.079
Per cent variance	30.360	15.431	11.574	7.902	5.995
Cumulative (%)	30.360	45.791	57.365	65.267	71.262
Factor loading/eigen vector					
Embryo length (mm)	0.553	0.424	0.005	0.428	0.052
Embryo width (mm)	0.701	0.088	0.229	-0.160	0.263
Grain length (mm)	0.197	**0.746**	0.013	-0.089	0.292
Grain width (mm)	0.028	**0.694**	0.224	0.230	-0.121
Coleoptile length (cm)	0.587	0.442	-0.112	0.127	0.229
NDVI1	0.139	0.008	0.045	0.063	**0.777**
NDVI2	-0.065	-0.317	0.690	0.434	0.265
NDVI3	0.018	-0.029	0.153	**0.850**	0.025
NDVI4	0.187	-0.060	**0.871**	0.171	0.096
Canopy temperature	0.009	0.485	0.647	-0.377	-0.070
No. of spikelets/head	**0.769**	0.140	-0.057	0.157	-0.125
Spike length (cm)	0.540	0.109	0.628	-0.080	0.023
No. of grains/spike	0.696	-0.101	0.140	-0.121	0.410
Plant height (cm)	**0.790**	-0.095	0.203	0.186	0.049
Tiller/m length	0.089	**0.759**	0.222	-0.220	-0.377
Test weight (g)	0.015	**0.736**	-0.182	-0.048	0.001
Days to heading	**0.821**	0.144	0.281	-0.188	-0.086
Days to maturity	0.395	0.272	0.639	0.157	-0.314

(Bold values indicate the eigen vectors within 10% of the highest factor loadings)

On the basis of eigenvalue three variables viz., number of spikelets per head, plant height and days to heading were selected from PC1 for multivariate correlation coefficient analysis. These variables were highly correlated (**P < 0.01) with each other. Phenological adjustment has essentially led to wheat adaptation to different ecologies as this crop regularly endures the terminal heat stress. The character therefore needs critical look under CA, as CA due to its inherent ability to modulate temperature, bolster crop for long span than the CTFB (Trethwon et al. 2012). The time taken for a variety to reach flowering, depends on vernalisation, photoperiod and thermal time requirements (Gupta and Yadav 2014). Sowing a variety outside of the sowing window increases the risk of flowering occurring at the wrong time, leading to frost damage or high temperatures at flowering and grain fill. In wheat, candidate genes have been identified for photoperiod (Scarth and Law 1983; Mohler et al. 2004) and vernalization response (*Vrn-A1*, *Vrn-B1* and *Vrn-D1*) (Law et al. 1976; Worland et al. 1987; Galiba et al. 1995) and are well studied. In our study all the genotypes copy same *Ppd* alleles, which are insensitive to photoperiod response for flowering, however, variation for *Vrn* genes has been detected among the genotypes (Yadav et al. 2014). Previous reports indicate that different pre-heading phases could be changed without modifying time to anthesis by exploiting available variability for vernalization, photoperiod and response to temperature (Slafer 1996; Gonzalez et al. 2002). Therefore, days to heading considered to be a part of MDS. Plant height has been reduced by exploiting various dwarfing genes, however, selection of gibberelin insensitive genes like *Rht* 1 and *Rht* 2 genes in wheat not only reduced height but also reduced the coleoptile length. Alternate *Rht* gene like *Rht* 8 and *Rht* 12 and do not affect gibberellin sensitivity at early stage of the crop growth but reduces overall plant height and therefore, produces long coleoptile of about 100 mm (Cornish and Hindmarsh 1988; Addae and Fearson 1992). Earlier studies showed that the varieties having shorter coleoptiles are less likely to emerge if sown at higher depth. To harness the residual moisture in the soil, and to cope up with the stubble-load under CA, seeds are to be placed at depth. Taller wheat with alternate dwarfing genes and longer coleoptiles emerges faster and establish good stand even under high residue load (Rebetzke et al. 2007). Keeping in view, the relationship between coleoptile length, plant height and stand establishment, plant height was also included in MDS. Number of spikelets per head and spike length may not always correspond to each other, longer panicle/spike may not always have large number of spikelets, if they are not compactly arranged on the rachis and therefore, it was pragmatic to include spikelet number as part of the MDS. In this way three traits were selected out of 1st PC are, number of spikelets per head, plant height and days to heading.

In PC2 four variables *viz*., grain length, grain width, test weight and tillers per meter were picked on the basis of eigen value for multivariate correlation coefficient. To reduce the number of variables for selection, redundant variables like grain length and seed width were identified through correlation and were dropped from MDS, leaving only grain weight as part of MDS. Seeding rate and establishment determine the plant population and can be an important determinant of tiller density and, at later stage, heading density. Wheat crop can compensate the yield by changing the number of tillers and the size of the heads with respect to change in the environmental conditions. Despite the crops ability to compensate, targeting a variety's optimum plant density at sowing makes the most efficient use of water and nutrients, thus the number of tillers/m was included as a part of the MDS.

For PC3 only one trait NDVI4 with highest factor loading was selected for MDS. Similarly, NDVI3, NDVI1 were picked up from PC4 and PC5. Thus, for this study NDVI emerged as a major trait for selection of genotypic performance with respect to yield. NDVI is a mathematical formula derived to form a single spectral based number, which is more sensitive than just a single wave length. It is defined as the ratio of the difference between near infrared and the red band to the sum of the two band, which is a measure of greenness (Sembiring et al. 2000). Grain development depend on the duration of grain filling and grain filling rate. Grain filling rate is decided by transfer of assimilate synthesized in green part of the plants which is near to sink. Therefore the rate of photosynthesis, which depends upon the chlorophyll content in leaves, is very important and can be measured through NDVI (Hu et al. 2010). So genotypes maintaining higher NDVI value during grain filling period may give higher grain yield. Sufficient genetic variation exist among genotypes for measuring NDVI, however, due to conflicting reports on relationship between NDVI and grain yield, NDVI can be used as an indirect selection criterion for identifying physiologically superior and high yielding wheat genotypes under heat stress only (Hazratkulova et al. 2012).

From all the PCs, eight traits were included as a part of MDS (Table 1). To checks how well this MDS fits the key of growth index and the tillage management, multiple regression was done using the indicator retained in the MDS as independent variable and yield and biomass as dependent variable.

MLR using yield, biomassas dependent variables showed R square value (R^2) of 0.661 and 0.605 repectively. Weighted factor calculated by dividing the individual PC score with the cumulative total of the all PCs, were 0.42, 0.23, 0.16, 0.09 and 0.08 for PC1, PC2, PC3, PC4 and PC5 respectively.

Indicator scoring as selection tool in breeding programme

GPI score was highest (0.806) in CA (2011-12) and was followed by CA 2012-13 (0.74), CTFB 2011-12 (0.617) and CT 2012-13 (0.58). GPI in both the years under study was much better in CA and therefore it can be roughly concluded that potential yield realization will be much higher under CA and therefore we must select under CA to identify potential high yielder. Both years during study were differing for terminal heat stress, with acute stress in 2012-13 and almost nill stress in 2011-12. In order to know the contribution of each of the indicators towards genotypic performance, their average nonlinear scores under each management treatment were computed (Fig. 1). During both years CA has higher genotypic performance index. However, the difference in two contrasting regime was explained on the basis that year (2011-12) as it was comparatively stress free.

Indicator scoring for superior genotype selection in plant breeding

The maximum score value of 1 was realised for genotype HD 3117 followed by HD CSW 18 (0.924) under CA. Both of these genotypes are identified for CA condition and are evolved through continuous selection under CA. The other two genotypes picked up for CT on the basis of indicator scores are HD 2967 and HD 3115 with score value of 0.68 and 0.69, respectively. Among these genotypes, HD 2967 is a mega variety, developed and released for CT, occupying maximum area in north western plane zone. The other genotype HD 3115 was also developed through systematic breeding and selection for conventional tillage. The heritability of component traits being higher than yield *per se*, the winner picked up by indicator score perfectly match their ecology for adaptation and therefore, these scores can easily be applied for identification of adaptability of a genotype in early as well as in advance generation.

Selection criterion usually differ from environment to environment and CA being a comparatively new environment, hardly any information related to the selection criterion is available in the literature. In this paper an attempt has been made to identify the characters which best express in particular environment so that the same can be involved to evolve selection indices. Key traits were identified on the basis of combined non linear score for CA and CT and these are: days to heading (0.141), no. of spikelets/ head (0.141), plant height (0.138), test weight (0.0724), no. of tillers/m (0.0704), NDVI4 (0.0580), NDVI3 (0.0367), NDVI1 (0.0294) with a corresponding contribution of 20.58 %, 20.58%, 20.10%, 10.52%, 10.23%, 8.42%, 5.33% and 4.27%, respectively. It is clear from stacked bar diagram presented in Fig. 2, that three characters namely, days to heading, no. of spikelets per head and plant height are equally important in all the environments, however, their order differ in different environment. It is tiller per meter which is enhancing overall performance of genotype on permanent bed under CA and therefore, has to be given due weightage while making selection under CA.

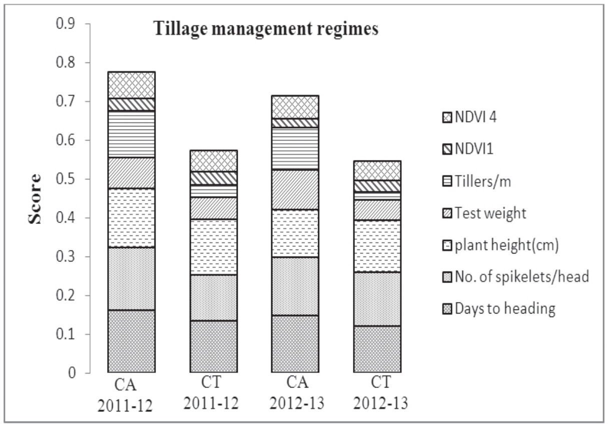

Fig. 2. **Genotypic performance index (GPI) values for different tillage management regimes of conservation agriculture (CA) and conventional tillage (CT)**

The average indicator score was 0.155 and 0.126 for days to heading, 0.155 and 0.127 for number of spikelets, 0.137 and 0.139 for plant height, 0.091 and 0.0532 for test weight and 0.113 and 0.026 for tillers per meter row length, respectively under CA and CT (Fig. 3). This shows that the indicators have a

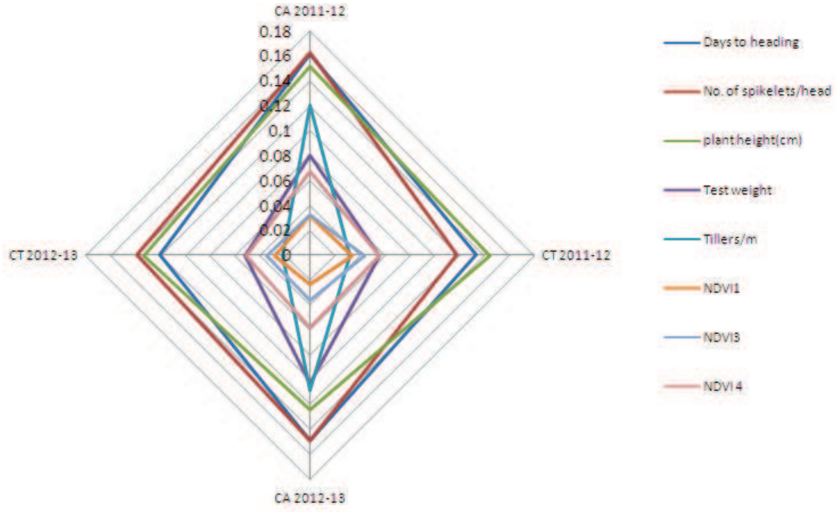

Fig. 3. **Average nonlinear scores of key indicators influenced by tillage management regime as depicted in Radar graph**

considerable role in plants overall performance and growth. Scoring function of all MDS indicator are presented in Fig. 4, which clearly establish their non linear pattern.

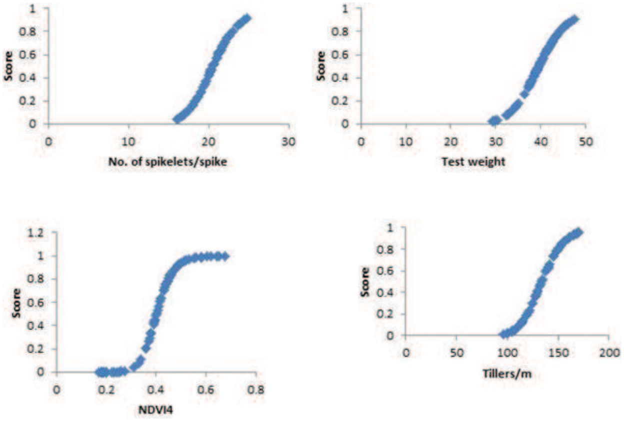

Fig. 4. Non-linear scoring functions for MDS indicators

Potential expression of key traits deciding yield formation is essential for effective selection in any breeding programme. The two years during the present experimentation were totally different in terms of plant growth and yield realization, with 2011-12 being a comparatively stress free year, whereas in 2012-13, heat wave at terminal stage affected the yield realization. The present study clearly established that yield realization was higher under CA in both the years and therefore, can be an effective environment for selection to make genetic gain. Yield *per se* being comparatively lesser heritable than component and other yield attributing traits, selection on the basis of yield it self is not going to be rewarding. Principal component and path analysis are some of the commonly used tools in plant breeding to establish relationship between yield and other traits. Indicator scoring system proposed in this paper is simple and taken into account the distribution pattern for each trait, which can be combined to make selection to identify the suitability of the genotype. In present investigation, yield and biomass were used as the ultimate variables affected by several other traits. The use of multivariate approach for plant performance index evaluation can be more effective than single parameter assessment. All the three component traits and one phenological trait contributed significantly toward indicator score but only under CA. There was reduced contribution of grain weight toward indicator score under CT and therefore, can not be a part of selection tool under coventional tillage programme. However, grain growth is an important trait for furthering yield gain and can not be ignored and grain weight along with like normalized index for vegetative index (NDVI) at maturity can form the part of selection strategy under CA to make additional genetic gain.

Table 2. Inter-correlation of highly weighted factor variables under different PCs

PC1 Variables	Days to heading	No. of spikelets/ head	Plant height	
Days to heading	1	0.618**	0.566**	
No. of spikelets/ head	0.618**	1	0.463**	
Plant height	0.566**	0.463**	1	
PC2 variables	Tillers/ m	Test weight	Seed length	Seed width
Tillers/m	1	0.486**	0.485**	0.451**
Test weight	0.486**	1	0.425**	0.368**
Grain length	0.485**	0.425**	1	0.377**
Grain width	0.451**	0.368**	0.377**	1

$^{**}P < 0.01$

Authors' contribution

Conceptualization of research (RY, VS); Designing of the experiments (RY, VS); Contribution of experimental materials (RY, KG); Execution of field/lab experiments and data collection (VS, RY); Analysis of data and interpretation (VS, RY, KG); Preparation of the manuscript (VS, RY, KG, SG).

Declaration

The authors declare no conflict of interest.

References

Addae P. C. and Fearson C. J. 1992. Variability in seedling elongation of wheat, and some factors associated with it. Austr. J. Expl. Agric., **32**: 377-382.

Andrews S. S., Mitchell J. P., Mancinelli R., Larlen D. L., Hartz T. K., Horwarth W. R., Pettygrove G. S., Scow K. M. and Munk D. S. 2002*a.* On farm assessment of soil quality in California's Central Valley. Agron J., **94**: 12-23.

Bastida F., Moreno J. L., Hernández T. and García C. 2006.Microbiological degradation index of soils in a semiarid climate. Soil Biol. Biochem., **38**: 3463-3473.

Bhardwaj A. K., Jasrotia P., Hamilton S. K. and Robertson G. P. 2011. Ecological management of intensively cropped agro-ecosystems improves soilquality with sustained productivity Agriculture. Ecosys. and Env., **140**: 419-429.

Brejda J. J., Moorman T. B., Karlen D. L. and Dao T. H. 2000. Identification of regional soil quality factors and indicators. I. Central and Southern High Plains. Soil Sci. Society America J*.,* **64**: 2115-2124.

Carr P. M., Horsley R. D. and Poland W. W. 2003b. Tillage and seeding rate effects on wheat cultivars: II. Yield components. Crop Sci., **43**: 210-218.

Cornish P. S. and Hindmarsh S. 1988. Seed size influences the coleoptile length of wheat. Aust. J. Expl. Agric., **28**: 521-523.

Erenstein O. U., Farooq R. K., Malik M. and Sharif. 2008. On-farm impacts of zero tillage wheat in South Asia's rice-wheat systems. Field Crops Res., **105**: 240-252.

FAO2009.http://www.fao.org/fileadmin/templates/wsfs/docs/Issues_papers/HLEF2050_Global_Agriculture.pdf

Fischer R. A. 2009. Farming Systems of Australia: exploiting the synergy between genetic improvement and agronomy, in: Sadras, V. O., Calderini, D. F., (Eds.), Crop physiology: applications for genetic improvement and agronomy. Academic Press, New York, pp. 23-54.

Galiba G., Quarrie S. A., Sutka J., Morgounov A. and Snape J. W. 1995. RFLP mapping of vernalization (*Vrn1*) and frost resistance (*Fr1*) on chromosome 5A of wheat. Theor. Appl. Genet., **90**: 1174-1179.

Gonzalez F. G., Slafer G. A. and Miralles D. J. 2002.Vernalization and photoperiod responses during wheat pre-flowering reproductive phases. Field Crops Res., **74**: 183-195.

Gupta R. and Yadav R. 2014.Sustainable Food Production in IndoGangeticPlainsRole of Improved Cultivars in Cropping System Intensification for Small Farm Holders. Advances in Soil Science: Soil Management of Small Holder Agriculture (Eds., Rattan Lal and BA Stewart): 113-143.

Hassan Z. and Hussain Akbar G. 2005. Effect of permanent raised beds on water productivity for irrigated maize-wheat cropping system. Evaluation and performance of permanent raised bed cropping systems in Asia, Australia and Mexico edited by C.H. Roth, R.A. Fischer and C.A. Meisner ACIAR Proceedings No. 121.

Hazratkulova S., Sharma R. C., Alikulov S., Islomov S., Yuldashev T., Ziyaev Z., Khalikulov Z., Ziyadullaev Z. and Turok J. 2012. Analysis of genotypic variation for normalized difference vegetation index and its relationship with grain yield in winter wheat under terminal heat stress. Plant Breed., **131**: 716-721.

Hu H., Bai Y. L., Yang L. P., Lu Y. L., Wang L., Wang H. and Wang Z. Y. 2010. Diagnosis of nitrogen nutrition in winter wheat (*Triticum aestivum*) via SPAD-502 and GreenSeeker. Chin. J. Eco-Agric., 748-752.

Joshi A. K., Chand R., Arun B., Singh R. P. and Ortiz R. 2007. Breeding crops for reduced tillage management in the intensive, rice-wheat systems of South Asia. Euphytica, **153**: 135-151.

Kharub A. S., Chatrath R. and Shoran J. 2008. Performance of wheat (*Triticum aestivum*) genotypes in alternate tillage environments. Indian J. agric. Sci., **78**: 884-886.

Kumar P. 1998. Food Demand and Supply projections for India, Agriculture economics policy paper 98-01 IARI, New Delhi, 141 pp.

Law C. N., Worland A. J. and Giorgi B. 1976. The genetic control of ear emergence time by chromosomes 5A and 5D of wheat. Heredity, **36**: 49-58.

Liang Y. L. and Richards R. A. 2012. Seedling vigor characteristics among chinese and Australian wheats. Commun. Soil Sci. Plan., **30**: 159-165.

Liu Z., Zhou W., Shen J., Li S., He P. and Liang G. 2014. Soil quality assessment of Albic soils with different productivities for eastern China. Soil Tillage Res, **140**: 74-81.

Martinez E., Fuentes J., Silva P., Valle S. and Acevedo E. 2008. Soil physical properties and wheat root growth as affected by no-tillage and conventional tillage systems in a Mediterranean environment of Chile*.* Soil Tillage Res., **99**: 232-244.

Mohler V., Lukman R., Ortiz-Islas S., William M., Worland A. J., Van B. J. and Wenzel G. 2004. Genetic and physical mapping of photoperiod insensitive gene *Ppd-B1* in common wheat. Euphytica, **138**: 33-40.

Rebetzke G. J., Richards R. A., Fettell N. A., Long M., Condon A. G., Forrester R. I. and Botwright T. L. 2007. Genotypic increases in coleoptile length improves stand establishment, vigour and grain yield of deep-sown wheat. Field Crops Res., **100**: 10-23.

Sagar V., Yadav R., Jain N., Gaikwad K. B. and Prabhu K. V. 2014b. Consolidating the yield gain by exploiting genotype × management interaction in wheat. Indian J. Genet., **74**: 157-165.

Sagar V., Yadav R., Jain N., Gaikwad K. B. and Prabhu K. V. 2014a. Decephering yield formation process under conservation agriculture and conventional tillage condition of wheat in India. Indian J. Genet., **74**: 506-510.

Scarth R. and Law C. N. 1983. The location of the photoperiodic gene, *Ppd2*, and an additional factor for ear-emergence time on chromosome 2B of wheat. Heredity, **51**: 607-619.

Sembiring H., Lees H. L., Raun W. R., Johnson G. V., Solie J. B., Stone M. L., DeLeon M. J., Lukina E. V., Cossey D. A., LaRuffa J. M., Woolfolk C. W., Phillips S. B. and Thomason W. E. 2008. Effect of growth stage and variety on spectral radiance in winter wheat. J. Plant Nutr., **23**: 141-149.

Slafer G. A. 1996. Diûerences in phasic developmentrate amongst wheat cultivars independent of responses to photoperiod and vernalization. A view point of the intrinsic earliness hypothesis. J. Agril. Sci. Cambridge., **126**: 403-419.

Trethowan R. M., Mahmood T., Ali Z., Oldach K. and Garcia A. G. 2012. Breeding wheat cultivars better adapted to conservation agriculture. Field Crops Res., **132**: 76-83.

Trethowan R. M., Reynolds M. P., Sayre K. D. and Ortiz-Monasterio I. 2005. Adapting wheat cultivars to resource conserving farming practices and human nutritional needs. Ann. Appl. Biol., **146**: 404-413.

Wander M. M. and Bollero G. A. 1999. Soil quality assessment of tillage impacts on Illinois. Soil Sci. Society America J., **63**: 961-971.

Worland A. J., Gale M. D. and Law C. N. 1987. Wheat Genetics. In: Lupton, F.G.H. (Ed.), Wheat Breeding. Chapman & Hall, New York, pp. 129-171.

Yadav R., Kumar L., Jat M. L. and Gupta R. 2011. Tailoring wheat genotypes for conservation agriculture in different cropping system: An innovative and much needed breeding paradigm. Resilient Food System for a Changing World. Proc. 5th World Congress of Conservation Agriculture. Brisbane, Australia. 444-445.

Yadav R., Sagar V., Jain N. and Gaikwad K. B. 2014.Agronomic association of *Vrn, Ppd, Rht* genes and identified QTLs under contrasting tillage condition in wheat. J. Wheat Res., **6**: 45-50.

Zadoks J. C., Chang T. T. and Konzak C. F. 1974. 'A decimal code for the growth stages of cereals'. Weeds Research, **14**: 415-42.

Zamir M. S. I., Ahmad A. U. H. and Javeed H. M. R. 2010. Comparative performance of various wheat (*Triticum aestivum* L.) cultivars to different tillage practices under tropical conditions. Afr. J. Agric. Res., **5**: 1799-1803.