

## LIST OF TABLES

S. No.	Title	After Page
1	List of selected Indian maize landrace accessions with the passport data and geographical coordinates	33
2	Geographical information of sites of evaluation of selected accessions	34
3	SSR loci analyzed in the study	37
4	List of genotypes used for analysis of nucleotide diversity in the 5' NTR region of <i>tb1</i> gene	42
5	Details of the forward and reverse primers designed for analysis of nucleotide variation and allele mining at 5' NTR region of <i>tb1</i>	43
6	SSR markers used for background analysis (population structure) in association analysis of <i>tb1</i> gene	45
7	Morphological description of selected maize accessions based on evaluation at different locations	50
8	Summary statistics of the morpho-agronomic traits measured in the maize accessions	50
9	ANOVA for various traits in maize accessions analyzed through multi-location trials (A) Bajaura, (B) Delhi and (C) Hyderabad	51
10	Means of various traits in the entries evaluated at Bajaura ( <i>Kharif</i> 2006)	51
11	Adjusted means of various traits in the entries evaluated at Delhi ( <i>Kharif</i> 2007)	53
12	Adjusted means of various traits in the entries evaluated at Hyderabad ( <i>Rabi</i> 2006-07)	55
13	Promising accessions identified based on their performance for grain yield and its components, including flowering behavior, in atleast two of the three phenotyping locations	57
14	Promising accessions identified based on their performances for various yield components and flowering behaviour at specific phenotyping locations	57
15	Cluster means of landrace accessions analyzed in the study of various morpho-agronomic traits	59
16	Summary of the results of Principal Component Analysis (PCA) of the grain yield and its components in the landrace accessions	60
17	Classification of clusters of maize accessions, based on distance and multivariate cluster analysis	61
18	Locus-wise details of SSR polymorphisms	62
19	Population-wise summary statistics based on SSR analysis	63
20	(a) The minicore of landrace accessions identified using advanced 'M strategy', along with mean values for various yield-related traits and flowering behaviour recorded at Bajaura; (b) Parameters of the 'minicore' representing the diversity of the initial collection	67
21	Mean phenotypic data for prolificacy for association analysis of <i>tb1</i> gene with prolificacy trait	68

S. No.	Title	After Page
22	ANOVA for prolificacy-related traits analyzed through trial at Bajaura	68
23	Percent homology estimated by comparing the sequenced alleles from 49 entries, with <i>tb1</i> sequence of <i>Zea mays</i> available in public domain	69
24	A summary of sequence variations observed in the 5' non transcribed region of <i>tb1</i>	70
25	Haplotypes identified in the 5' NTR region of <i>tb1</i> gene based on the nucleotide sequencing of 49 entries	72
26	General Linear Model (GLM) analysis, indicating significant associations ( $p < 0.05$ ) of specific polymorphic sites in the 5' NTR of <i>tb1</i> alleles with the prolificacy traits	75
27	Mean number of ears per plant and grain yield per plant in each of the six generations in different experimental crosses evaluated at three locations	78
28	Partitioning of the variances into various components, and heritability of prolificacy trait in the progenies of the three crosses based on trials undertaken at different locations	78