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Research Article

Development and evaluation of early maturing white-grained finger millet (*Eleusine coracana* L.) genotypes for cultivation in sub-mountain Himalayan region of India

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Abstract
White grained finger millet genotypes has become a thrust area in finger millet breeding due to increased demand of non-glutinous food products and lesser acceptability of brown grained finger millet. Sixteen white grain finger millet lines were developed by crossing extra early maturing brown grained finger millet genotypes including adapted varieties with late maturing white grained finger millet genotypes. The quantitative data of 16 lines along with parents were subjected to multivariate analysis. A wide range of variation was observed for all the studied traits. The parental lines of brown and white grained finger millet genotypes exhibited extreme values for grain yield and days to maturity whereas, the developed white grained genotypes showed moderate values. Projections of genotypes in PCA biplot showed close association of newly developed white grain genotypes VL 427, VL 360, VR 485, VR 443, VL 366, VR 425B, VR 425A and VL 356 with VL 201 (brown type) because of earliness and high yield potential. The cluster analysis further indicated that white grained genotypes from second cluster are probable candidates for further testing and release, and further refinement in breeding strategy by hybridizing white genotypes from second cluster with brown genotype in third cluster for incorporating earliness and high yield.

Key words
White grained finger millet, Early maturity, PCA, Cluster analysis, Himalayan region

Introduction

Finger millet (*Eleusine coracana* L. Gaertn) is cultivated as a subsistence farming crop in Asian and African continents. Global area under finger millet is 4-4.5 million hectares with the production of 5 million tonnes (Anonymous, 2012). The crop has a wide range of seasonal adaptation from sea level (in parts of Andhra Pradesh and Tamil Nadu) to about 2400m above mean sea level in hills of Uttarakhand in India. Finger millet seeds are consumed in variety of forms, such as unleavened bread (roti), mudde, thin or thick porridge, and fermented porridge, and also used in brewing. Demand for finger millet grains has picked up in the urban areas and baking industry in the recent times due to high fibre and other health benefits associated with its consumption. However, the dark colour of grains has been the major hindrance for its acceptability in baking and food industry. Among both brown and white grain types, white grain types are preferred because of high protein, low fibre, low tannins and higher consumer acceptability (Sharathbabu *et al*., 2008). However, the yield potentiality of all white grain types is significantly lower than the brown types. In addition, all the white grained finger millet genotypes were late maturing, making them unsuitable for Himalayan region as only early and medium maturity duration (≤100 days) genotypes are preferred by the farmers. This necessitated the breeding towards developing early maturing white grained finger millet genotypes suitable for cultivation in hill regions.

Materials and methods

Twenty-three genotypes including 16 early maturing white grained finger millet advance cultures, three early maturing brown grained parental lines (GEC 447, GEC 450 and VL 201) and four late maturing white grained genotypes (WR 1, WR 2, WR 10 and OUAT 2) were selected for the present study. All the 16 white grain genotypes were developed through back cross breeding at ICAR-VPKAS, Almora by using white grained genotypes as recurrent parent (female) with extra early maturing brown types i.e. GEC 447, GEC 450 and VL 201 as donors, in order to develop early maturing white grained genotypes suitable for Himalayan region.

Hot water emasculation method (Rao and Rao, 1962 and Raj *et al*., 1984) was used with slight modifications. The female panicles in appropriate stage were immersed in hot water at a temperature of 48ºC for five minutes. Air dried treated panicles were tied with male panicle at appropriate hybridization stage by intertwining the fingers of male panicle inside the female panicle. The tied panicles are covered with butter paper bag for protection and exclusion from external pollination.

The 16 white grain breeding lines developed from these crosses along with parents were evaluated for

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various yield traits and suitability in the region. The crop was raised at the experimental farm of the ICAR-Vivekananda Institute of Hill Agriculture (79°39'E latitude and 25°35'N longitude, 1250 m above msl) during *Kharif* 2011. Each genotype was grown in three rows of 3 m length with row to row spacing of 22.5 cm in randomized complete block design with two replications. Thinning was practiced within a month after sowing to maintain plant to plant spacing of 10 cm within the rows. The recommended package and practices were followed to raise the crop.

The data on nine quantitative traits was recorded in 10 plants randomly in each plot as per the descriptors of finger millet (IPGRI, 1985). The traits include plant height (PH in cm), productive tillers (PT in number), flag leaf length (FLL in cm), flag leaf width (FLW in cm), peduncle length (PL in cm), finger length (FL in cm), fingers per ear (FPE in number), grain yield (GY in g per plot) and fodder yield (FY in Kg per plot). The grain yield and fodder yield values were converted to q/ha for statistical analysis. The data on days to flowering (DTF) and days to maturity (DTM) were recorded on plot basis. The data was analyzed using the JMP 2009 and statistical package SPSS (Statistical Package for Social Science, SPSS Inc., Chicago, IL). For multi-factorial comparison, principal component analysis (PCA) was used to display the correlations among the various morphological and related characters and their relationship with different finger millet genotypes. Two way cluster analysis was done using JMP 2009.

Results and discussion

Development of white grained finger millet genotypes: Due to small floret size of finger millet crossing emasculation and hybridization is difficult. The contact method of hybridization is an easy choice for breeders (Ayyangar, 1934 and Ravikumar, 1988) but requires more resources, time, space and labour. Since, the temperature requirement of water for emasculation may vary with the location and growing conditions, we have standardized the temperature and treatment duration for effective emasculation using hot water technique in finger millet. In all the crosses only few seeds were set in the female panicle, most of which gave rise to hybrid plants. In F_1 generation brown grained plants were selected as hybrid plants as brown colour is dominant over white (White grain plants of selfed seeds were also observed in F_1 generation). The crosses were further confirmed in F_2 generation by observing the segregation for brown and white grain plants.

A total of 180 early maturing brown grained plants were selected as single plant selections in F_2 generation in each cross. The number of single plant selections and number of plants/ progenies grown in each generation are depicted in figure 1. The selection was deferred and early maturing white grained plants were selected in F_4 onward generations. Homogeneous early maturing white grained progenies were bulked in F_5 and F_6 generations (Fig 1).

Patterns of genetic variation: Wide range of variations was observed among finger millet genotypes for all the studied traits (Table 1). The maturity duration of parental lines varied from 86 in GEC 447 (brown) to 117 in WR 1 (White), whereas developed white grained genotypes varied from 97 (VL 356 and VL 360) to 113 (VL 355). Although all the white grained parental lines were late maturing, some of the stabilised white grained lines (VL 356, VL 360, VR 441 and VR 443) were early and matured in ≤100 days. The variation for days to flowering and days to maturity among the stabilised lines offers great flexibility to the breeders for developing improved varieties suitable for various agro-ecologies or regions, which have variable length of growing period and also suit to various cropping systems. It also guides finger millet breeder to develop a variety, which can tolerate early cold in the hills by improving traits such as days to maturity in the required direction.

Variation in number of fingers per ear, finger length and grain yield per plant implies the possibility to develop a variety with higher grain yield. In the present study, the variation has also been created for selecting desired white grained genotypes suitable for the hill ecosystem. The plant height ranged from 81 cm (GEC 447) to 135 cm (OUAT 2). The developed white breeding genotypes were taller than the brown parental genotypes. This is desired since fodder is scarce in hills and a considerable requirement of fodder is met from finger millet straw. However, the variation in plant height and tillering capacity also indicate the possibility to combat lodging problem in finger millet. The mean values for PT, FLL, FLW, PL and FL in developed white breeding genotypes were similar to white and brown parental lines. But GEC 450 exhibited higher FPE (13), which did not translate in developed white breeding genotypes. The highest GY was recorded in brown parental line GEC 450 (33.04 q/ha). The developed white grained genotypes VR 427 (23.61 q/ha), VR 487 (22.08 q/ha), VR 363 (21.43 q/ha), VR 486 (21.49 q/ha) and VR 483 (20.84 q/ha) out yielded VL 201 (early maturing variety used as parent).

Among these white grained genotypes, VR 427 matured in 100 days but the plants were dwarf in comparison to other white lines which was reflected in its low fodder yield. Among the developed white grained lines, VL 366 recorded

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highest fodder yield (66.67 q/ha), followed by VL 356 (64.20 q/ha), VR 486 (61.73 q/ha) and VR 487 (61.73 q/ha). Wide phenotypic variability for several traits in finger millet including days to maturity and grain yield was also observed by Gowda *et al*. (2008), Dhanapal *et al*. (2008) and Reddy *et al*. (2009).

Principal component analysis: The first four principal component axes revealed a total variation of 82.4% extracted from the mean values of 11 traits on 23 finger millet genotypes (Table 2). A variance of 42.6, 18.91, 11.33 and 9.60 per cent were extracted from the first to the fourth components, respectively. The traits *viz*., DTF, PH, PL, FL, DTM and FLL were the major contributors for the first principal component axis, GY, FPE and FLL for the second axis, PT and FY for the third axis and FY and FLL for the fourth axis. Projections of genotypes on first two PCs showed that all three brown parental lines were on the left side of the plot and white parental lines were on right side of the plot (Fig 2). The genotype GEC 450 was on left top of the plot as outlier because of its significantly higher number of fingers per ear and grain yield per plot. Similarly, the genotype GEC 447 was also outlier because of its high fodder yield. Some of the developed white seeded lines VL 427, VL 360, VR 485, VR 443, VL 366, VR 425B, VR 425A and VL 356 along with VL 201 (brown type) were on left side of the plot because of earliness and good yield potential. The remaining late maturing developed white grained genotypes along with late maturing white grained parental genotypes were on the right side of the plot. The stabilised early maturing white grained lines clustering along with adapted variety, VL 201 could be the probable candidates for further testing and release of white grained finger millet for hills.

Evaluation of VL 356 and VL 360 along with 38 other white seeded genotypes bred at different centres in multi-location trials at six locations in Southern India showed that both these entries were earliest in maturity (less than 100 days) with average grain yield of 23.49 and 21.91 q/ha, respectively.

Only three traits occupied left side of the bi-plot and rest all were on the right side of the bi-plot. The projections also indicated that PT had least contribution, followed by FY, FLW and FLL in increasing order towards principal components. GY, FPE, DTF, DTM, PL, FL and PH were the major contributors for principal components (Fig 2). Lule *et al*. (2012) and Wolie and Belete (2013) have highlighted the importance of traits based on PCA for different agro-ecological conditions in brown grained finger millet.

Cluster analysis: The two way hierarchical cluster analyses of 23 finger millet genotypes formed three clusters (Fig 3). The first cluster contained nine genotypes including stabilised late maturing white grained genotypes *viz*., VL 355, VL 363, VR 428, VR 483 and VR 484 along with all four white grained parental lines *viz*., WR 1, WR 2, WR 10 and OUAT 2. These genotypes were clustered together based on high values of DTF, DTM, PH, FL and PL. The second cluster contained thirteen genotypes including two brown grained parental lines (VL 201 and GEC 450) along with eleven (VR 441, VL 360, VR 425A, VR 425B, VR 443, VL 356, VR 427, VL 366, VR 485, VR 486, VR 487) early maturing white grained stabilised lines. This grouping was due to earliness in maturity, moderate plant height, FL and PL, good fodder yield and grain yield. The third cluster had only single brown grained genotype (GEC 447), which had the lowest value for DTF, DTM, PH, FL and PL; with highest value for FY and lowest value for GY.

Two-way cluster analysis broadly separated the accessions based on trait variability. The first cluster had all the white grained genotypes, second had both white and brown grained genotypes and third had a single brown genotype. This validated our right selection of parents for developing new white grained genotypes. The clustering also indicated that a diverse material of white grained genotypes falling in first cluster along with white grained parental lines are similar for agro-morphological traits to white grained parental lines; and the white grained genotypes falling in second cluster with two brown parental lines had similarity of traits with brown parental lines VL 201 and GEC 450. This indicated that development of extra early maturing white grained finger millet genotypes is possible by crossing white grained genotypes from cluster 2 with GEC 447 of cluster 3.

Relationship between traits: The correlation coefficients between traits are presented in Table 3. It was interesting to observe that DTM, DTF, PH and FLL were significantly positively associated with PL and FL. The other significant positive associations were DTF with DTM; PH with DTF, DTM and FLL. GY was significantly positively associated with FPE, and FY showed significant negative association with FL. Positive association of finger number per ear with grain weight per ear was also observed by Sonnad *et al*. (2008). Data on character associations could be used to identify a few traits which are less relevant and could be of low priority in the germplasm evaluation (Upadhyaya *et al*., 2006). This simplifies the work and saves resources. Association studies among different traits are important for white grained finger millet breeding in effective selection of desirable types. The

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association analysis suggests that more fingers per ear should be given high weightage while selection and least emphasis should be given on finger length during breeding for optimum grain and fodder yield. Strong positive association of number of fingers per ear with grain yield was recorded by Sonnad *et al*. (2008). However, finger length has been reported as important yield contributing trait by Ganapathy *et al*. (2011).

Conclusion

The selection of parental lines is of utmost importance in developing high yielding early maturing white grained finger millet genotypes for Himalayan region. The white grained breeding genotypes generated from hybridization of late maturing white genotypes bred at southern region and early maturing adapted brown genotypes of Himalayan region revealed considerable variability for morpho-physiological traits. PCA and cluster analysis showed that the early maturing white grained finger millet genotypes with matching yield potential could be generated but further refinement in breeding strategy and hybridizing the white grained genotypes from second cluster with brown genotype in third cluster for incorporating earliness could be a fruitful approach in this direction. Association analysis suggested selecting plants with more number of fingers per ear for higher grain yield during selection process while developing of early maturing white grained finger millet genotypes could be an important strategy.

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Table 1. Mean values of agro-morphological traits in 23 finger millet genotypes

Genotypes	DTF	DTM	PH	PT	FLL	FLW	PL	FL	FPE	GY	FY
VL 363	73	108	128.0	1.0	40.5	23.5	8.3	1.3	7.5	21.43	59.26
VR 441	70	99	126.5	1.5	38.2	26.4	6.4	1.3	8.5	20.10	41.98
VL 366	68	103	123.0	2.5	35.9	21.5	6.1	1.2	7.0	19.90	66.67
VR 443	64	99	112.5	1.5	32.9	23.5	6.0	1.2	7.5	19.76	27.16
VR 483	74	112	130.5	2.5	35.9	24.2	7.9	1.4	7.5	20.84	49.39
VR 484	73	108	126.5	2.5	41.5	22.7	8.6	1.4	7.5	14.67	49.38
VR 485	70	103	109.5	2.0	33.2	20.4	6.3	1.2	8.0	19.76	59.26
VR 486	71	104	124.5	2.0	36.9	22.4	6.8	1.3	8.5	21.49	61.73
VR 487	74	107	125.0	1.5	32.6	22.5	7.0	1.3	7.5	22.08	61.73
VL 356	64	97	103.0	2.0	30.5	24.1	5.0	1.2	7.0	19.21	64.20
VL 360	64	97	116.5	2.0	36.1	25.5	6.2	1.2	8.5	20.45	41.98
VL 355	74	113	128.5	1.5	35.1	24.5	8.4	1.3	7.0	18.57	37.04
VR 425A	64	100	112.5	2.0	33.0	27.1	5.8	1.2	7.5	19.41	44.45
VR 425B	64	103	119.5	1.5	30.2	24.9	6.1	1.3	8.0	19.61	46.92
VR 427	66	100	95.5	2.5	35.5	23.5	6.7	1.2	7.5	23.61	46.91
VR 428	71	104	120.0	2.0	36.9	24.5	8.0	1.4	7.0	19.41	49.39
OUAT 2	77	115	135.0	1.5	40.0	26.8	9.0	1.3	7.5	19.91	39.51
GEC 447*	54	86	81.0	1.5	30.6	23.9	3.8	1.0	9.0	11.90	69.38
GEC 450*	62	96	117.5	2.0	37.3	21.4	6.4	1.3	13.0	33.04	34.57
WR 1	79	117	121.5	2.5	31.9	26.2	7.3	1.3	6.0	15.01	37.04
WR 2	76	113	131.0	1.5	36.9	25.6	8.9	1.3	8.0	19.86	46.92
VL 201*	60	89	95.5	2.0	34.7	22.0	5.1	1.2	6.5	20.79	34.57
WR 10	77	115	128.0	2.0	28.1	23.3	5.4	1.3	7.0	16.79	41.98
CD	2.75	3.65	13.12	1.53	7.56	3.44	1.21	0.12	1.37	7.42	23.07
CV (%)										18.21	23.48

*- brown finger millet genotypes
DTF-Days to 50% flowering; DTM-Days to maturity; PH-Plant height; PT-Productive tillers; FLL-Flag leaf length; FLW-Flag leaf width; PL-Peduncle length; FL-Finger length; FPE-Fingers per ear; GY-Grain yield; FY-Fodder yield.

Table 2. Principal component analysis based on agro-morphological traits of 23 finger millet entries, and first four principal components with the original variables

Trait	PC1	PC2	PC3	PC4
DTF	**0.92**	-0.21	0.16	0.07
DTM	**0.90**	-0.26	0.09	-0.01
PH	**0.91**	0.11	-0.03	0.09
PT	-0.01	-0.09	**0.77**	-0.44
FLL	0.50	0.51	0.00	0.34
FLW	0.31	-0.36	**-0.70**	-0.21
PL	**0.90**	0.15	-0.01	0.20
FL	**0.90**	0.16	0.13	-0.10
FPE	-0.27	**0.82**	-0.14	0.08
GY	0.04	**0.89**	0.04	-0.20
FY	-0.40	-0.24	0.29	**0.77**
Eigen value	4.69	2.08	1.25	1.06
Percent of total variation	42.6	18.9	11.3	9.6
Cumulative value	42.6	61.5	72.8	82.4

DTF-Days to 50% flowering; DTM-Days to maturity; PH-Plant height; PT-Productive tillers; FLL-Flag leaf length; FLW-Flag leaf width; PL-Peduncle length; FL-Finger length; FPE-Fingers per ear; GY-Grain yield; FY-Fodder yield.

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Table 3. Correlations between variables and factors in finger millet genotypes

Trait	DTF	DTM	PH	PT	FLL	FLW	PL	FL	FPE	GY
DTF										
DTM	0.956**									
PH	0.827**	0.815**								
PT	0.051	0.042	-0.114							
FLL	0.272	0.156	0.426*	-0.029						
FLW	0.210	0.274	0.232	-0.220	0.030					
PL	0.771**	0.747**	0.752**	-0.070	0.691**	0.232				
FL	0.769**	0.728**	0.853**	0.067	0.447*	0.113	0.775**			
FPE	-0.389	0-.368	-0.076	-0.144	0.190	-0.235	-0.145	-0.179		
GY	-0.112	-0.137	0.127	-0.016	0.280	-0.297	0.103	0.195	0.635**	
FY	-0.201	-0.246	-0.293	-0.032	-0.125	-0.294	-0.272	-0.430*	-0.007	-0.302

* Significant at P<0.05; ** Significant at P<0.01
DTF-Days to 50% flowering; DTM-Days to maturity; PH-Plant height; PT-Productive tillers; FLL-Flag leaf length; FLW-Flag leaf width; PL-Peduncle length; FL-Finger length; FPE-Fingers per ear; GY-Grain yield; FY-Fodder yield.

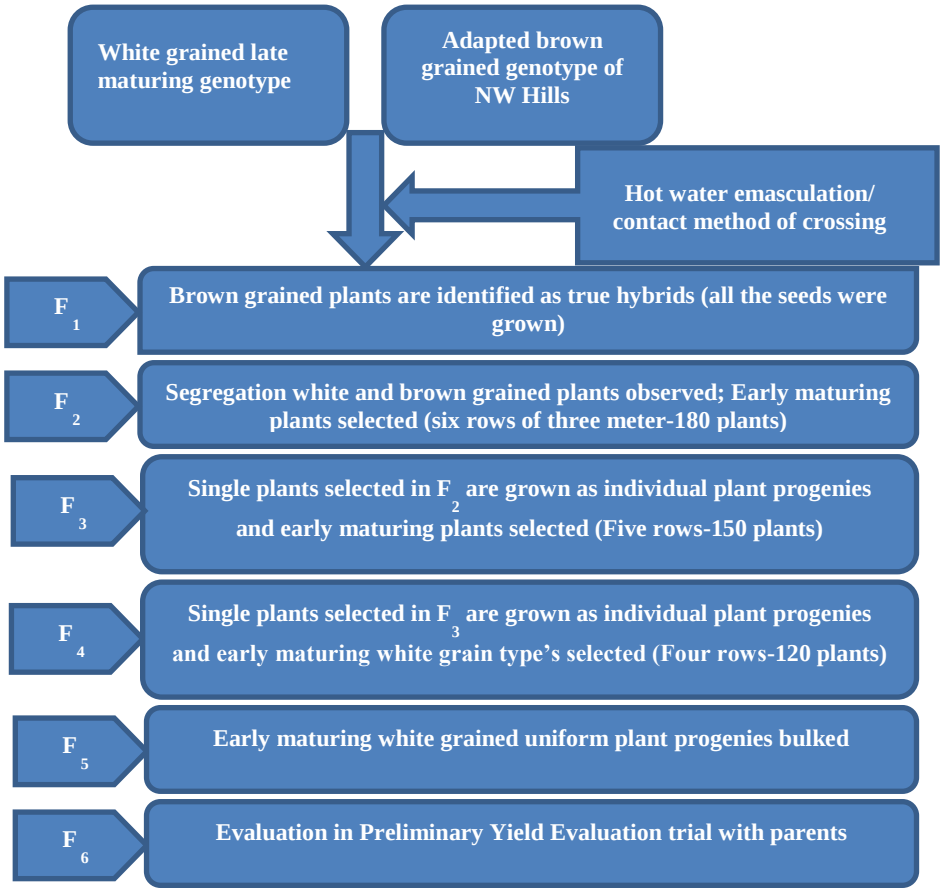

Fig. 1. Development of early maturing white grained finger millet genotypes for hills

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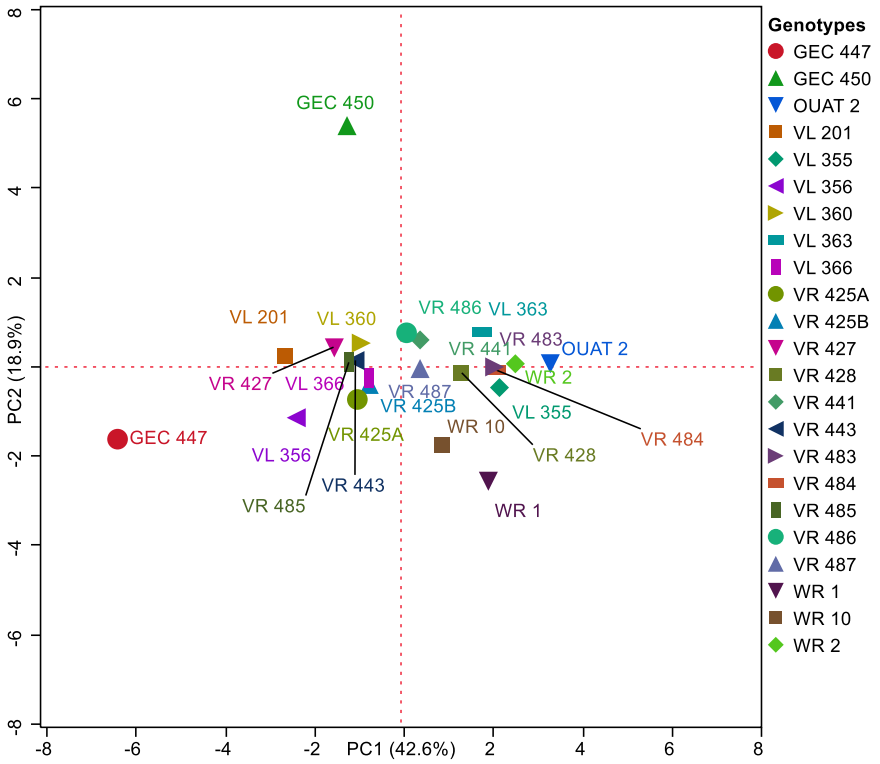

Fig. 2. Score plot of PC1-PC2 for finger millet genotypes

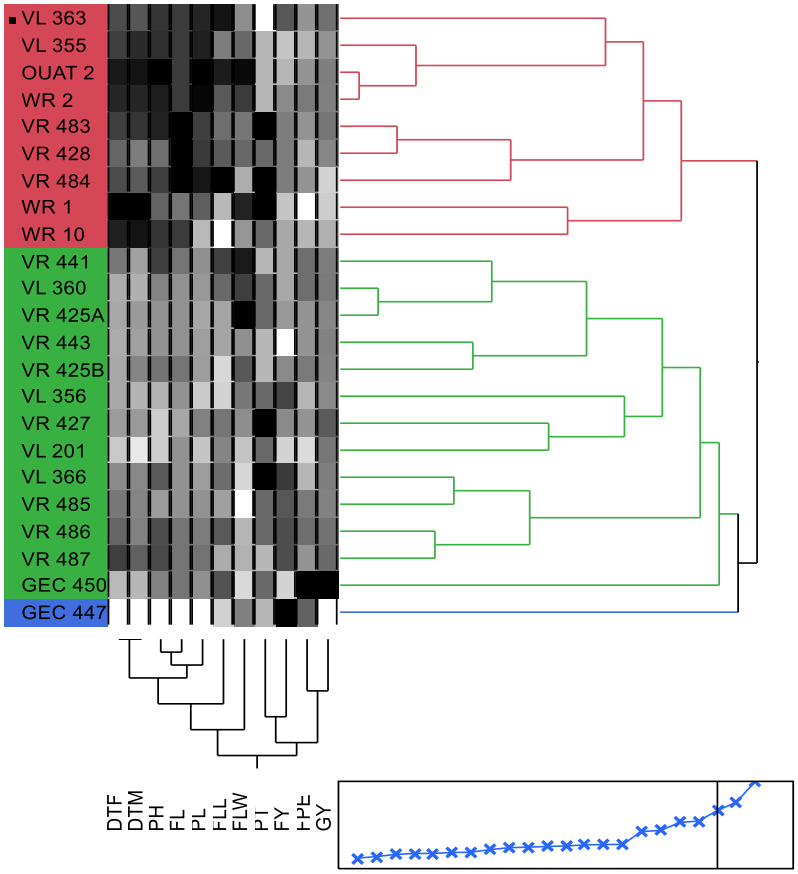

Fig. 3. Two way hierarichal clustering of Finger millet genotypes