Introduction

1. *Sesamum - The oil crop:*

*Sesamum indicum* L. (family Pedaliaceae) is perhaps the oldest annual oilseed crop known to man. On the basis of its ancient history of cultivation, availability of diversity of forms of cultivated varieties and occurrence of the wild sesame, *Sesamum indicum* var. *malabaricum*, India is considered to be the basic center of origin of the crop (Brar and Ahuja, 1979). 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 seed yield, however, is lowest of all major oilseeds in India mostly because it is grown under adverse climatic and cultural conditions. As a result the genotype which is hardy but poor yielding got selected as cultivars (ICAR, 1977 and 1978). Moreover, the best cultivars of exotic origin gave poor performance under different soils, climatic and cultural practices in India (Brar and Ahuja, I.C.). Seasame is an important self-pollinated annual crop in the tropics and warm sub tropics. Practically 100% of world’s Seasame area is found in developing countries with the largest areas in India, Mayanmar, China, Sudan, Nigeria and Uganda. India produced 0.9 million tonnes of Seasame from 2.7 million ha during 1995 (Ashri, 1998). The corresponding world figures were 7.8 million ha and 2.7 million tonnes. Seasame is usually grown as a catch crop in the pre-kharif season in West Bengal. The bottle neck in increasing its productivity and exploiting its genetic potentiality is in the shattering of mature capsules before harvest as well as the span of time taken for continuous flowering and capsule setting which prevents early harvest. The two traits counteract minimizing the quantum of harvestable seeds.

Moderately fertile, free draining, sandy loam soil is ideal for obtaining good yield from sesame under minimal intercultural practices. Therefore, the identification of genotypes for optimum response under high, low and zero input conditions is necessary to evaluated their competence for objective genetic manipulation to increase the yield as well as to eliminate the attributes adversely affecting the yield. For genetic improvement of the efficiency of both seed and oil production the basic necessities are the availability of donor genotypes which would show unambiguous superiority of the relevant character/characters and a clear understanding of the genetic background of such characters. Seasame is an important self-pollinated annual crop in the tropics and warm sub tropics.
It is not that some improvement in yield has not been achieved and apparent high yielders being evolved for cultivation in India. In spite of that, the average yield of sesame in India is only 213 kg/ha as compared to the 980 kg/ha in the United Arab Republic (Weiss, 1971). So far as West Bengal is concerned, this State produces only 1.02 lakh tonnes of oil seeds, 30% of which is contributed by sesame (Agriculture Situation in India, 1984). Paucity of genotypes well adapted to the diverse edapho-climatic conditions of sesame cultivation in the State reduces perforce the yield at a level lower than the national average. It is imperative therefore that, with a view to optimizing the return and maximizing the productivity of this crop in this State, approaches with new parameters as selection criteria and appropriate breeding protocol should be taken up to achieve a quantum jump in yield. The mean seed yields of Sesame are very low (about 3.5 q/ha). The low yields are due to lack of improved cultivars, low harvest index, susceptibility to diseases, pests and environmental stresses, seed shattering, indeterminate growth habit and asynchronous capsule ripening that accentuates seed shattering; low rainfall and prolonged dry periods and lack of inputs.

Much of the available knowledge on the genetic control of various trades in Sesames stems from the pioneering studies of Lingham (1945a, 1945b, 1946, 1947a, 1947b). The studies of inheritance mechanisms in Sesame were reviewed by Joshi (1961), Weiss (1971, 1983) and Brar and Ahuja (1979).

Yukawa et.al (1996) investigated the structure and expression of two seeds specific cDNA clones encoding stearoyl-acyl carrier protein desaturase (SACPD).

From the perusal of literature it becomes clearly evident that Sesame seed yields and harvest indices are often low. Higher seed yields are a major breeding goal and many authors evaluated the relative importance and/or the genetic control of the different yield components namely: number of branches/plant, number of capsule/plant, number of carpels/capsule, number of seeds/capsule, seed weight as well as harvest index (Ashri, 1998). Special efforts are needed to improve germplasm resources. This include collection of germplasms, evaluation and documentation of accessions using both conventional and nonconventional tools which may provide the breakthrough in breeding which may provide significant effect on Sesame yields, especially in West Bengal and rest part of the country.

Understanding the diversity and phylogeny of a plant species or genus (or even higher levels) is of great significance, primarily because of its connection to many branches of biological sciences. From the diversity point of view, the presence of variation in a population particularly at the molecular level is important both in determining the opportunity
to improve the population through selection of pre-existing variation or new mutations (Barrett & Schluter 2008) and in quality (Fitzgerald et al. 2009) and disease control (Zhu et al. 2000). Moreover, genetic diversity has a significant effect on ecological processes such as primary productivity, population recovery from disturbance, interspecific competition, community structure, and fluxes of energy and nutrients (Hughes et al. 2008). Genetic diversity gives species the ability to adapt to changing environments, including new pests and diseases and new climatic conditions. The pattern of genetic variability within and among population is influenced by mutation, genetic drift, mating system, gene flow and selection (Nebauer et al. 1999). The loss of genetic variation, however, is detrimental to the plant population as it reduces its ability to respond to environmental change leading to enhanced probability of extinction or limited opportunity for evolution (Aguilar et al. 2008). From the phylogenetic point of view, a well-corroborated phylogeny would provide a means for evaluating character evolution (Les et al. 1999; Borsch et al. 2008), molecular evolution (Grimm et al. 2007), and global changes (Edwards et al. 2007). Phylogenetic reconstructions may also aid in the discovery of greater plant diversity and assist biologists in choosing areas or species to prioritize in their conservation efforts (Cameron 2011).

The range of morphological characters currently available for evaluation are extremely useful but most often the desired phenotypic characters are phylogenetically inherited and highly influenced by environmental conditions. The recently developed DNA based molecular markers have been proved to be valuable tools in the characterization and evaluation of genetic diversity within and between species and populations. It has been shown that different markers might reveal different classes of variation (Powell et al. 1996; Russell et al. 1997). It is correlated with the genome fraction surveyed by each kind of marker, their distribution throughout the genome and the extent of the DNA target which is analyzed by each specific assay (Dávila et al. 1999). The advent of the polymerase chain reaction (PCR) favored the development of different molecular techniques such as RAPD, SSR, ISSR, AFLP, RAMP, STS (Wu et al. 1994). Despite the recent discovery, marker technologies have already been used to study genetic diversity, genetic relationships, and phylogeny in several crops. The variation detected by the DNA based markers is far more compared with morphological markers and is seldom influenced by the environment and geographical location. This also helps in identifying suitable accessions and hybrids at seedling stage itself for further crop improvement program (Tanksley 1983). Biochemical and genetic markers for identification of varieties and finger printing a vast number of species and varieties to avoid
confusion and for Plant Varietal Rights (PVR) is essential. Detailed plant variety profiling methodologies are instrumental to strengthen Intellectual Property Protection (IPP) and patenting through their abilities to provide positive identification of germplasm. With this background the present work three objectives have been undertaken with the following aspect:

a) To assess the phenotypic diversity and yield components using biometrical tools like ANOVA, Duncan test, GCV, PCV, ECV, Heritability, GA, Correlation, Path analysis, $D^2$ etc. in selected germplasms of sesame growing in West Bengal.

b) To assess oil and fatty acids composition using GLC in selected germplasms of sesame.

c) To assess genetic diversity using molecular marker in selected germplasms of sesame.