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EVALUATION OF PHOTOPERIODIC RESPONSE AND  
CHARACTERIZATION OF POPULATION STRUCTURE OF PEARL  
MILLET GERMPLASM FROM WEST AND CENTRAL AFRICA

Submitted by

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On the basis of our results we conclude that both genetic distance based and model based grouping methods worked equitably well to an extent in clustering the inbred lines of pearl millet. Model based method gave the inferred ancestry of an individual; however it does not provide information about sub-groups in each cluster. Whereas in genetic distance based methods the subgroup information was also available. Understanding the population structure of the WCA pearl millets is a prerequisite for future studies aimed at association mapping where regions of genome can be associated with phenotype of interest.

## CHAPTER FOUR

### 4. Summary

Pearl millet (*Pennisetum glaucum*) is one of the staple crops of the arid and semi-arid tropics of Africa and Asia with high adaptability to harsh climatic conditions. The photoperiodic sensitivity observed among local landraces is one of the key adaptation traits of this cultivars over generations in marginal environments. The flowering time response of 200 inbred lines derived from local cultivars grown across West and Central Africa to photoperiod were evaluated in field experiments at two different planting dates. The difference in the vegetative cycle between the first planting date (June 15<sup>th</sup> corresponding to long day treatment) and second planting (July 16<sup>th</sup> corresponding to short day treatment) was used as photoperiod response index (PRI) which indicates the sensitivity of the genotype and which were categorized into eight groups from 0-7. The mean values of two replications for “days to 50 % flag leaf emergence” were considered as the length of the vegetative cycle. Approximately 61% of the inbred lines from West and Central Africa were found to be photoperiod sensitive and the sensitivity varied quantitatively showing a large range of PRI values. We observed a vast variation for flowering response and other morphological traits among inbred lines from the same country of origin. Lines were characterized for their diversity in “flag leaf emergence”, “flowering”, “plant height” and “panicle length”. The flowering response showed a north south latitude gradient, with early flowering lines were found more towards north and late flowering types were found more towards south. We observed an enormous range of morphological diversity among pearl

millet inbred lines across WCA and also among inbred lines within one country of origin for “flowering”, “plant height” and “panicle length” characters.

In the second part of the study, these two hundred inbred lines were subjected to a genetic diversity analysis using 22 molecular markers (SSR) including the investigation of the population structure of these materials. We detected 347 alleles over 22 loci and the selected markers were proven to be highly informative i.e. showing high PIC values. The results showed high genetic diversity among the inbred lines across WCA and also within their countries of origin using statistical values like “gene diversity”, “allele polymorphism” and “genetic distances”. A genetic distance based and a model based clustering analysis was performed to group all the inbred lines into clusters. A model based cluster analysis assigned all the inbred lines to five distinct groups based on their inferred ancestry with 41% of the accessions being identified as admixtures. Clustering using Roger’s genetic distance gave similar results, with some inbred lines grouping differently from that of the model based clustering. The genetic distance ( $D_R$ ) values observed between the inbred lines and also among sets of inbred lines varied highly. Principal coordinate analysis performed with all the accessions using allelic data again demonstrated the diversity of these inbred lines within their countries of origin and across WCA.

This study constitutes a part of larger joint research project titled “Availability of allele specific molecular markers for genes controlling photoperiod sensitivity of flowering time in pearl millet and sorghum” at University of Hohenheim in collaboration with the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) centre in Niamey, Niger. The study results established here will be further used in the project as the basis for an association mapping study to identify the molecular variation responsible for photoperiod sensitivity at the genome level among inbred lines. Further, the germplasm which has been characterized both phenotypically and genotypically in this study can be used in future breeding programmes for the selection of varieties with enhanced adaptation to local environments and for production of hybrids.