Oat is an important fodder crop of northern and central India. The relative performance of existing varieties different from location to location and over year by the influence of environment conditions. There is therefore urgent need to examine the stability of genotypes for fodder yield in order to develop high yielding varieties with stable performance. The information on this aspect is rare in oat. An attempt was therefore made in this study to determine the stability of fodder yield and crude protein yield in ten genotypes of oat by regression analysis technique.

Ten genotypes including Kent and OS 6 as national check were evaluated in randomized complete block design with there replication at four location viz., Jabalpur, Rahuri Uralikanchan and anand during rabi season of 2002-03. Each genotypesa was sown in ten rows plot to 0.4m length and row- to- row distance of 22.5m. Recommended agronomical practices were adopted for optimum crop growth and better harvest for fodder yield. The inner eight rows were harvested to record the fodder yield (kg/ha), which was converted into fodder yield (q/ha). The dry sample of fodder was used for estimation of nitrogen content by the method described in AOAC (1965). The estimated nitrogen content was multiplied by factor 6.25 to determine the protein percentage and consequent crude protein yield (q/ha). The method of Berhart and Russel (1966) was adopted for stability analysis. The analysis was carried out by using statistical package IRRISTAT developed at International Rice Research Institute, Manila, Phillipines.

The analysis of variance (Table-1) revealed significant differences among the genotypes and environments for fodder yield and crude protein yield. It further indicates the presence of sufficient variability among the genotypes and environments. The mean square for genotypes x environment interaction was also significant for both the traits. It indicates the differential response of genotypes in different environment, hence satisfying the requirements of stability analysis.

OL 125 recorded the highest fodder yield (660.60 q/ha) but it was responsive to favorable conditions and unstable having greater than one regression coefficient and high estimates of deviation from regression. Similarly, the second third tanking genotypes SKO 1.2 and SKO 20 were responsive to favourable condition and unstable. OS 6, JHO 2001-1 and UP 272 were average yielder, average responsive to change in environment and stable for fodder yield. These genotypes also showed the maximum estimates of R². These genotypes can be recommended for general cultivation in order to stabilize the productivity in fodder oat.
Crude protein yield ranged from 10.6 to 14.78 q/ha. Genotypes SKO 12 followed by Kent and SKO 20 recorded the maximum crude protein yield. However, Kent, JO 6 and JHO 2001-3 were average responsive and stable for this character having unit regression coefficient and deviation from regression around zero. Genotypes SKO 12, SKO 20 and JHO 2001-1 were responsive to favourable conditions and stable for crude protein yield.

It can be concluded from present study that genotypes OSD 6, UPO 272 and JHO 2001-1 for fodder yield and Kent, JO 6 and JHO 2001-3 for locations in order to identify the stable genotypes.

**ACKNOWLEDGEMENTS**

Author is grateful to the scientists of different locations for conducting the trial and ICAR, New Delhi for providing the funds for this study.

**REFERENCES**
