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Genetic diversity of mango (*Mangifera indica*) bioactive components

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Previously the main objective of mango hybridization was to develop high yielding varieties, with attractive colour, less fibre and resistant to pest and diseases (Ram and Rajan, 2003), but now the priorities have shifted to nutritionally rich cultivars because of health consciousness among the people. Breeding to develop an ideal mango variety with high nutritional attributes requires prior quantitative assessment of genetic divergence in the available gene pool, especially parental lines to be used in hybridization. If the parents are diverse for the characters then there is a greater chance of getting wide spectrum of recombinants (Vasugi *et al.* 2013). However, little efforts have been made for genetic characterization of diversity in commercially grown mango genotypes and their potential mango breeding is indistinct (Rajan *et al.* 2009). In a highly out crossing species like mango, knowledge of the magnitude of genetic variation among fruit nutraceuticals and its heritability is lacking. Therefore, the present investigation reports the heritability, genotypic and phenotypic coefficients of mango genotypes and correlation for bioactive compounds.

The 40 mango genotypes (Table 1) were selected for this study. Experimental site is located at 26.92^0 N, 80.72^0 E and an average elevation of 128 metres at ICAR-Central Institute for Sub-tropical Horticulture, Lucknow (2015–16). The fruit pulp was homogenised separately and required quantity of the extract was used for analysis of different biochemical compounds, whereas the colour reading was recorded immediately after cutting the fruits. The results were expressed in mg/100 gram of fresh weight of edible portion. The fruit pulp extracts containing total phenolic compounds (Bloor, 2001 and Singleton *et al.* 1999), total flavonoids (Dewanto *et al.* 2002), total antioxidant activity (Apak *et al.* 2004) and total carotenoids (Ranganna 1997), were estimated by UV-VIS spectrophotometer method. Pulp colour was determined longitudinally at three equidistant points on freshly cut fruits by ColorLlite sph850 spectrophotometer. In L*, a*, b* scale, L is the measure of lightness, the positive values of a* are in direction of redness and positive values of b* are the vector of yellowness**.** The negative values of 'a' is towards greenness and negative values of b* depicts blueness (Higby 1962).

Wide range of variation was observed among the genotypes for all the biochemical compounds (Table 1). Particularly 'Alphonso' has recorded highest phenolic content (234.72 mg/100 g of pulp). Genotype 'Amrapali' has highest flavonoids as well as total carotenoids content of 37.07 mg/100 g and 10.37 mg/100 g respectively. The highest total antioxidant activity was observed in genotype 'Langra' (1.51 µmol trolax/100 g). Analysis of variance revealed that the total phenols attributed greater variability among the genotypes studied. Wider the variation among the genotypes there is an ample scope for selection of superior types in breeding programme (Choham and Dhaliwal 1994 and Pandey *et al.* 2002). The PCV was slightly higher or almost equal to their respective GCV for all the components studied but the narrow difference between PCV and GCV showed the presence of sufficient genetic variability which can be utilized for crop improvement programme. The estimates of PCV ranged from 40.53 (total antioxidants) to 60.30% (total phenols) and the estimates of GCV varied from 39.27 (total antioxidants) to 60.04% (total phenols). Apart from this, total antioxidant had comparatively low PCV than other components. This less variation indicated the stable nature of the trait. The difference between GCV and PCV was lowest for total phenols indicated the least influence of environment on the trait, so this may be considered as a valuable trait in crop improvement (Table 1). However, only GCV is not sufficient for determining the amount of heritable variation. Therefore, heritability in broad sense was estimated. High heritability estimates were observed for all the components which ranged from 93 (total carotenoids) to 99% (Total phenols and flavonoids) (Table 1). High heritability for different traits and closeness of their genotypic and phenotypic variation indicated that reliable selection could be made for these traits on the basis of phenotypic expression being less influenced by environment. For more reliable and maximum genetic

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Table 1 Genetic variability among mango genotypes for major nutraceuticals and colour characteristics

Genotype	Total Phenols (mg/100 g)	Total Flavonoids (mg/100g)	Total Antioxidants (µmol/100 g)	Total carotenoids (mg/100 g)	L	a	b
13-1	50.28	6.60	0.82	5.10	47.13	14.33	41.38
Alphonso	234.72	32.27	1.21	2.66	46.67	11.99	37.57
Ambika	56.25	13.33	0.79	4.07	45.34	10.92	38.69
Amin khurd	150.14	20.87	0.38	4.77	47.08	16.59	38.41
Amrapali	69.44	37.07	0.75	10.37	45.77	20.03	42.99
Arunika	71.39	9.80	0.66	7.55	50.42	20.23	43.80
Banganpalli	38.61	9.73	0.62	2.30	59.12	7.90	42.77
Banglawala	40.28	17.47	0.55	4.77	47.08	16.59	38.41
Bangalora	33.19	7.00	0.30	1.86	47.09	15.59	36.18
Baramasi	38.19	18.40	0.56	3.00	47.09	10.69	36.18
Bombay Green	55.00	27.40	0.64	4.39	42.13	13.66	40.73
Dashehari	61.67	30.33	0.67	6.98	49.04	18.64	46.73
Ellaichi	93.61	9.40	0.93	4.31	57.24	11.99	33.61
Fazri	53.06	10.07	0.43	1.83	47.09	15.59	35.18
Gilas	51.81	17.47	0.57	2.66	46.67	11.99	37.57
Gourjeet	73.19	26.13	0.78	3.29	51.56	17.07	50.92
Gulabkhas	48.33	23.13	0.66	5.43	54.84	22.65	56.61
Himsagar	57.36	28.20	0.65	4.61	54.97	18.17	57.64
Kensington	47.22	14.13	0.70	2.81	55.78	9.78	45.24
Kesar	51.11	8.13	0.42	9.62	47.04	21.19	52.69
Kitchner	34.72	6.07	0.51	2.34	53.48	6.85	42.97
Langra	156.25	27.93	1.51	4.95	57.29	10.11	49.31
LuknowSafeda	68.89	24.20	0.82	3.00	48.21	8.71	35.46
Mallika	120.14	28.13	1.28	3.77	45.05	12.62	40.22
Mankhrad	99.58	26.20	0.94	6.48	49.82	15.48	43.91
Moovandan	36.11	12.07	0.43	3.00	47.09	10.69	36.18
Mulgoa	55.69	25.80	0.68	7.63	48.49	17.61	46.04
Neeluddin	44.17	7.80	0.37	3.32	62.65	7.78	36.92
Neelum	119.31	9.73	1.03	2.88	55.78	9.87	45.21
NisarPasand	55.00	30.20	0.55	6.14	46.26	16.53	43.39
Pairi	33.61	8.13	0.24	4.23	45.67	12.67	43.00
PusaArunima	55.00	33.40	0.81	9.63	57.93	14.38	53.78
Sangam	62.92	6.87	0.48	9.17	55.61	13.36	53.65
Sharad Bhog	48.47	23.80	0.59	3.89	61.23	7.78	36.58
Sindhu	87.50	17.80	0.75	6.00	47.05	12.81	39.73
Surkha Burma	41.25	22.13	0.41	3.03	47.09	9.86	36.18
Tommy Atkins	40.56	24.60	0.36	4.35	47.41	10.80	41.92
Vanraj	40.56	16.20	0.49	3.79	49.17	14.01	39.38
Vellio	36.67	4.40	0.55	3.26	43.11	3.09	28.95
Zardalu	93.19	29.13	0.79	6.58	47.51	17.26	49.40
SE	3.089	0.715	0.044	0.493			
Mean	67.611	18.788	0.667	4.745			
CV (%)	5.596	4.658	8.048	12.723			
Range	201.528	32.667	1.27	8.544			
σ^2 g	1647.963	86.343	0.07	4.938			
σ^2 e	14.316	0.766	0.003	0.365			
σ^2 p	1662.28	87.109	0.073	5.303			
GCV	60.042	49.457	39.727	46.829			
PCV	60.302	49.676	40.534	48.527			
H^2	0.991	0.991	0.961	0.931			
GAM	83.265	19.057	0.535	4.418			
GA (%)	123.153	101.432	80.208	93.093			

*$P \leq 0.01$, GA, Genetic advance; H^2_b, Heritability in broad sense; σ^2 g, genotypic variance; σ^2 e, environment variance; σ^2 p, Phenotypic variance; CV, coefficient of variability; PCV, Phenotypic Coefficient of variation; GCV, Genotypic coefficient of variation; GAM, genetic advance in per cent means.

Table 2 Correlation coefficients among nutraceuticals and colour characteristics

	Total Phenols	Total Flavonoids	Total Antioxidants	Total carotenoids	L	A	b
Phenols	1.00						
Flavonoids	**0.44**	1.00					
Antioxidants	**0.68**	0.44	1.00				
Carotenoids	-0.01	**0.34**	**0.03**	1.00			
L	-0.02	-0.11	0.10	-0.10	1.00		
a	0.06	0.40	-0.02	0.64	-0.12	1.00	
b	-0.03	0.36	0.11	0.39	0.38	0.61	1.00

information heritability estimates coupled with genetic advance should be considered (Burton 1953). The highest value of genetic advance as per cent mean were obtained for total phenols (83.2%) indicated the influence of environment on the expression of these characters to certain extent. It is quite clear from the estimate of genetic advance as per cent mean ranged from 80.2 (total antioxidants) to 123.15% (total phenols). The highest value of genetic advance and per cent mean value of total phenols showed that the parameter is under control of additive gene (Table 1). This is in confirmation with the results of Kumar *et al.* (2002). Panse (1957) also pointed out that high heritability coupled with higher genetic advance is mainly attributed to the additive gene action. Higher heritability coupled with high GA was observed for total phenols, which may be due to additive gene action and thus selection would be effective for this component for further improvement. In this study correlation between the components showed an interesting relationship. Total phenols had a significant positive correlation with total antioxidants (0.68) (Table 2). The a* and b* value of colour had a significant positive correlation with the total carotenoids content (0.64 and 0.39

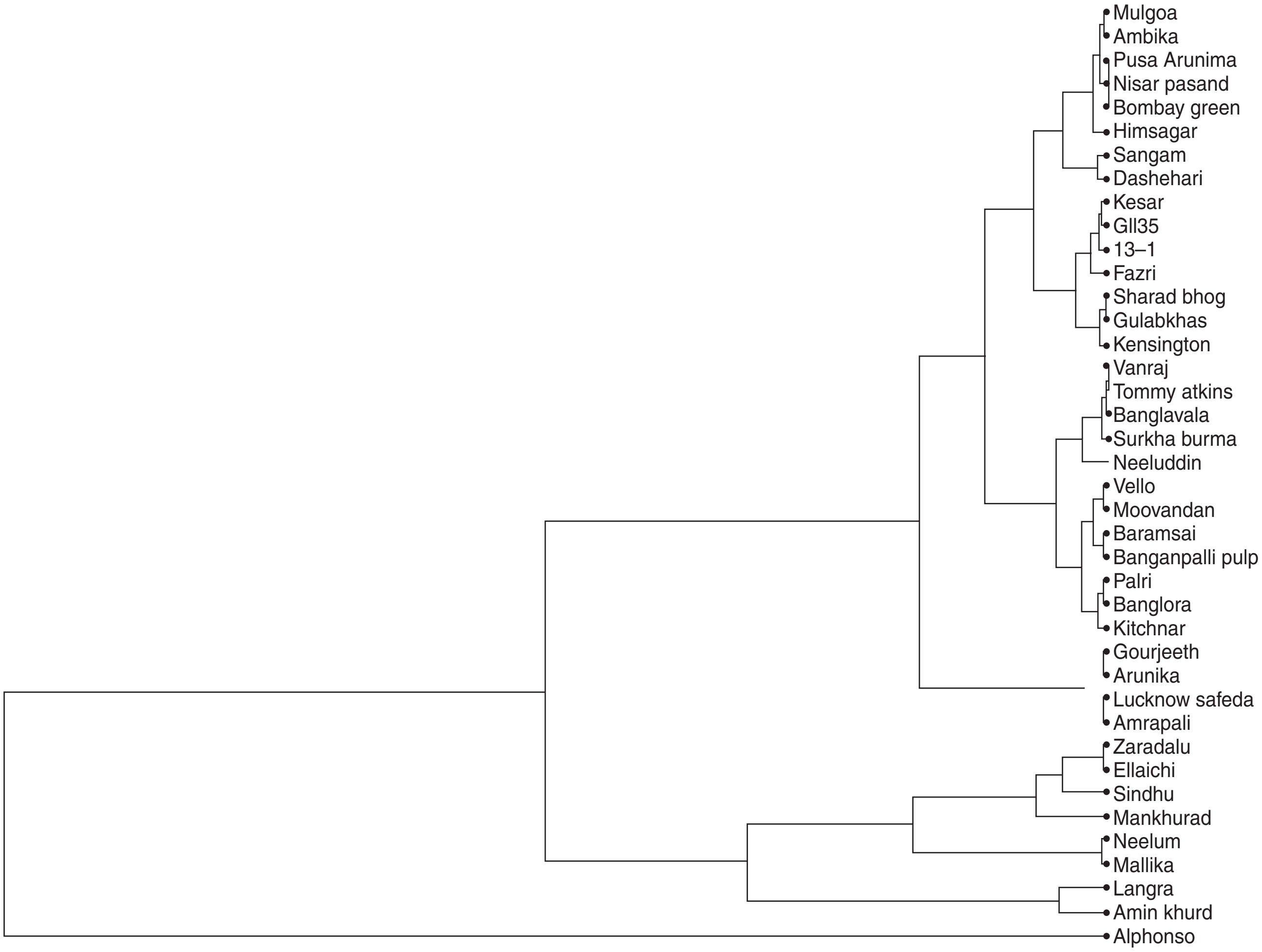

Fig 1 Hierarchical Clustering of 40 mango genotypes based on total phenols content.

respectively) (Table 2). Whereas L* value of the spectra is negatively correlated with the total carotenoids. This can be used as a direct selection criterion for selection of carotenoids rich genotypes in mango.

Hierarchical clustering was done using darwin software based on total phenols content, where 40 mango genotypes were mainly grouped into two clusters i.e, A and B (Fig 1). cluster A was grouped separately which consist of genotype Alphonso, stand as an out group because of highest amount of total phenolic content (234.72 mg/100 g).The number of inter and intra clusters showed the diverse nature of mango genotypes due to heterogeneity and genetic architecture of populations (Murty and Arunachalam 1966, Bajpai *et al.* 2015).

SUMMARY

The move towards fruit with high concentration of specific nutritional components will help the breeders to select appropriate genotypes which can be used as key drivers in nutritional breeding. Consequently, the present study illustrated that, wide variation exists in the major nutraceuticals of mango which provides opportunities for genetic gain through selection or hybridization. The study showed wider genetic variability among the genotypes for biochemical components. Genotypes Amrapli, Alphonso, Langra and Aminkhurd are good source of phenols, carotenoids and antioxidants. Total phenols were indicated as the parameter under the control of additive gene which can be considered for further improvement through selection and it is also having a significant positive correlation with total antioxidants and total flavonoids. The a* and b* value of colour can be considered as a direct selection criterion for carotenoids rich genotypes. Thus, the selection may be possible for these traits or can be used as potential parents in hybridization programme for developing nutritionally rich genotypes in mango.

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