CHAPTER-VI

SUMMARY
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The experimental material of 50 diverse genotypes of forage oats (Avena sativa L.) was evaluated at the research area of the Division of Crop Improvement, Indian Grassland and Fodder Research Institute, Jhansi and Forage Research Section, Department of Plant Breeding, CCS Haryana Agricultural University, Hisar under normal and late sown conditions during the rabi season of 1999-2000, thereby comprising four environments in all. Each genotype was planted in a randomized block design replicated thrice in two rows of 4 m length spaced 30 cm between rows and 10 cm between plants. The observations on five randomly selected plants from each genotype in each replication in each environment were recorded for days to 50% flowering, plant height (cm), number of tillers per plant, stem diameter (mm), number of leaves per plant, leaf length (cm), leaf breadth (cm), leaf: stem ratio, green and dry fodder yield per plant (g), crude protein content (%) and in vitro dry matter digestibility (%). The data of four environments were pooled after conducting the Bartlett’s test and subjected to estimate the genetic variability components, genetic divergence, associations, path-coefficient analysis and phenotypic stability of various fodder yield and quality traits. The salient findings of this study are summarized as under:

1. Significant differences for various traits in all the environments indicated that ample variability existed among the genotypes.

2. An adequate variability was observed for various traits and estimates of genotypic and phenotypic coefficients of variation were quite close to each other, suggesting little role of environment. The estimates of heritability were high for all the characters, whereas moderate to high genetic advance was observed for all the characters. High heritability
coupled with high genetic advance was observed for most of the traits, particularly green and dry fodder yield per plant.

3. The analysis of genetic divergence through Mahalanobis D² statistics revealed considerable genetic diversity among genotypes. The genotypes were grouped into 8 homogenous clusters in E₁ and E₂, 9 in E₃ and E₄ and 10 in pooled basis. Cluster I composed of maximum 13, 14, 14, 16 and 11 genotypes followed by Cluster II having 8, 12, 8, 9 and 10 genotypes in E₁, E₂, E₃, E₄ and pooled basis, respectively, whereas Cluster VIII (E₁, E₂), IX (E₃, E₄) and X (pooled basis) contained a single genotype. No correspondence was observed between the geographical and genetic diversity in all the environments.

4. The intra-cluster distances were relatively smaller than inter-cluster distances indicating homogenous nature of groups and presence of narrow genetic variation within a cluster in all the environments. The maximum inter-cluster distance was observed between cluster III and V followed by V and VII, III and IV and I and V; between clusters V and VII followed by VI and VII, IV and VII and III and VIII; between clusters V and VII followed by VII and IX, III and VII and V and VI; between clusters II and IV followed by IV and VIII, II and VI and II and V; between clusters IX and X followed by I and X, IV and X and III and IX in E₁, E₂, E₃, E₄ and pooled basis, respectively. The use of genotypes in hybridization from these clusters having most of the desirable characters is likely to produce more transgressive segregrants. The D² analysis further indicated that high variation for various fodder yield contributing traits had maximum contribution towards genetic divergence.

5. In general, genotypic correlation coefficients were found to be higher than their corresponding phenotypic correlation coefficients. Green and dry fodder yield per plant was found to be positive and significantly
correlated with plant height, stem diameter, number of leaves per plant, leaf length and leaf breadth in all the environments.

6. Path-coefficient analysis further confirmed that the characters such as plant height, stem diameter, number of tillers and leaves per plant, leaf length and leaf breadth were the major component traits of green and dry fodder yield and hence these should be given priority in selection in view of their high heritability coupled with high genetic advance also.

7. The joint regression analysis indicated significant differences among the genotypes for all the characters. The environments of experimentation also differed significantly. The G x E interaction and its two components viz., heterogeneity between regression and remainder were significant for all the traits indicating importance of both linear and non-linear components of G x E interaction. There was preponderance of linear components for days to 50% flowering, plant height, number of tillers per plant, number of leaves per plant, green fodder yield per plant, dry fodder yield per plant and IVDMD and hence prediction of genotypes appeared possible for these traits. However, non-linear components of G x E interaction was higher than linear components for stem diameter, leaf length, leaf breadth, leaf: stem ratio and crude protein content indicating that prediction could not be made easily for these characters.

8. Based on environmental index, \( E_1 \) was the best and most favourable environment for all the characters. \( E_2 \) was good for number of tillers and leaves per plant and leaf: stem ratio, \( E_3 \) for days to 50% flowering, plant height, stem diameter, leaf length, leaf breadth, crude protein content and IVDMD. However, \( E_4 \) was the poorest for most of the characters except days to 50% flowering and leaf: stem ratio. Performance of genotypes for different characters in normal sown environments (\( E_1 \) and \( E_3 \)) was better than that of late sown environments (\( E_2 \) and \( E_4 \)).
9. The estimation of stability parameters for individual genotypes indicated that the proportion of genotypes exhibiting predictable behaviour was more for leaf breadth, crude protein content and IVDMD.

10. The genotypes JHO-822, JHO-889, OL-805, OS-189, OS-7, OS-174, and HJ-8 were found stable and high yielding for both green and dry fodder yield. As far as yield and quality is concerned, the genotypes HJ-8, JHO-889 and JHO-822 were found stable and high in crude protein content and better in digestibility.

11. Considering both genetic divergence and phenotypic stability together, the selected genotypes can be used as promising parents for hybridization. The most promising genotypes selected include: JHO-95-1, JHO-822, JHO-889, OS-189, HJ-8, JHO-99-6, OS-174, OL-805, OS-7 and OS-237.

Thus, the present study was a successful attempt in identifying the elite genotypes based on genetic divergence, genetic variability, stability, their performance and the understanding of complex interrelationship among attributes involved in genetic control of fodder yield and quality of oat. Therefore, these results will provide valuable added guidelines in future breeding programmes for improving the fodder yield and related traits as per the need of this crop in order to enhance over all quality forage production in the country.