

Genetic variability, correlation and path analysis in fenugreek (*Trigonella foenum-greacum* L.)

Devraj Singh, PP Singh, IS Naruka and SS Kushwah

Received : July, 2011 / Accepted : April, 2012

Fenugreek (*Trigonella foenum greacum* L.), 2n=16 popularly known as “Methi” is an important seed spice crop grown in India during Rabi season. Fenugreek seed has both food and medicinal value particularly against digestive disorders. Being a leguminous crop, the root nodules enrich the soil with atmospheric nitrogen. The importance of fenugreek seed has further increased due to the presence of alkaloids ‘diosgenin’ and ‘trigonellin’ having pharmaceutical use. It is one of the crops in which both leaves as well as seed are consumed in one or the other form.

Fenugreek is grown in a large area of Malwa region and particularly in Ratlam, Mandsaur and Neemuch districts due to this region has been designated as agri - export zone for fenugreek.

Study of variability is a prerequisite for improvement of yield in any crop. At present no standard cultivar is being grown in this region. Farmers sow their own seed year after year. Hence there is an urgent need to assess and improve the existing genotype and develop high yielding cultivars suitable for this region. The present investigation was undertaken with a view to ascertain the relative variability present in yield contributing characters and to utilize them in the genetic improvement of fenugreek.

The experiment was laid out at the “Bahadri farm” College of Horticulture, RVSKVV, Mandsaur, (M.P.) during “Rabi” season of 2009-10. The soil was black loamy in texture, with low in availability of nitrogen, low in phosphorus and high in potassium status. The experiment consisted of twenty six genotypes, laid in randomized block design with a plot size of 2m² keeping 30 cm row to row and 10 cm plant to plant spacing. The recommended cultural practices were followed to raise good crop. Data were recorded on ten randomly

selected plants in each plot for plant height (cm), No. of primary branches/ plant, days to flowering, No. of pods/ plant, pod length, No. of seeds/ pod, 1000 seed wt (g), chlorophyll content (mg/g), protein content (%), dry matter content (g), biological yield (g) and seed yield / plant. The protein content (%) was estimated by the method of Lowry *et al.*, (1951) using folin cio-calteau reagent. The analysis of variance was calculated as per the method suggested by Federer (1956), heritability in broad sense as per Hanson *et al.* (1956) and Genetic advance as per Johnson *et al.* (1955) for all traits. The genotypic and phenotypic correlations were estimated according to Johnson *et al.*, 1955. Path analysis was done to partition total correlation into direct and indirect effects as suggested by Dewey and Lu (1959).

Significant difference among 26 lines for days to 50 per cent flowering, plant height, primary branches per plant, pods per plant, pod length, seeds per pod, biological yield, seed yield per plant, chlorophyll content and protein content in seeds of fenugreek indicated the existence of enough variability among genotypes. When the variation was compared on the basis of coefficient of variation, the magnitude of phenotypic variance was higher as compared to genotypic variance for all the characters in the present investigation indicating a positive effect of environment on the characters. The difference between GCV and PCV was low. High phenotypic coefficient of variation was recorded for biological yield followed by dry matter content, while lowest phenotypic coefficient of variation was observed for days to 50 per cent flowering followed by protein content. Similar results were also reported by Kumar and Choudhary (2003) and Sharma and Sastry (2008). High genotypic coefficient of variation was recorded for biological yield followed by dry matter content. While, the lowest genotypic coefficient of variation was recorded in days to 50 percent flowering followed by protein content. These results corroborate the findings of Sharma *et al.* (1990). The broad sense heritability was found to be higher for almost all characters. Highest heritability was