Summary

Sesame (*Sesamum indicum* L.), which originated in Africa, is probably the most ancient oil seed plant cultivated in many parts of the world. Currently, China, India, and Myanmar (Burma) are the world’s largest producers of sesame, followed by Sudan, Nigeria, Pakistan, Bangladesh, Ethiopia, Thailand, Turkey and Mexico (Desai, 2004). The genus *Sesamum* contains more than 30 species of which *Sesamum indicum* is the commonly cultivated (Nayar & Mehra 1970; Kobayashi *et al.* 1990). Sesame is self-pollinating, although differing rates of cross pollination have been reported by Yermanos (1980); Sarker (2004) and Ashri (2007). The pollination process occurs at the time the flowers open (Kafiriti and Deckers 2001; Langham 2007). Yermanoos (1980) found less than 1% when the sesame was surrounded by cotton and other crops.

Sesame seed oil is valued for its high quality and stability. It is used as salad and cooking oil as well as in the manufacture of margarine, vanaspati, soap, paints and insecticides. Sesame cake is also a rich source of protein, carbohydrates, mineral such as calcium, amino acids like tryptophan, methionine and a nutritious feed for dairy cattle. So sesame seeds are in high demand because of its significance in the confectionary industry universally.

Plant genetic resources are very important for food security, health care and welfare of human race. Increase demand due to population growth, loss of cultivated lands and emergence of new disease and pest have made man to depend more on the utilization of plant genetic resources effectively.

PCR based molecular techniques like RAPD, ISSR, AFLP etc. have unambiguously established their worth in germplasms characterization, conservation and utilization for the benefit of mankind. These techniques focus on the detection of variability in the genetic material particularly the DNA, which is stable, heritable hence, preferred over many other methods of study.

The present research work was started with the following objectives and the important research finding that we have achieved could be presented as follows:

This research work started with the estimation of the genetic variation with in the germplasms of *Sesamum indicum* L. using agromorphological and chemical parameters and to identify important germplasms of different districts in West Bengal. ANOVA followed by DMRT revealed significant differences among fifteen different germplasms of *Sesemum* species with
respect to oil content and other associated characters. Among the 15 different germplasms maximum oil was obtained from germplasms V-JTS-8 of Murshidabad district of north zone. Genetic variability was also evidenced by the GCV and PCV results which help us to conclude that there was adequate scope of selection for improvement of certain traits. High heritability and genetic advance (GA) values indicated that these characters are simply inherited and there is a chance of selection for further improvement. A number of significant correlations (genotypic, phenotypic, environmental and simple) between the characters were observed and there was very little variation between the genotypic and phenotypic correlations. So from the results so far obtained we can conclude that environment play very little role for expression of traits. Path analysis results revealed that different causal characters had different level of direct and indirect effects on oil content which helps us to select suitable plant material for generating plants with higher oil content.

The sesame seeds collected from different districts of West Bengal contain the total lipid/oil (w/w) ranging from 12.44% to 31.94%. The seeds also contain six major fatty acids such as palmitic acid (ranging from 11.2% to 15.5%), stearic acid (ranging from 4.4% to 5.7%), oleic acid (ranging from 39.3% to 44.4%), linoleic acid (ranging from 37.5% to 41.3%), γ-linolenic acid (ranging from 0 to 0.2%) and α-linolenic acid (ranging from 0.2% to 0.8%).

Assessment of genetic diversity on polymerase chain reaction (PCR) using RAPD marker proved an efficient means for estimating genetic relatedness among the plant species, to distinguish cultivars and allow excellent advantages for re-examination of the taxonomy classification of important species delimitation. Several studies have highlighted the assessment of genetic diversity in crops (Levi & Rowland 1997; Demeke et al. 1992; dos Santos et al. 1994; Scott et al. 1996; Novy et al. 1994; Transue et al. 1994; Shah et al. 1994; Demeke et al. 1996).

The objective of this presentation was to report the RAPD analysis of selected germplasms of *Sesamum indicum* L. collected from different districts of West Bengal grouped into 4 distinct zones to access the similarity/dissimilarity at DNA level. The RAPD analysis was carried using 25 RAPD primers in 15 selected germplasms of *Sesamum* species. Out of the 25 primers, 10 primers showing distinctly different banding patterns in these selected germplasms which were equally prominent. In order to assess the utility of RAPD analysis in the germplasms variation study, the performance of the RAPD marker was evaluated with various parameters such as percentage polymorphism, polymorphic information content, EMR, marker index, resolving power and was presented in chapter 4. The POPGENE
programme version 1.31 (Yeh et al. 1999) is used to calculate pi value. The binary data matrix was used to calculate Jaccard’s similarity coefficient between pairs of accessions using the Simqual module of NTsys-PC (Numerical Taxonomy System version 2.1) (Rohlf 1993). These distance coefficients were used to construct dendrogram using the Unweighted Pair Grouped Method Arithmetic Average (UPGMA) employing the Sequential Agglomerative Hierarchical and Nested (SAHN) algorithm for determining the genetic diversity and relationships among the accessions. In order to highlight the resolving power of the ordination, Principle coordinate analysis (PCA) was performed using the EIGEN and PROJ modules of NTSYS Pc.

A high level of genetic diversity was observed among the 15 germplasms of Sesame. Although Sesame is generally follow self-pollination but cross pollination have been reported between 5 and 60 % in this species (Yermanos 1998; Joshi 1961; Mazzani 1983; Brar and Ahuja 1979; Ashri 1989). Approximately 10 to 20 % of the genetic diversity among the population is due to out crossing could explicate the high genetic variability noticed in the present study. Our results are in conformity with the results of earlier workers based on RAPD and morpho-agronomic traits which have reported high genetic diversity in Sesame germplasms (Ashri 1998; Bhat et al. 1999; Ercan et al. 2004; Salazar et al. 2006; Pham et al. 2009; Akbar et al. 2011).

The present study detected a high level of polymorphism for Sesame between the different geographical areas of West Bengal. A considerable level of genetic diversity was noticed among diverse Sesame germplasms collected from various geographical regions of West Bengal, it was found that some germplasms situated geographically fur apart grouped together in the same cluster such as V1 and V6 (from North Zone) and V11 (from South Zone) grouped together in cluster I. Similarly in the cluster II germplasms of North Zone (V3 and V5), East Zone (V8 and V10) and West Zone (V13 and V15) were clustered together. Furthermore, in the cluster III germplasms collected from different regions of West Bengal appeared in the identical group such as North Zone (V2, V4 and V7), South Zone (V12), East Zone (V9) and West Zone (V14). This could be an outcome of fairly large movement of West Bengal farmers to different regions (West Bengal) carrying sesame seeds for cultivation into their new geographical locations. Germplasms collected from the same zone were found to have a close genetic relationship for example cluster I included germplasms V1 and V6 from North Zone and V8, V10 from East Zone in cluster II. Interestingly, all the 3 clusters included germplasms collected from North Zone (Murshidabad district) which may be a
consequence of largely substantial movement of farmers of Murshidabad district to different regions of West Bengal for collection of diverse germplasms of sesame for cultivation.

Using the RAPD results attempts have been made to analyses the genetic diversity from the 4 different geographical zones of West Bengal. From the result it can be summarized that least gene diversity was among the germplasms collected from the South Zone or South 24 Parganas district and highest among germplasms of North Zone or Murshidabad district. The same order of genetic heterogenety was discerned to Shannon’s information index (North Zone › West Zone › East Zone › South Zone).

These basic findings will facilitate for designing crop improvement programme through molecular marker assessment selection with respect to qualitative and quantitative characters.