GENERAL INTRODUCTION
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India is one of the 12 mega biodiversity countries in the world. The country is divided into 10 biogeographic regions. The diverse physical features and climatic conditions have caused the formation of diverse ecological habitats like forests, grasslands, deserts, wetlands, as well as coastal and marine ecosystems each harboring typical biodiversity. This has contributed to the richness of genetic resource in this sub continent. Again, being situated at the tri-junction of three realms - Afro-tropical, Indo-Malayan and Paleo-Arctic realms, the biodiversity available in this region includes characteristic elements from each of these domains. The country is one of the 12 primary centers of origin of cultivated plants. It is considered to be the homeland of 167 important plant species of cereals, millets, fruits, condiments, vegetables, pulses, fiber crops and oilseeds. About 4,900 species of flowering plants are endemic to the country. These are distributed among 141 genera belonging to 47 families. Much of the rich plant genetic resource is concentrated in the floristically rich areas of North-East India, the Western Ghats, North-West Himalayas and the Andaman and Nicobar Islands. Of these, North East India and Western Ghat constitute two of the world’s 18 hot spots.

Medicinal plants play an important role in supporting healthcare system in countries with record of ancient civilization. According to the World Health Organization (WHO), 80% of the rural population in developing countries utilizes locally available medicinal plants for their primary healthcare needs. Through the years different systems of traditional Indian medicines have stood the test of time. In India a number of alternative medicine system viz., Ayurveda, Unani, Siddha along with folk medicines in tribal communities are in use. These are predominantly based on plant based raw
materials that are used in herbal medicine preparations and formulations. About 8000 species of medicinal plants are in current use by local communities all over India. About 90% of the country's medicinal plants are found in forest habitats. Only 10% of the medicinal plants are distributed among other landscape elements like open grasslands, agricultural pastures and in and around fresh water bodies. Availability of medicinal plants together with its medicinal potential makes these plants useful and has drawn attention of International scientific community. India is one amongst those nations which possess a historical track record of having made a significant contribution globally, towards use of herbal medicine. In the 21st century, given the global resurgence of consumer interest in natural products, India's rich medicinal plant heritage of 8000 species and an estimated 40,000 herbal formulations stands out significantly; conservation and sustainable utilization of Indian medicinal plants thus have global relevance. Thus there is an urgent need to conserve wild medicinal plant diversity in prioritized forest (wild vegetation) regions of India.

Use of biological resources based on local knowledge systems and practices is ingrained in Indian ethos. With the globalization based growing focus on herbal medicine, greed / wider need of medicinally important plants without thought for conservation has led to unwarranted loss of much of the rich plant genetic resource in the country. Biopiracy by multinational companies have added to this predicament. Realization that plant genetic resource should be conserved and sustainably used led to the concept of environmental protection which is enshrined in the Indian constitution in articles 48a and 51a(g). To protect plants from bio-piracy, it is important to establish fool proof identification / authentication that may establish owners' right of possession of the
medicinal plant. The strategies for conservation and sustainable utilization of biodiversity include providing special status and protection to biodiversity-rich areas by declaring them as national parks, wildlife sanctuaries, biosphere reserves, ecologically fragile and sensitive areas. Other strategies include offloading pressure from reserve forests by alternative measures for fuel wood and fodder and simultaneous afforestation of degraded areas and wastelands and creation of ex-situ conservation facilities such as gene banks.

The growing awareness of inequalities between countries or communities that have abundant resource, an important partner being India, and those waiting to harvest the same resource without sharing the commercial benefits derived from the natural resource, prompted United Nations to host the "World Commission on Environment and Development" (WCED) that endorsed the urgent need for conserving the world’s rich biodiversity; special emphasis was laid on the biodiversity-rich tropical areas where plant genetic diversity constitute an important component. Subsequently the "Earth Summit" held under the auspices of the United Nations Conference on Environment and Development (UNCED) at Rio-de-Janeiro 1992, adopted a "Convention on Biological Diversity" (CBD) that calls for Conservation, precise Documentation and Sustainable utilization of Biodiversity. The main implementation measures for the CBD are through national strategies, legislation, and administrative instruments to be developed in accordance with the country’s conditions and capabilities. This plan aims at consolidating the on-going efforts of conservation and sustainable use of biological diversity, identifying gaps in various sectors and providing a policy and programme regime to ensure attainment of the three objectives of the CBD. The multinational
convention, viz CBD signed by 193 countries (https://www.cbd.int/information/parties.shtml), including India, stressed on the need for precise documentation of Biodiversity to facilitate Benefit Sharing of useful plant genetic resource (through Prior Informed Consent) An important appendix to such endeavor constitutes Evaluation of germplasm and Bio-prospecting of useful genes. This calls for precision in Documentation and Evaluation of valuable (medicinal) plant genetic resource.

The demand for medicinal plants is growing at a rapid pace. In 1947, the annual turnover of the herbal industry was Rs. 2,000 million which is expected to touch Rs. 40,000 million by the end of 2020. This is why India supplies 12% of the world's requirements of medicinal plants. Today, 90% of the medicinal plants consumed domestically and exported are collected from the wild, and only 70 out of around 700 species in the trade are obtained purely from cultivated sources. The plant resource needed for such health curing systems constitute natural wealth of our country and have been used as the starting materials of many allopathic drugs developed world-wide. The Herbal Drug Market, globally is expected to grow to US$ 5 Trillion by the Year – 2050; (Joshi-et-al 2004). In this, India with its rich natural plant resource and commendable traditional knowledge and wisdom for the medicinal value of these plants is expected to be involved as a major partner. It is important to authentically characterize and precisely evaluate the rich medicinal plant diversity of our country using modern biotechnological tools. To ensure fair benefit sharing and to prevent un-warranted biopiracy of indigenous plant genetic resource; urgent efforts are necessary to develop unambiguous inventory of our plant diversity using a precise documentation system.
The use of biochemical techniques and maker compounds once taken as a superior (over Morphological / Anatomical Parameters) assessment protocol for standardizing botanical preparations has limitations because of their variable sources and chemical complexity. With the availability of DNA based techniques, DNA finger printing that provides the ultimate in individualization, remaining unchanged through changes in season / environment / period in life cycle, now appears to be the method of choice (in combination with comparative studies on chemical finger printing) in unambiguously documenting valuable medicinal plants.

During the past decade DNA based techniques viz. DNA finger printing have been widely used (Hui-et-al 2000) for authentication of plant species of medicinal importance. Morphologically similar plants that are sometimes used as adulterants / substitutes for the prescribed drug usually causes reduced efficacy of plant based medicines / drug formulations. A common example in this context is *Desmodium Gangeticum*, which is an important ingredient of ‘Dasamularista’ – a common Ayurvedic tonic. This is a Polymorphic species (with respect to phenotypic characters). Notwithstanding co-ordinated efforts on DNA based identification of medical plants of our country, extensive documentation of plant genetic resource of the country is still largely lacking. In this age of focus on herbal medicine and global benefit sharing of the resource, it is urgently necessary to take up advanced research on DNA fingerprinting methodology for precise identification of the wide diversity of plant genetic resource. It is important to establish:
Species specific DNA markers for checking adulteration of prescribed medicinal plants required by the Industry and authentication of drug plants in production of herbal medicine.

Trait related DNA markers from study of wild land races as well as cultivated plants (using correlative studies between DNA fingerprinting data and biochemical analysis data of medicinally important compounds) to be used as diagnostic probes for assessment of medicinal potential in plants.
CURRENT STATUS OF RESEARCH AND DEVELOPMENT IN THE SUBJECT

DNA Fingerprinting is universally accepted as the ultimate in identification of genotypes and thus documentation of genetic resource. Such DNA characterization methods help to fulfill the needs for documentation mandated under the WTO (World Trade Organization) and CBD (Convention of Biological Diversity) and also its associated India National Biodiversity Act, 2002. DNA profiling / fingerprinting is thus considered the ultimate in individualization and documentation of plant genotypes.

DNA based Molecular documentation of genotypes helps in:

a) Management of accessions of Gene Banks
b) Developing Passport Data for export of crop bio-resource
c) Resolving IPR (International Property Right) conflicts
d) For facilitating prior informed consent procedures under the CBD regime
e) DNA Fingerprinting also helps in supplementing drug assessment / authentication protocols that is essential for preparing authentic herbal medicine of uniform efficacy in different batches by the pharmaceuticals industries (Hui-et-al 2000).

A major problem faced in herbal drug development is lack of precise parameters that could unequivocally identify and document plants possessing desired medicinal potential. Morphologically similar plants that are sometimes used as substitute for prescribed drug usually results in development of low efficacy drugs and / or inclusion of harmful plant components in preparation of medicines / drug formulations. It is thus important that prescribed plants are correctly identified.

Several methods of DNA finger printing, Viz. RAPD, CAPS, SCAR, SSR, ISSR, AFLP, SNP (Laxmikumaran, 2003) are now available for use as appropriate, depending
on genome size of the plant under study and the expected level of distinction sought between the individuals. DNA based unique characterization of desirable plants is particularly important for closely related plants that are not readily distinguishable by morphological / anatomical characters. Consequently the European Scientific Co-Operative on Phototherapy (ESCOP) has clearly specified the requirement for standardization of phyto-pharmaceuticals on the basis of Bio-makers that are unique to that species (Vasudevan, 2004). Accurate identification of plant species is also considered as the basis for modernization of Chinese drugs (Hui et al, 2000; Cheng et al, 1997).

Comprehensive understanding of a genotype requires a combination of three types of markers viz. (1) Morphological (also classical or visible) markers that identify phenotypic traits of characters; (2) Biochemical markers, which include allelic variants of enzymes called isozymes; and (3) Molecular (DNA) markers, which reveal variation in DNA sequence.

❖ **Morphological Markers**:

Morphological characters are the simplest, easily recording parameters that have been the subject of numerous studies in population genetics and agriculture and used for identification of families, species and genera. Such identifying features i.e. markers are usually visible phenotypic characters such as flower colour, seed shape, growth habit, pigmentation. Such traits sometime exhibit one to one correspondence with the genes controlling the traits. In such cases, morphological characters (i.e., phenotypes) can be used as reliable indicators for specific genes and are useful as genetic markers on
Chromosomes. Several morphological markers have been studied and mapped for human, mouse, drosophila, maize, tomato and many other plants and animal species. Till date, in Rice about 170 morphological markers have been assigned to 12 linkage groups, through conventional segregation analysis (Khush & Kinoshita, 1991). However, their usefulness is limited by the low number of available morphological markers. Further, most of the morphological markers are influenced by environment (Mohan et al., 1997), exhibiting epistemic and pleiotropic effects (Kumar, 1999). Morphological markers thus do not constitute dependable parameters for unambiguous characterization and documentation of the genotypes. Thus, for precision in plant identification / documentation, conventionally used morphological parameters need to be supplemented with precise markers such as biochemical (viz. isozyme) and more preferably molecular (viz. DNA) markers.

❖ Biochemical Markers:

The most commonly used biochemical markers involve isozymes that specifically represent allelic variants of several enzymes viz. isozymes (Mcmillin D. E. 1983; Weeden & Wendel, 1989). Isozyme makers reveal differences in enzyme isoforms detectable in different genotypes or even in the same genotype at different developmental state / tissue. Isozymes are detectable by eletrophoretic separation followed by specific staining that reveals enzyme activity (activity staining). In 1959, Markert and Moller introduced the term isozyme to define each one of the possibly many multiple forms of an enzyme existing in the same population of an organism. Glaszmann (1987, 1988) developed a valuable classification system based on 15
Polymorphic Isozyme loci for resolving rice germplasm into 6 varietal groups. In rice twenty-two Isozyme loci has been assigned to the respective chromosomes through trisomic analysis (Pham et al., 1990; Ranjhan et al., 1988). Isozyme linkage maps have been established for several plant species, including important crops such as Tomato (Tanksley & Rick, 1980) and Rye (Wehling et al., 1985). Once map positions of Isozyme genes have been established, they could be used to locate other genes, which may be linked (Tanksley & Rick, 1980). Use of Isozyme as identifying markers of genotypes is however limited, not only due to their limited number in any crop species but also because they are subject to post translational modifications (Staub et al., 1982), and are often restricted to specific developmental state or tissue. Thus, despite the ease of precise detection, by electrophoresis and specific staining, Isozymes have not been useful as independent makers. The best marker system suitable for precise authentication of genotypes should be free of variation in (a) environment (Mohan et al., 1997) and (b) Variation of stage of life cycle (Winter and Kahl, 1995).

**Molecular markers**:

The best marker system suitable for precise authentication of genotypes should be free of variation due to (a) environmental changes (Mohan et al., 1997) and (b) different stages of life cycle (Winter and Kahl, 1995). A marker system, free of such variations is provided only by DNA based markers; such markers provide dependable genotype characterization. Such genotype specific DNA characterization viz. DNA fingerprinting if correlated with trait-related Morphological / Biochemical parameters may also lead to development of trait-related DNA marker.
To avoid problems associated with use of morphological markers for genotype characterization, molecular markers that are not subject to variation in environment constitute the desirable means of precise identification and authentication of plants (Teixeira da Silva et al., 2005). DNA characterization techniques revealing different levels of polymorphism in DNA of closely related plants lead to development of species specific DNA markers. DNA markers for individualization of genomes typically consist of small DNA fragments; a) generated by amplification of selected segments of the DNA under study and, b) arranged along the gel length due to electrophoretic separation, appearing as bars along a lane on the gel. The patterns thus developed are referred to as 'DNA Fingerprints'; this term was introduced for the first time by Jeffrey et al., (1985) to denote the bar-code like patterns of DNA fragments generated by primer induced amplification of DNA segments followed by visualization of the amplified products after electrophoretic separation. 'DNA Fingerprints' of an individual is unique and this technique is currently considered to be the ultimate tool for the identification of organisms. Various DNA fingerprinting techniques viz. RAPD, AFLP, SSR, ISSR have been used for genotype characterization. Of these, AFLP analysis of genome provide a particularly efficient and reproducible marker system compared with RAPD and RFLP (Garcia-Mas et al. 2000; Garcia et al. 2004; Lanteri et al. 2003) and also with SSR (Jones et al. 1997) markers. A specific pattern for a genotype is taken as the genotype specific DNA Markers / genetic Markers. The most important properties of good quality genetic Markers are: a) Highly polymorphic nature, b) Co-dominant inheritance (which can determine both the homozygous and the heterozygous states of diploid organisms), c) Frequent occurrence in Genome, d) Easy
& fast assay, e) High reproducibility, f) Low or Null interaction among markers allowing the use of many markers at the same time in a segregating population and, g) Easy exchange of Data between laboratories. Depending on the type of study to be undertaken, a marker system can be selected that would fulfill at least a few of the above characteristics (Weising et al., 1995). Such methods of DNA characterization provide for development of good genotype-specific markers. All the methods used for developing DNA Markers provide visual representation of polymorphism between genomes, represented as banding pattern that appear as in fingerprints—hence coinage of the term DNA fingerprinting (Jeffery, 1985). Characterization of genotypes, exploring through the coding and non-coding regions of the genome and represented by DNA fingerprinting provides the ultimate in individualization, thus allowing extensive comparison between genotypes. DNA Markers may be used to properly assess genetic diversity (IRRI, 2002) revealing inter-relationship between genotypes and also help in avoiding duplication (Virk et al., 1996) in genotype accessions. This also helps to promote greater use of stored collections due to more precise characterization of inventories at the molecular level, facilitating detection of allelic diversification along with location of loci on genome maps. DNA markers also provide dependable means, through Marker Assisted Selection (MAS), of monitoring & facilitating plant improvement through breeding based introgression of genes from wild species into cultivated gene pools.
Based on the techniques used for detection of polymorphism in DNA, DNA markers may be two types:

- **Hybridization based markers** – Here DNA polymorphism is generated by hybridizing restriction enzyme-digested DNA to a labeled probe (a DNA fragment of known origin or sequence). This analysis is based on restriction enzyme-revealed differences in genomes seen as different sized DNA fragments generated by specific restriction enzymes. The DNA fragments separated on gels produces specific DNA fingerprinting pattern.

![Diagram of Hybridization based marker analysis](image)

**Figure - Basic principle of Hybridization based marker analysis**

Use of specific "probe" i.e labeled segment of a desirable gene of known sequence are often used to derive useful information regarding the genome. Although providing useful information, the requirement of probes of interest based on prior known DNA sequence makes such methods less convenient for characterizing previously not
characterized (unknown) genotypes. Such studies may also be used for phylogeny exploration and also for introgression studies. Hybridization based markers include Restriction Fragment Length Polymorphism (RFLP), Sequence-Tagged Sites (STS), Expressed Sequence-Tagged (EST), Single Strand Conformation Polymorphism (SSCP) and Restriction Land Mark Genomic Scanning (RLGS).

- **Polymerase Chain Reaction (PCR) based markers**— The earliest used marker system viz. RFLPs have not stood the test of time mainly due to the requirement for prior knowledge in selection of probes. Progressive research in the field of molecular markers have provided alternative means for amplification of discrete DNA fragments using the polymerase chain reaction (PCR) method. Here development of markers involve *in vitro* amplification of DNA sequences or loci with the help of specifically or arbitrarily chosen oligonucleotide sequences (primers) and a thermo stable DNA polymerase enzyme viz. *Taq* Polymerase for the primer initiated in vitro synthesis of small fragments of DNA.
Some of the PCR based markers are Random Amplified Polymorphic DNA (RAPD), Simple Sequence Repeat (SSR), Inter Simple Sequence Repeat (ISSR), Amplified Fragment Length Polymorphism (AFLP) which are used for detecting genetic polymorphism among plant genotypes viz. between species (Williams et al., 1990; Welsh & McClelland, 1990; Aruna et al., 1990) and also between cultivars (Nybom, 1990; Nkongolo et al., 2002) and as well as for studying genetic diversity and population differentiation (O’Hanlon et al., 2000). These PCR based methods require small amount of DNA and are technically simple and cost effective (Dos Santos et al., 1994). RAPD analysis of genomes is thus the conventionally used method for routine
comparative studies on large number of genotypes. More stringent methods of DNA characterization e.g. AFLP are also available for further precision in characterizing specific germplasm. Choice of the method to be used in genome characterization is generally based on the question being asked, the extent of stringency required and the resource available for the study (Karp et al., 1997). Of the different Molecular marker techniques developed till date, RAPD and AFLP in DNA fingerprints are most commonly used molecular markers that are conventionally used in crop Biotechnology.

RAPD has a number of advantages that make it easily applicable for efficient detection of DNA Polymorphism and related identification of trait related DNA Marker. It is relatively inexpensive, fast and reliable and utilizes short random synthetic deoxyribonucleotides of arbitrary sequence as primers for analysis of a wide range of genotypes (Williams et al., 1990; Newbury and Ford-Lloyd, 1993) and does not require specific sequence information for the design of amplification primers. Polymorphism generated by RAPD assays have been used for assessments of genotypic variation (Williams et al., 1990; Welsh & McClelland, 1990); genotype related fingerprinting (Caetano-Anolles et al., 1991; Klein-Lankhorest et al., 1991), cultivar (Caetano-Anolles et al., 1991; Hu and Quiros 1991; Subramanian et al., 2000; Rajora and Rahman, 2003), pathotype (Crowhurst et al., 1991; Goodwin and Annis 1991); systematic classification (Horwell et al., 1994); and genetic mapping (Williams et al., 1990; Reiter et al., 1992). Pedigree evaluation and paternity testing through RAPD markers are useful in resolving disputes regarding germplasm identity, parentage and ownership of variety. In correlation of trait related specific biochemical parameters, the RAPD system of DNA Polymorphism may be used for developing trait related DNA marker.
The main drawback of RAPDs is their low reproducibility (Schierwater & Ender 1993), and hence highly standardized experimental procedures are needed. RAPD analyses generally require purified, high molecular weight DNA, and precautions are needed to avoid contamination of DNA samples because short random primers are used that are able to amplify DNA fragments in a variety of organisms. Altogether, the inherent problems of reproducibility make RAPDs unsuitable markers for transference or comparison of results among research teams working in a similar species and subject. As for most other multilocus techniques, RAPD markers are not locus-specific, band profiles cannot be interpreted in terms of loci and alleles (dominance of markers), and similar sized fragments may not be homologous. RAPD markers were found to be easy to perform by different laboratories, but reproducibility was not achieved to a satisfactory level (Jones et al. 1997) and, therefore, the method was utilized less for phylogenetic analysis nowadays.

AFLP can be applied in studies involving genetic identity, parentage and identification of clones and cultivars, and phylogenetic studies of closely related species because of the highly informative fingerprinting profiles generally obtained. Their high genomic abundance and generally random distribution throughout the genome make AFLP a widely valued technology for gene mapping studies (Vos et al. 1995). AFLP markers have successfully been used for analyzing genetic diversity in many plant species such as peanut (Herselman, 2003), soybean (Ude et al. 2003), and maize (Lübberstedt et al. 2000). AFLP markers are useful in genetic studies, such as biodiversity evaluation, analysis of germplasm collections, genotyping of individuals and genetic distance analyses. This technique is also useful for breeders to accelerate plant
improvement for a variety of criteria, constructing molecular genetic maps for marker-assisted selection and positional cloning for special characters. The strengths of AFLP lie in their high genomic abundance, considerable reproducibility, the generation of many informative bands per reaction, their wide range of applications, and the fact that no sequence data for primer construction are required.

In recent days AFLP can be analyzed in automated DNA sequencer using software based analysis which makes the interpretation more reliable and error free. If done manually (without the use of an automated DNA sequencer), the AFLP study represents a labour intensive method and is thus not selected for large scale comparative genome analysis.

• Single Nucleotide Polymorphism (SNP) as Molecular Marker:
In recent years a novel class of markers namely Single Nucleotide Polymorphism (SNP) has emerged as an important tool in genomics and is increasingly being used as molecular markers for diverse applications. As suggested by the acronym, an SNP marker is just a single base change in a DNA sequence, with a usual alternative of two possible nucleotides at a given position. For such a base position with sequence alternatives in genomic DNA to be considered as an SNP, it is considered that the least frequent allele should have a frequency of 1% or greater. SNPs possess unique merits that make them preferred over the other class of markers. They have rich information content and depict extremely high level of polymorphisms. They are highly amenable to automation thus eventually become cost effective. They occur in virtually unlimited numbers as differences of individual nucleotides between individuals and every SNP in
single copy DNA is a potentially useful marker. Due to their abundance in genome they are extremely useful for creating high-density genetic map. This density cannot be achieved with other genetic marker classes. As SNPs are largely biallelic in nature, which makes them less informative per locus examined than multiallelic markers such as RFLPs and microsatellites (Xiong and Jin 1999) but this problem can be overcome by their abundance which allows the use of more number of loci. Kruglyak (1997) determined that a 4cM map of 750 SNP based markers was equivalent in the information content to a 10cM map of 300 microsatellite markers (Kruglyak, 1997). SNPs in coding region (cSNPs) may have functional significance if the resulting amino acid change causes the altered phenotype. SNP markers associated with phenotype changes pinpoint functional polymorphism (Jehan and Lakhanpaul, 2006). SNPs found in coding region can be used in Marker Assisted Selection (MAS). SNPs present in close proximity to the coding sequences and showing <100% association can also be used in MAS. SNPs are less mutable as compared to other markers. The low rate of recurrent mutation make them evolutionary stable. They are excellent markers for studying complex genetic traits and for understanding the genomic evolution. This also makes them suitable and easier to apply in population genetics (Jehan and Lakhanpaul, 2006).
Although numerous approaches for SNP discovery have been described, including some also currently used for genotyping, the main ones are based on the comparison of locus-specific sequences, generated from different chromosomes. The simplest, when targeting a defined region for instance containing candidate genes, is to perform direct sequencing of genomic PCR products obtained in different individuals. However, on a large scale, this approach tends to be costly due to the need for locus-specific primers, is limited to regions for which sequence data is available, and produces a diploid sequence in which it is not always easy to distinguish between sequencing artefacts and polymorphism when double peaks, as expected in heterozygotes, are observed.
❖ Species / Genotype Specific DNA Markers

DNA Fingerprinting is universally accepted as the ultimate in identification of genotypes and thus documentation of genetic resource. DNA characterization / fingerprinting patterns often referred to as genotype related DNA Markers. DNA markers are stable (Boggini et al., 1990) and do not vary with change in external environmental conditions (Prasad et al., 2000) and are also not affected by internal factors such as phase of life cycle. The limitations of conventional markers in assessing genetic diversity in cultivated and wild plant species have thus largely been circumvented by the development of DNA Markers (Weising et al., 1995). DNA Fingerprinting also proves to be very important in plant taxonomy for species-specific molecular marker identification. Species specific marker have been developed in many plants (Lin et al., 1996, soybean; Waugh et al., 1997, barley; Degani et al., 2001, strawberry; Saunders et al., 1999, 2001, marijuana and opium, respectively; Percifield et al., 2007, Hypericum perforatum L.; Misra et al., 2010, Swertia sp). SNP markers also have been used for development of species specific marker as in case of close related species of Picea (Germano and Klein, 1999)
Trait Related DNA Marker

Gradual disappearances of landraces due to adoption of new varieties for cultivation in available land calls for conservation of precisely evaluated germplasm in gene banks. This is particularly essential for germplasm that are not maintained in cultivation due to change in consumer preference related farmers’ choice. For full utilization of available genetic resource for crop improvement programs with an aim to incorporating desirable traits into otherwise elite varieties, it is essential to precisely evaluate available germplasm with reference to traits of preference. Molecular (DNA) analysis of genotypes correlated with trait of interest allows identification of hitherto unknown genotypes with superior quality. Selection of genotypes through use of Trait Related DNA Markers would be useful for Marker Assisted Selection (MAS). Further, MAS of progenitor and hybrids in breeding endeavors should also help in rapid development of new genotypes through introgression of appropriate genes for enhancing not only market value of consumer’s preference but also survival strategies for successful crop stand establishment under stressful conditions. During the last two decades, DNA-based molecular markers associated with traits of importance have been extensively studied. Some such markers are: one drought tolerance associated RAPD marker (in *Camellia sinensis* – Mishra and Senmandi. 2004), nine SSR and four RAPD markers associated with mite resistance (in *Cocos nucifera* – Shalini et al. 2007), four ISSR markers associated with protein content (in *Morus* sp. – Kar et al. 2008), five markers associated with forage yield and seven markers for fall growth by RFLP and SSR (in *Medicago sativa* – Maureira-Bulte et al. 2007), four SSR markers associated with fiber length (in *Betula platyphylla* – Wang, 2007), twenty three AFLP markers associated with
many agronomic traits (grain and groat yield, panicle emergence, plant height and lodging as well as kernel quality) (in Avena sativa — Achleitner et al. 2008), two AFLP markers associated with resistance and another two for susceptibility against downy mildew (in Medicago sativa— Obert et al.2000).
OBJECTIVES

(i) To establish species specific DNA markers through AFLP for three species of *Zingiber* genus (*Z. officinale* Roscoe, *Z. montanum* (J. Koeing) Link ex A. Dietr and *Z. zerumbet* (L.) Roscoe ex Sm).

(ii) DNA fingerprinting analysis of different wild landraces of ginger (*Zingiber officinale* Roscoe) collected from different localities of North Bengal using AFLP and other appropriate methods viz. RAPD, SNP for molecular documentation of these valuable wild genetic resource.

(iii) To evaluate medicinal potential (active principle content/ antioxidant potential) by appropriate analytical methods to determine the variation in medicinal potential among the different landraces of *Zingiber officinale* Roscoe and *Dendrocalamus hamiltonii* Nees & Am. ex Munro.

(iv) To develop Trait (medicinal potential) related DNA marker(s) for association of DNA fragments with the important medicinal trait in *Zingiber officinale* Roscoe and *Dendrocalamus hamiltonii* Nees & Am. ex Munro. landraces.

(v) DNA fingerprinting of different edible and non-edible species of Bamboo, Collected from in and around Manipur state for documentation and characterization of individual taxa and for assessing phylogenetic relationships among them.