Chapter VI

Summary
SUMMARY

Maize (Zea mays L.) belongs to the grass family, Poaceae (syn. Gramineae), subfamily, Panicoideae, which includes the majority of grasses in tropical and sub-tropical regions throughout the world. Whereas most grasses have perfect flowers. Maize is a monoecious plant and it develops inflorescence with unisexual flowers that are always borne in separate parts of the plant. Maize is one of the few food plants that is diploid with a basic set of ten chromosome ie. 2n= 20.

Maize, a nutritious cereal is used for human consumption besides feed and fodder. In spite of many beneficial uses, it has not so far received adequate attention from the point of view of fodder genetic improvement and management. The crosses involving diverse parents are expected to generate considerable amount of genetic variability, in order to select diverse parents from existing genetic stock stratification of diversity is important. The nature and magnitude of various genetic parameters, character association and G x E interaction under changing environments serves as complementary information.

In the present study a core collection comprising of one hundred genetic lines of diverse origin were collected from the maize genetic stock being maintained at Gene Bank of Indian Grassland and Fodder Research Institute (IGFRI), Jhansi. These representatives were initially collected from the state of Madhya Pradesh, Rajasthan and Uttar Pradesh. The crop accessions were evaluated against the check variety African Tall in randomized block design with three replication during three consecutive years 2001-2003 in Kharif season.
Each entry was replicated thrice in two rows of 4 m length keeping 0.50 m distance between the rows and 0.15 m between the plants. Standard agronomic practices were followed and recommended fertilizer dose were applied during the course of experiment. Observations on three randomly selected plants from each accession in each replication of each environment were recorded for days to 50% silking, plant height (cm), leaf blade length (cm), sheath length (cm), leaf width (cm), stem girth (cm), green fodder yield/plant (g), dry fodder yield/plant (g), leaf-stem ratio, crude protein content (%), days to maturity, cob length (cm), cob width (cm), number of kernel rows, kernels per row, kernel length (cm), kernel width (cm), 100-seed weight (g) and seed (kernel) yield/plant (g). The data of three environments were pooled and subjected to estimate the genetic variability, genetic divergence, character association and phenotypic stability of various fodder, and seed yield traits with the help of statistical procedures. The salient findings of this study are summarized as under following sections:

Analysis of variance showed considerable genetic variation in the accessions for different fodder and seed yield characters and its component traits. The potential of the accessions with respect to various traits was studied, and a number of potential strains for fodder, seed and fodder cum seed yield and quality traits were identified for their exploitation in future breeding programmes.

Visual parameters (qualitative traits) showed maximum number of accessions with dark green colour of sheath and leaf blade. There was no colour variation in midrib colour while maximum number of accessions was showing light green stem colour. Among seed traits, maximum number of accessions with light yellow kernel, regular kernel row arrangement, medium size with shrunken kernels and cylindrical cob shape. On the basis of mean performance of each accession, five major classes were formed and the maximum number of accessions was placed in class II followed by class III for most of the traits.
Considering mean performance of the accessions, the accession IC-335056 and IC-334973 were observed to be earliest for days to 50% silking as they flowered in 43 and 48 days respectively, whereas, the genotype African Tall and IC-334833 were considered late in this trait as they flowered in 59 and 54 days respectively. For plant height African Tall and IC-334855 were found to be taller as compared to others. The accessions identified, as dwarf in plant height are IC-335060 and IC-335056. The genotype producing maximum number of leaves is African Tall and IC-335035. Maximum green fodder yield was observed in genotypes like African Tall and IC-334846 whereas maximum dry fodder yield was recorded for African tall and IC-334833.

Being a cereal crop, maize is not rich in protein content, however, few accessions like IC-334841 and IC-334920 were identified to be very promising as they contain about 11.0 -12.24% crude protein whereas African Tall had very low crude protein content (8.66%) amongst the accessions evaluated.

Among the seed yield traits, the germplasm lines like IC-335111 and IC-335069 were found as early maturing type, whereas, African Tall and IC-334904 were found late in maturity. Maximum cob length was recorded for African Tall and IC-335024. Maximum cob width was reported for IC-334932 and IC-334877. IC-334942 and IC-334947 was rich in number of kernel rows and Maximum kernels/row was observed in IC-335094 and IC-335120. Biggest shank size was observed in African Tall and followed by IC-33496. Accessions like IC-334954 and IC-334853 had highest kernel length while IC-334869 and IC-334846 were found with highest values for kernel width. Maximum test weight was recorded for African Tall and IC-334853. African Tall also showed maximum seed yield/plant followed by IC-335024.

High genotypic coefficient of variation was observed for green fodder yield/plant whereas it was moderate for dry fodder yield/plant. Similarly, among seed yield traits genotypic coefficient of variation was high for number of
kernels/row and moderate for seed yield/plant. There was a close relationship between phenotypic and genotypic coefficient of variation in almost all the characters. However, phenotypic coefficient of variation was slightly higher than their corresponding genotypic coefficient of variation.

For fodder yield and its contributing traits, the range of heritability (broad sense) estimates were high as compared to seed characters. Among fodder traits the highest heritability was observed for green fodder yield, dry fodder yield and days to 50% silking. The remaining characters showed low to medium level of heritability. Similarly in case of seed traits and its contributing traits, days to maturity along with days to 50% silking were showing high level of heritability.

Expected genetic advance for various traits showed that green fodder yield/plant exhibited the highest genetic advance and the moderate values of genetic advance was showed by plant height and dry fodder yield/plant. The remaining characters were showing low to very low genetic advance. Similarly for seed traits it was high to number of kernels/row, days to maturity and seed yield/plant.

The analysis of genetic divergence through non-hierarchical Euclidean cluster analysis revealed considerable genetic diversity among the accessions. Entire number of evaluated accession were grouped into eight clusters for fodder and seed traits as well, in combined form. Among eight clusters, cluster III comprised of 26 accessions was identified as the largest group followed by cluster VII which included 19 accessions. Cluster V was noticed as digenotypic and cluster IV as monogenotypic. Accessions belonging to same eco-geographical regions were scattered over different clusters showing substantial genetic diversity.

The intra-cluster distances were relatively smaller than inter-cluster distances showing homogenous nature of groups and presence of narrow
genetic variation within a cluster. The maximum inter-cluster distance was observed between cluster IV and V followed by I and IV, III and IV, IV and VII, IV and VI and II and IV. The use of accessions in hybridization from these clusters having most of the desirable characters is likely to produce more transgressive segregants.

The accessions belonging to cluster IV had the highest dry fodder yield as well as seed yield. Days to 50% silking and maturity were found short for clusters V while they were prolonged for cluster IV. The accessions belonging to cluster IV had taller plants, long leaf blade length and sheath length, wide leaf width and thick stem. Cluster IV showed highest values for leaf-stem ratio and crude protein content were higher for cluster I.

Of the three isozymes used for the assay, maximum polymorphism was observed for the esterase and peroxidase isozymes UPGMA based dendrogram indicated that there was no relationship among geographical, agronomic and isozyme diversity. However, generally, accessions from the same state tend to be together. IC- 334836 and IC- 334853, both from Rajsamand (Rajasthan) were relatively far apart which was also reflected in the cluster analysis. It was also evident that accessions belonging to the same cluster based on quantitative fodder and seed yield trait had no corresponding placement in the isozyme based dendrogram.

Estimates of phenotypic correlation coefficients revealed dry and green fodder yield/plant was found to be positive and significantly correlated with each other and their contributing traits like days to 50% silking, plant height, number of leaves/plant, leaf blade length, sheath length, leaf width and stem thickness. Similarly for seed yield, it was positive and significantly associated within order 100-seed weight, number of kernels row, kernel width, kernel length, shank diameter and cob length.
When fodder and seed yield components considered together, dry fodder yield had positive and significant correlation with the seed yield/plant and its contributing traits like days to maturity, 100-seed (kernel) weight. Kernel length and cob length. Similarly, component characters of seed yield per plant were also correlated with fodder traits like number of leaves per plant, days to 50% silking, plant height, stem girth, sheath length, leaf length, leaf width and 100-seed (kernel) weight. Where these traits were positive and significantly associated with various seed yielding characters.

Path-coefficient analysis further confirmed that the characters like days to 50% silking, plant height, number of leaves/plant, leaf length, sheath length, leaf width and stem girth were the major component traits of dry fodder yield. Whereas, for seed yield these components were number of leaves/plant, dry fodder yield/plant, cob length, cob width, number of kernels/row, shank diameter, kernel length, kernel width and 100-seed weight.

Analysis of variance of 101 maize accessions over three environments carried out for important fodder, seed and quality characters showed significant difference amongst the accessions for these characters. Further, the environment (linear), genotype x environment (linear) components of variance and the pooled deviations were also significant which showed that accessions could not maintain consistency in performance with respect to these characters as such there is a need for studying stability of the individual accession.

The estimation of stability parameters for individual accession indicated that the proportion of accessions exhibiting predictable behaviour was more for stem girth, days to 50% silking and plant height for fodder yield and for seed yield these traits were number of kernel rows, number of kernels/row and cob width.

The accession like IC- 334834, IC- 335164, IC- 334872 and African Tall were found stable with promise for yield potential of green as well as dry fodder/
plant. Amongst the seed yielding traits, all accessions were stable for this trait except IC-334974, IC-334872 and IC-334887. Out of stable accessions IC-334974, IC-335043 and African Tall were having maximum seed yield/plant.

Thus, the present study was a successful attempts in identifying the elite accessions based on genetic variability, divergence, stability, their performance and the understanding of complex interrelationship among attributes involved in genetic control of fodder, seed yield and quality of maize. The results will provide valuable guidelines in planning future breeding programmes for improving fodder yield, seed yield and quality in order to enhance over all quality forage production and/or to develop dual-purpose materials in maize.