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Genetic variability and character associations in vetiver (*Vetiveria zizanioides* L. Nash)

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ABSTRACT

Forty genetic stocks of vetiver (*Vetiveria zizanioides* L. Nash) were screened for high oil yield. The considerable amount of natural and genetic variability in morpho-metric traits was recorded. The estimate of heritability ($\hat{h}^2_{BS}$ %) and corresponding genetic advance (GA), both were high for plant height ($\hat{h}^2_{BS}$ % = 98.48 and GA = 64.83). Genetic (G) and phenotypic (P) associations coefficients among the seven traits indicated that plant height was highly and significantly correlated with tillers/plant (0.399**G, 0.389**P); fresh root with dry root yield (0.905**G, 0.769**P) and oil content with oil yield (0.397**G, 0.390**P) at both genotypic and phenotypic level. The plant height with root length was also positively correlated with each other at both genetic (G) and phenotypic (P) levels (0.282*G, 0.278*P). The path coefficient under study revealed that the highest direct contribution to total oil yield was made by fresh root yield (0.514) followed by oil content (0.386), tillers/plant (0.149) and root length (0.086) in percent.

1. Introduction

The genus *Vetiveria* is a small genus of perennial grasses occurring mainly in tropical countries of old world. In India, only two species of vetiver are found *Vetiveria zizanioides* and *Vetiveria lawsoni* syn. *Vetiveria nemoralsis* belongs to family Poaceae, is native to India and is found growing wild in almost all parts of the country (Ramanujam and Kumar, 1964; Lavania, 2000; Lal, 2012). However, it is only the former, i.e. (*V. zizanioides* (L.) Nash), chromosome number: $2n = 20$, which is of great significance as a high class perfume as well as indigenous systems of medicine since time dating back to 1103 AD (Virmani and Datta, 1975; Akhila et al., 1981; Hussain et al., 1984; Lal, 2012). Its aerial parts have other potential economic values also, such as for fodder, mulch, animal bedding, thatches, handicrafts, in paper industries, vermi compost, in making tiles, etc. (Pareek, 1994; Lal et al., 1997a,b; Lal et al., 1999a,b), thus non-part of vetiver plants goes waste. It grows luxuriously in parts of Utter Pradesh, Madhya Pradesh, Bihar, Rajasthan and several tracts in southern and peninsular India particularly along the river banks and over marshy lands (Virmani and Datta, 1975; Hussain et al., 1984; Lal, 2012). The total world production of vetiver oil is estimated to be 300–350 tonnes per year (Lal, 2012). The annual consumption and demand is likely to increase further. In India, about 100 tonnes of oil is produced annually, which is far below to meet our internal demand of the oil for perfumery, masticatory, attar and soap industries.

In our research programme on vetiver improvement, a large number of genetic stocks/clones were assembled from different places of India. Three exotic genetic stocks were also obtained from Haiti, Reunion Island and Indonesia for genetic study. This study have planned to sort out promising genetic stock(s) suitable for high root and oil yield of better quality purpose. Since, a priori knowledge of the range of variability and character associations having great significance for further breeding, all these genetic stocks were maintained and studies for the required genetic parameters.

2. Materials and methods

A large number of genetic stocks of vetiver (*V. zizanioides* (L.) Nash) were assembled from wild/cultivated sources of vetiver from various places in India and abroad. Out of 125 genetic stocks, a new set having forty genetic stocks of vetiver (*V. zizanioides* L. Nash) from Uttar Pradesh (30), Rajasthan (1), Delhi (3), Travancore (2) and Odakali (1) in India and one each from Indonesia, Haiti and Reunion Island were screened for high oil yield of better quality (Table 2, Fig. 1). The genetic stocks were grown in a randomized block design with two replications at the research farm of the CSIR–Central Institute of Medicinal and Aromatic Plants, Lucknow, India in the two consecutive years 2009–2010 and 2010–2011 under normal fertility regime (80:40:40) kg N, P_2O_5 and K_2O/ha, respectively, with plot size of single row of 2.5 m each 50 cm apart. Plants were uprooted

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Fig. 1. Genetic variability in plants, roots and in essential oil of vetiver genetic accessions.

12 months after planting of the experiments. The experimental site at the institute research farm was located at 26.5° N latitude and 80.50° E longitude, and 120 m above mean sea level. The climate is semiarid to subtropical in nature.

Morpho-metric observations were recorded for seven economic traits, namely plant height (cm), tillers/plant, fresh and dry root yield (g/plot), root length (cm), oil content (%) and oil yield (g/plot). Oil content was estimated by hydro-distillation of shade dried roots of each clone for 16 h in Clevenger's apparatus (Clevenger, 1928).

2.1. Statistical analyses

Statistical analyses were done using the Statistical Software 4.0 version, available in the Division of Genetics and Plant Breeding of the Institute, which is based on the standard methods in Panse and Sukhatme (1967) and Singh and Chaudhary (1979). The pooled mean values of 2 years for the all seven characters were subjected to correlation and path coefficient analyses (Dewey and Lu, 1959; Lal et al., 2001a,b). Various statistical parameters, including correlation and path coefficient, namely variance components genetic (σ^2g), phenotypic (σ^2p) and environmental (σ^2e), coefficient of variation genotypic (GCV), phenotypic (PCV) levels and heritability in broad sense (h^2_{BS}) computed per the following formula:

Analysis of variance (ANOVA).

Source of variation	d.f.	Mean sum of squares (MSS)	*F*	Expectations
Replications	01 $(r-1)$	MSr	–	–
Genotypes	39 $(g-1)$	MSg	MSg/MSe	$\sigma^2e+r\sigma^2g$
Error	39 $(g-1)(r-1)$	MSe	–	σ^2e
Total	79 $(gr-1)$	–		

2.2. Estimates of genetic parameters

Heritability in broad sense (h^2_{BS}) %: It is the ratio of genotypic variance to the phenotypic variance = $(\sigma^2g/\sigma^2p)\times 100$, where, $\sigma^2g = (MSg - MSe)/r$ and $\sigma^2p = \sigma^2g + \sigma^2e$; MSg = mean sum of squares of genotypes; MSe = mean sum of squares of error.

2.3. Correlation coefficient (r)

Correlation coefficients were used to measure of the associations between two or more than two variables.

(i) Genotypic correlation (r_g) between two traits *X* and *Y* = [{Genotypic covariance (*XY*)}/√{genotypic variance (*X*) × genotypic variance (*Y*)}]where Genotypic covariance = (MSPg − MSPe)/*r* and Genotypic variance = (MSg − MSe)/*r*

(ii) Phenotypic correlation (r_p) between two traits *X* and *Y* = [{phenotypic covariance (*XY*)}/√{phenotypic variance (*X*) × phenotypic variance (*Y*)}]where phenotypic covariance = (MSPg − MSPe)/*r*; phenotypic covariance = $\sigma^2g + \sigma^2e$; and *r* = number of replications.

Co-heritability value of a character contribution suggests that the increases in one of the characters of those contributions will be coupled in the increasing trend in its co-heritable character. Where, Co-heritability (1,2) = genotypic covariance/phenotypic covariance of traits 1 and 2.