V SUMMARY AND CONCLUSIONS
1. Indian and African populations of *E. africana* are spatially isolated since last 3 millennia. Genome divergence and differentiation in these two populations was analyzed in this work. Chromosome pairing data from African/Indian populations, hybrids indicate that genomes of these two populations have diverged through one large translocation. Poor crossability and low level of fertility in F1 and F2 indicate genomic differentiation in Indian populations of *E. africana*.

2. *Eleusine coracana* and *E. africana* shows regular 18 II formation during meiosis and this pairing behaviour suggests their allotetraploid origin. Finger millet species *E. coracana* is a direct domesticate of wild African grass *E. africana*. Therefore, genomes of these two species are basically similar. Genomic symbol of AABB is proposed to them. Progenitor species *E. africana* being allotetraploid must have originated as a result of hybridization between two diploid species having AA and BB genomes followed by chromosome doubling. In an attempt to discover A and B genome donors to *E. africana/ E. coracana* and to establish genome relations of diploid species with above two tetraploid taxa, all the six diploid species were crossed to *E. coracana* and *E. africana*. Following
five triploid hybrids, *E. tristachya* x *E. coracana*, 
*E. intermedia* x *E. coracana*, *E. africana* x *E. indica*, 
*E. africana* x *E. floccifoilia* (2x) and *E. intermedia* x 
*E. africana* were generated and analyzed.

3. Mean chromosome pairing of 9.4 I + 8.9 II + 0.0 III + 
0.1 IV per cell was found in *E. tristachya* x 
*E. coracana* triploid hybrids. About 82% of the 
PMCs exhibit 9 I + 9 II. This pairing data indicate 
that *E. tristachya* genome is homologous with one of the 
two genomes of cultivated cereal *E. coracana* (AABB). 
Does this diploid *E. tristachya* represent A or B 
genomes? It is well established that *E. indica* is the 
A genome donor to finger millet species *E. coracana* and 
89% of the cells in *E. tristachya* x *E.indica* hybrid 
reveal 9 II bivalents. Thus *E. tristachya* belongs to A 
genomic group of diploid Eleusines. This diploid 
species no where grows near *E. coracana/E. africana* and 
it is not a direct participant in the evolution of this 
millet species or its progenitor *E. africana*. Genomic 
symbol AtAt is assigned to this species.

4. In *E. intermedia* x *E. coracana* triploid hybrids mean 
chromosome pairing of 8.7 I 8.5 II + 0.0 III + 0.3 IV 
per cell was found. About 80% of PMCs reveal typical 
9 I + 9 II configuration. This pairing behaviour
indicates that *E. intermedia* diploid genome is homologous with one of the two genomes of cultivated cereal *E. coracana* (AABB). *E. intermedia* represent AA genome because its genomes are fully homologous with pivotal A genome of *E. indica*. *E. intermedia* and *E. indica* belong to A genomic group of diploid Eleusines and genomic symbol of A\textsubscript{im}A\textsubscript{im} and A\textsubscript{i}A\textsubscript{i} is proposed to them respectively.

5. African allotetraploid wild grass *E. africana* is the direct progenitor of millet species *E. coracana* and genomes of these two taxa are similar (AABB). In an attempt to identify A and B genome diploid participant in the speciation of *E. africana*, all the diploid Eleusines were crossed to it and following three combinations *E. africana* x *E. indica*, *E. africana* x *E. floccifolia* (2x), *E. intermedia* x *E. africana* were successful and these were analyzed. Morphologically diploid *E. indica* (n=9) is similar to allotetraploid *E. africana*. In *E. africana* x *E. indica* triploid hybrids 74% of the PMCs showed 9 I + 9 II chromosome configuration. This pairing behaviour indicates that *E. indica* (AA) genomes are homologous with two genomes of *E. africana* (AABB). Thus from morphological and chromosome pairing data, it is proposed that *E. indica*
6. In *E. africana* x *E. floccifolia* triploid hybrids mean chromosome pairing of 8.4 I + 8.5 II + 0.0 III + 0.04 IV per cell was found and nearly 72% of the PMCs revealed 9 I + 9 II configuration. This pairing behaviour suggests that *E. floccifolia* genome is partially homologous with one of the genomes of *E. africana*. *E. floccifolia* genome is known to be homologous to *E. indica* AA genomes. Thus *E. floccifolia* belongs to A genomic group of diploid Eleusines. Morphologically *E. floccifolia* is quite different than tetraploid *E. africana* and is not a genome donor to it but belongs to A genomic group of diploid Eleusines. Genomic symbol of EfEf is assigned to this species.

7. Mean chromosome pairing of 8.2 I + 8.2 II + 0.0 III + 0.4 IV per cell was found in *E. intermedia* x *E. africana* triploid hybrid. Nearly 54% of the PMCs exhibited 9 I + 9 II pairing configuration. This chromosome pairing data indicate that *E. intermedia* genomes are partially homologous with one of the genomes of *E. africana* (AABB). As evident from present
studies *E. intermedia* genomes are homologous and basically similar to *E. indica* (AA) A genomes. Thus perennial *E. intermedia* belongs to A genome group of diploid Eleusines and it is not a participant in the evolution of *E. africana*. Similar conclusion has been reached from breeding experiment with *E. coracana* also. A genomic notation of \( A_{im}A_{im} \) been assigned to *E. intermedia*.

8. Chromosome pairing data from triploid hybrids of *E. coracana* \((n=18)\) x diploid Eleusines and *E. africana* \((n=18)\) x diploid Eleusines suggests that *E. indica* (AA) to be A genome participant in the evolution of *E. africana/E. coracana* cereal. Other diploid species *E. intermedia* \( (A_{im}A_{im}) \), *E. tristachya* \( (A_tA_t) \) and *E. floccifolia* \( (A_fA_f) \) belong to A genomic group of diploid Eleusines and form a close genetic assemblage within the genus *Eleusine*.

9. Large number of tetraploid x tetraploid species crosses were made to establish genome homology and differentiation among tetraploid taxa. Only *E. africana* x *E. floccifolia* and *E. africana* x *E. kigeziensis* hybrids were successful and these were analyzed. Pollen parent *E. floccifolia* appears to be an autotetraploid race with \( A_fA_fA_fA_f \) genomes. Where
as, female parent *E. africana* with AABB genomes is an allotetraploid taxa. The chromosome pairing data in *E. africana* x *E. floccifolia* hybrid suggests that the duplicated genome of autotetraploid (AAAA). *E. floccifolia* is partially homologous with A genome of *E. africana* (AABB).

10. The female parent *E. africana* (AABB) (n=18) is an allotetraploid and apparently AA genome is derived from *E. indica*, with no clue of B genome donor. The pollen parent allotetraploid *E. kigeziensis* (n=19) is believed to have originated from cross between *E. indica* (n=9) and *E. jaegeri* (n=10) followed by chromosome doubling. Morphological characters of *E. kigeziensis* supports this origin. In *E. africana* x *E. kigeziensis* hybrid, mean chromosome pairing of 0.9 I + 16.8 II + 0.05 III + 0.19 IV per cell was found and nearly 69% of the PMCs revealed 18 regular bivalents and one univalent. This pairing data indicates that genomes of *E. africana* (AABB) and *E. kigeziensis* are homologous but for one chromosome of *E. kigeziensis* which has no homology in A/B genomes and remains as univalent. Out of two genomes of *E. kigeziensis* (AABB) AA genome has probably come from *E. indica* and BB genomes possibly from *E. jaegeri*, in which one chromosome has no
homology with AB genomes and remain as univalent in the hybrids. Thus *E. africana* and *E. kigeziensis* have AA genome from *E. indica* and BB genome from *E. jaegeri*. It appears that BB genome might have come to *E. africana* from some diploid species closely related to *E. jaegeri*. Present work for the first time provide a clue regarding the B genome donor to *E. africana*/*E. coracana*.

11. Genome homology and differentiation in diploid Eleusines were studied through chromosome pairing in interspecific diploid hybrids and their fertility in subsequent generations. All the diploids were intercrossed among various combinations and following interspecific hybrids: *E. intermedia* × *E. indica*, *E. intermedia* × *E. floccifolia* and *E. tristachya* × *E. intermedia* were generated and analyzed. In *E. intermedia* × *E. indica* hybrids mean chromosome pairing of 0.28 I + 8.76 II + 0.02 III + 0.01 IV per cell was found. About 94% of the PMCs exhibited 9 bivalents. Obviously genomes of *E. intermedia* and *E. indica* are fully homologous. *E. indica* is a pivotal A genomic parent of *E. africana* has A_iA_i genomes. Obviously *E. intermedia* also has AA genomes. Thus genomic symbol of A_imA_im is assigned to
E. intermedia. Thus along with E. indica (A₁A₁), E. intermedia (AᵢₘAᵢₘ) belong to A genomic group of diploid Eleusines.

12. From various evidences it is proposed that annual E. indica has descended from E. intermedia. Genomes of these two species are differentiated through cryptic structural hybridity. It acts as an efficient isolating barrier to prevent the gene flow among these two species in nature.

13. E. intermedia and E. floccifolia are perennial primitive diploid species. In their interspecific hybrid mean chromosome pairing of 0.3 I + 8.7 II + 0.0 III + 0.1 IV per cell was found. Nearly 79% of the PMCs showed 9 II and hybrids are sterile. This suggests that AA genomes of E. intermedia is homologous to E. floccifolia genomes. Thus E. floccifolia (AᵢF) along with E. intermedia (AᵢₘAᵢₘ) and E. indica (A₁A₁) belong to A genomic group of diploid Eleusines. E. intermedia and E. floccifolia are distinct primitive species. In spite of good chromosome pairing hybrids are sterile. Genome differentiation among these two species is through cryptic structural hybridity and subsequent hybrid sterility.
14. South American species *E. tristachya* and endemic African *E. intermedia* are typical diploid. In *E. tristachya* × *E. intermedia* hybrids mean chromosome pairing of 0.44 I + 8.54 II + 0.0 III + 0.02 IV per cell was found. About 78% of the PMCs revealed 9 II. This chromosome pairing data indicate that genomes of both the species are homologous. Thus *E. tristachya* also has AA genomes and genomic symbol of $A_tA_t$ is assigned to it. These two diploid species are differentiated by one large translocation. Geographic isolation appears to be the major isolating barrier between North American *E. tristachya* and endemic Kenyan *E. intermedia*.

15. Chromosome pairing data from diploid hybrids indicate that *E. indica*, *E. intermedia*, *E. floccifolia* and *E. tristachya* all belong to AA genomic group of diploid species. These diploid species form a close genetic assemblage within the genus *Eleusine*. These genomes have substantially differentiated during the course of evolution and developed the various isolating barriers against gene flow between these taxa in nature.

16. Prolamin proteins of nine *Eleusine* species involving 15 accessions were fractionated by SDS-PAGE method to
elucidate the genome hoology and differentiation in Eleusines. Considerable degree of prolamin diversity was displayed by different species of Eleusines examined. Totally ten polypeptides were resolved with Mw ranging from 12 to 23 kD. Within the species prolamin diversity is low.

17. Prolamin profile of *E. africana* is similar to cultivated millet species *E. coracana* and exhibit same two polypeptides. The average similarity index value of protein homology among there two species is 83%. Thus prolamin data confirms the earlier cytogenetics conclusion of finger millet species *E. coracana* being a direct domesticate of wild grass *E. africana*.

18. Diploid species *E. intermedia*, *E. indica* and *E. floccifolia* possess prolamin profile which is similar to *E. africana/E. coracana*. Prolamin data suggests that *E. indica* is A genome participant in the evolution of *E. africana/E. coracana*. Low level of prolamin heterogeneity in *E. africana/E. coracana* precludes the identity of diploid B genome donor to progenitor *E. africana*.

19. With the exception of *E. tristachya* all the A genomic group of diploid Eleusines, *E. indica*, *E. intermedia*
and *E. floccifolia* share similar prolamin polypeptides and support the idea of their assemblage into A genomic group of species.

20. *E. tristachya* prolamin profile is quite different than A genomic group of species. Thus prolamin studies do not support the concept that *E. tristachya* is closely related to A genomic group of diploid *Eleusine*. Prolamin data support the distinct genomic status of *E. multiflora* (CC).

21. Among *E. africana* and *E. kigeziensis* the similarity index value as a parameter of protein homology is very low. Prolamin studies do not support that *E. kigeziensis* and *E. africana* share similar (AABB) genomes.