India is one of the world’s seventeen mega biodiversity centers with the presence of over 45,000 different plant species, out of this about 15,000 - 20,000 plants have good medicinal properties of which only about 7,000 - 7,500 are being used by traditional practitioners whether directly as folk remedies or the medicaments of the different indigenous systems of medicine or indirectly in the pharmaceutical preparation of modern medicine (Ballabh and Chaurasia, 2007), but they have not been followed any standard protocols for formulation of drug. Hence, adulteration and substitution have become common. To overcome this situation, measures are needed to promote the cultivation of medicinal plants, to improve methods of collection, to ensure effective quality control and to regulate commerce so as to protect both the producer and the consumer (Olayiwola, 1991).

**Genetic diversity**

Estimation of genetic diversity and identification of superior genotypes are some of the prime objectives of any crop improvement programme. Highly diverse genotypes or accessions can be utilized as parents in hybridization programmes to produce superior varieties / hybrids. Therefore there is a need to evaluate available genotypes for their genetic diversity. The genetic diversity analysis among the genotypes shows the genetic distance and similarity on the whole genome basis that is, difference in their genetic makeup throughout the genome. If the genetic diversity in the germplasm is considerably less, measures should be taken to widen the available gene pool and germplasm and analyzed time to time to reveal genetic diversity.
**Molecular markers**

With the advent of molecular markers, DNA based molecular markers have acted as versatile tools and have found their own position in various fields like taxonomy, physiology, embryology, genetic engineering etc. Thus giving new dimensions to concerted efforts of breeding and marker-aided selection that can reduce the time span of developing new and better varieties and will make the dream of super varieties come true (Swati et al., 2008).

**RAPD markers**

Random Amplified Polymorphic DNA technique has been used for the identification of genetic polymorphism. RAPD markers are amplification products of anonymous DNA sequences using singly, short and arbitrary oligonucleotide primers, and thus do not require prior knowledge of a DNA sequence. Low expense, efficiency in developing a large number of DNA markers in a short time and requirement for less sophisticated equipment has made the RAPD technique valuable although reproducibility of the RAPD profile is still the centre of debate (Fevzi, 2001).

Runo et al., (2004) carried a study using RAPD markers to assess genetic diversity within and between populations in order to suggest appropriate conservation and management strategies. In this study, 8 RAPD primers generated 38 scorable polymorphic bands. AMOVA indicated significant genetic differentiation between populations in the eastern and the coastal regions with 21.1 % of the total variation attributed to differences between these regions. These differences may be due to ecogeographical association with
genetic variation and should be conserved to retain the full breadth of genetic variation of the species.

Gilani et al., (2009) reported the genetic diversity of 7 populations of Withania coagulans from the districts of Kohat and Karak in Pakistan using molecular markers. This finding showed higher diversity within population and lower diversity among population like percentage of populations was 50 to 71.95 % with gene diversity of 0.192 to 0.298. AMOVA result showed genetic diversity among populations 17 % and gene flow 2.494. Conservation measures for the species existence are also recommended for current survival of the limited fragmented populations.

Padmalatha and Prasad, (2007) reported inter and intra population diversity analysis using RAPD markers in Rauwolfia serpentina collected from six locations of Andhra Pradesh, India. A total of 379 markers were amplified. A high proportion of polymorphism (70 %) was found with 23 unique markers. Intra-population diversity in R. serpentina collected from Dulapally mostly exhibited monomorphism, which prove the maintenance of homogeneity. Hence the result of the study can be seen as a starting point of future research on the population and evolutionary genetics of the species.

Rout and Das, (2002) studied the genetic integrity of Plumbago zeylanica using RAPD markers. 20 arbitrary decamers were used to amplify genomic DNA from in vitro and in vivo plant material to assess the genetic fidelity. All RAPD profiles from micropropagated plants were monomorphic and similar to those of field grown mother plants. The results demonstrated that RAPD markers can be applied to rapid evaluation of genetic fidelity of micropropagated plants for the conservation of genetic richness.
**Alam et al., (2009)** analyzed the genetic diversity among the 28 genotypes of Podophyllum hexandrum distributed in 11 geographical regions from Himachal Pradesh using RAPD markers. The genetic diversity was high among the genotypes as measured by percentage of polymorphic bands was 92.37 % and Shanon information index was 0.50. The mean coefficient of gene differentiation was 0.69, which indicated that 33.77 % of the genetic diversity resided within the genotypes. Based on the observed genetic variations among the genotypes of Podophyllum, they recommend for their in situ conservation and germplasm collection expeditions in future conservation plans.

**Palacios and Gonzalez, (1997)** worked in *Limonium dufourii* belonging to the family plumbaginaceae. Genetic variation and populations structure in this species has been studied using RAPD markers. 12 primers provided 124 reliable bands of which 33 were polymorphic among 165 individuals analyzed. Several methods for statistical evaluation have been used for intra and interpopulation analysis of genetic variability. Most of the variation found in this species is due to differences among populations as shown by the analysis of molecular variance. These results have been used to understand the evolutionary and demographic history of *L. dufourii*, which is a requisite in order to establish efficient conservation measures for this species.

*Limonium cavanillesii* is an extremely endangered plant species endemic to the east Mediterranean region of Spain. The genetic variation was analyzed in this species using RAPD. 29 individuals were analyzed and 11 different primers were produced 131 monomorphic bands. This results could be explained both by the apomictic reproductive system of this species and by the passage through a severe bottleneck in recent times, after
which there has been no chance for mutation to restore detectable genetic variation (Palacios and Gonzalez, 1997).

Biswas et al., 2010 reported that the RAPD markers were used to evaluate the genetic diversity in the 14 Phaseolus vulgaris populations from three eco-geographical regions of Bangladesh. Out of the 20 primers only, 6 yielded polymorphic banding patterns. In total, 40 different DNA bands were reproducible. Pair-wise variety comparison of the varieties showed that inter-variety similarity indices for PV004 versus PV005 (98.51) was higher than all other varietals pairs. On the other hand, inter-cultivar similarity index for BARI 01 versus PV009 (59.58) cultivar was lower than all other cultivar pairs. Therefore, the inherent simplicity and efficient of RAPD analyses will be to facilitate the construction of RAPD-based genetic linkage maps in Phaseolus vulgaris.

Finger et al., (2010) estimated the genetic diversity of 49 accessions of Capsicum chinensis through analyses of 12 physicochemical traits of the fruit, eight multi-categorical variables and 32 RAPD primers. Nine clusters were formed from the quantitative data based on the generalized distance of Mahalanobis using Tocher’s method. The accessions were distributed into 14 groups using Tocher’s method and no significant correlation between pungency and origin was detected. Uni and multivariate analyses permitted the identification of marked genetic diversity and fruit attributes capable of being improved through breeding programs.

Mohapatra et al., (2008) assessed that genetic variation in nine populations of T. wallichiana from western part of the Himalayan ranges. Average heterozygosity was 0.3715 and Molecular Variance was 0.0855. Most part of the genetic variation was present
within the populations. However, between populations variation was low but significant, which suggested that the sampled populations might not constitute a single panmictic population. Cluster analysis and Mantel’s correlation revealed that genetic differentiation broadly followed geographic distribution of the populations. *T. wallichiana* thus urgently needs to be conserved using both in situ and ex situ conservation approaches.

**Bilal et al., (2010)** analyzed the intraspecific variation of *Withania somnifera* using molecular markers. Analysis of the genetic diversity provided evidence that wild and cultivated genotypes are not different only on morphological, chemical and molecular basis. This study supports the wild and cultivated genotypes of *W. somnifera* are quite distinct. Thus, it could be concluded that molecular markers may be useful in screening more individuals and populations before any conclusion is drawn in phylogeny.

**Muchugi et al., (2006)** assessed the pattern of genetic variation in *Prunus africana* an important medicinal plant using RAPD markers. AMOVA which employed 39 RAPD markers, indicated that a significantly greater proportion of total country variation for conservation strategies. Data also shed light on the evolutionary history of *P. africana* stands. Data suggested that conservation strategies for *P. africana* should place relatively more emphasis than currently on the status of surrounding phytocoria.

**Salim Khan et al., (2010)** studied the authentication of *Cuscuta reflexa* and its adulterant *Cuscuta chinensis*. Thirty two decamer oligonucleotide primers were used to amplify the genomic DNA isolated from the dried stems as well as seeds of both the species. Out of the thirty two primers used, fourteen did not amplify, eleven gave faint and non-reproducible, while seven gave species-specific reproducible unique bands. The
unique bands obtained in PCR amplification clearly discriminated the two species, having similar morphology and thus, RAPD may serve as a complementary tool for quality control.

Genetic diversity was analyzed using RAPD primers among six accessions of *Azima tetracantha* collected from different locations of Tamilnadu, India. Genetic distances were calculated using Nei’s coefficient. Dendrogram was constructed on the basis of the similarity matrix data by unweighed pair group method with average (UPGMA) cluster analysis. The analysis with RAPD markers revealed wide variation within *A. tetracantha* that reflected a high level of diversity within this species (*Thendral Hepsibha et al., 2010*).

*Barbosa et al., (2010)* evaluated the genetic structure of nine natural populations of *P. coriacea*, totaling 168 individuals, collected in the States of Goiás and Bahia using RAPD markers. This species showed a high level of genetic diversity, with He values varying between 0.259 and 0.338, with an overall mean of 0.296. Analysis by AMOVA revealed that 23% of the total variability was between populations and 77% was within populations. The estimate of apparent gene flow (Nm) was 0.83. The degree of interpopulational differentiation was relatively high, which allows us to recommend a strategy of sampling for the *ex situ* conservation of genetic variability, utilizing a larger number of populations. For *in situ* conservation, they suggest preservation of a larger number of areas in the Cerrado, where this species naturally occurs.

*Mo et al., (2009)* analyzed the genetic diversity and differentiation degree of five *Lonicera confusa* populations using RAPD markers. A total of 100 loci were obtained for
all populations using ten primers, 87.00% of which were polymorphic (PPL = 87.00%). Analyzed by POPGENE, the average percentage of polymorphic loci was 58.86%. Nei's genetic diversity (H = 0.2647) and Shannon's information index (I = 0.4022) indicated that *Lonicera confusa* had a higher level of genetic diversity. Management strategies were proposed for species conservation and resource utilization of *Lonicera confuse*.

The utility of RAPD markers in assessing genetic diversity in 48 genotypes of *Persea bombycina* collected from northeast India was studied. Thirteen RAPD primer combinations generated 93 bands. On average, seven RAPD fragments were amplified per reaction. In a UPGMA phenetic dendrogram based on Jaccard's coefficient, the *P. bombycina* accessions showed a high level of genetic variation, as indicated by genetic similarity. The study concluded that the high level of genetic diversity in the *P. bombycina* accessions may be attributed to the species' outcrossing nature. This study may be useful in identifying diverse genetic stocks of *P. bombycina*, which may then be conserved on a priority basis (*Bhau et al.*, 2009).

*Mossi et al.*, (2007) studied the intra and inter populational genetic variability in three populations of *M. ilicifolia*, focusing on the genetic conservation of this species, which has been threatened by anthropogenic action. RAPD markers were used to analyze 30 plants of each of the three populations collected in the Alto Uruguai Gaúcho region. Fourteen selected primers generated a total of 158 bands, 71.5% of which were polymorphic.

*Rout et al.*, (2006) reported the genetic variation within 15 clones of *Tinospora cordifolia* through RAPD markers. Analysis was made using forty decamer primers. A
A total of 138 distinct DNA fragments ranging from 0.2 to 3.2 kb were amplified using 15 selected random primers. The genetic distance was very close within the clones. Thus, these RAPD markers have the potential for identification of species and characterization of genetic variation within the population. This study will be helpful to know the genetic background of the medicinal plants with high commercial value, and also provides a major input into conservation biology.

**Smita Nair and Keshavachandran, (2006)** characterized 18 phenotypically and biochemically distinct *Gymnema sylvestre* accessions representing different geographical regions of Kerala using RAPD markers. In the RAPD assay, 123 amplified products were generated. Overall, molecular fingerprinting revealed the existence of considerable genetic variations in the *Gymnema* germplasm collected from Kerala. Identification of ideal genotypes and for extraction of drugs by correlating the molecular fingerprints with desirable morphological and biochemical features. It will also help in devising strategies to protect the genetic diversity of this species.

**Padmalatha and Prasad (2006)** reported the molecular variations in *Rauwolfia tetraphylla* collected from 7 locations of Andhra Pradesh, India, which was carried out using RAPD markers. A total of 205 scorable polymorphic markers out of 397 total markers were generated. Polymorphism of 51.6% was found with 3 unique markers. Cluster analysis based on Dice coefficient showed two major groups indicating the high levels of differentiation among accessions which existed independent of geographical distance. Hence, the results of the present study can be seen as a starting point for future researchers on the population and evolutionary genetics of this species. Understanding
such variation would also facilitate their use in various conservation management practices, rootstock breeding and hybridization programmes.

*Costus speciosus* an important medicinal plant species found in the Andaman and Nicobar Islands, was collected from 14 localities for assessing genetic variability using RAPD. Four primers showed appreciable intra species variation or molecular polymorphism at amplicon levels. UPGMA analysis showed 35% variation in the collections, which is seemed to be useful in formulating sound conservation strategies of the precious medicinal plant species under the humid tropics of Bay Islands (*Mandal et al., 2007*).

Genome variability of 23 ginseng plants *Panax ginseng* grown in Primorskii Krai was studied using RAPD method. Using five primers, it was demonstrated that the genetic polymorphism of the cultivated plants is lower than that in nature (7.6% and 10.6%, respectively). Dendrograms of genetic relatedness are in accord with genetic differences between individuals of planted *P. ginseng* belonging to different morphotypes. This suggests that the plant in various areas of the currently fragmented natural habitat and cultivated plants of different origin have retained a significant proportion of their gene pool. The mean genetic heterozygosity may be helpful in estimating gene diversity of the populations of rare and endangered plant species (*Artyukova et al., 2004*).

Sebastian *et al., (2010)* assessed the genetic diversity of *Tylophora rotundifolia* using RAPD markers. Nei’s gene diversity (*HE*) ranged from 0.1778 to 0.5 and the average expected heterozygosity (*HE*) was 0.2643. The mean Shannon index (*Ho*) was 0.3985.
Principal coordinate analysis shows that the first two components account for 61.17% of the total variation. The average percentage of polymorphic bands is 46%. The data indicate a restricted gene flow among populations and calls for immediate conservation measures.

Nidhi Shukla et al., (2003) worked in genetic variability in Boerhavia diffusa between accessions of different geographical origin within the Indian Territory through RAPD markers. Jaccard’s and Nei’s similarity coefficient values amongst the accessions were in the range of 0.22 to 0.89 and 0.33 to 0.93, respectively. Association of RAPD markers with the leaf characteristics, flower colour as well as with geographical locations has been made. This shows that RAPD markers are also useful for the study of genetic structure of Boerhavia populations.

Cunila galioides is a popular aromatic and medicinal plant of South Brazil. 20 populations collected from Rio Grande do Sul and Santa Catarina States, were analyzed by RAPD and generated 239 scorable bands. The analysis with RAPD markers revealed wide variation within C. galioides that reflected a high level of diversity within this species. However, analyzing the present data in the light of paleontological and phytogeographical information, and considering the seed dispersal properties of C. galioides, they suggest an explanation for the actual distribution of the chemotypes of this species and its relation with the genetic variability (Fernando Fracaro et al., 2005).

Arya et al., (2011) analyzed the genetic diversity of C. occidentalis collected from various places of Haryana. 12 RAPD primers gave 111 bands, an average of 9.25 bands
per primer with 79 bands showing polymorphism (71.17%). Dendrogram revealed two major clusters. It showed rich genetic diversity among *C. occidentalis*.

**Muthusamy Govarthanan et al., (2011)** analyzed the genetic diversity among coleus spices using RAPD markers. The opw 6 and opw 7 gave reproducible bands profiles among *C. amboinicus, C. aromaticus and C. forskohlii* and it determines the level of genetic similarity among them.

**Sandigawad** and **Patil, (2011)** analyzed the genetic diversity in *Cinnamomum zeylanicum* Blume, using RAPD markers. 11 primers produced 89 % polymorphic bands. This study showed the variation occurs in *Cinnamomum zeylanicum* due to cross pollination by mammals.

**ISSR markers**

ISSR involves amplification of DNA segments present at an amplifiable distance in between two identical microsatellite repeat regions oriented in opposite direction. The primers used can be either unanchored (**Meyer et al., 1993; Gupta et al., 1994; Wu et al., 1994**) or more usually anchored at 3′ or 5′ end with 1 to 4 degenerate bases extended into the flanking sequences. The annealing temperature depends on the GC content of the primer used and ranges from 45 to 65°C. The technique is simple, quick and the use of radioactivity is not essential. ISSR markers usually show high polymorphism (**Kojima et al., 1998**).

**Catalina Egea - Gilabert et al., (2009)** evaluated the genetic diversity of 50 individuals of *Eruca vesicaria* from 5 accessions of Spain using morphological,
agronomical and ISSR data. A total of 395 DNA bands were produced, 247 of which were polymorphic. Nei’s genetic distance was 0.36. In general, a high variation was observed for most of the 16 morphological and 6 agronomical traits showing significant differences. Morphological parameters together with the high degree of genetic homogeneity found could make the local accessions a good candidate for a future breeding programme.

ISSR technique was employed to study genetic diversity in Italian *Asparagus acutifolius*. A total of 228 polymorphic fragments were used to evaluate genetic variation. The distance UPGMA tree grouped together the genotypes strictly according to their geographical origin, showing that each sample is genetically structured and can be considered as a distinct population. The results suggest that ISSR markers are useful in distinguishing the populations of *A. acutifolius* according to geographical origin, and confirm the importance of genetic studies for designing germplasm conservation strategies (Maria Sica et al., 2005).

**Hui Zhong Wang et al., (2009)** worked in genetic diversity of the genus *Dendrobium* collected from Yunnan region of China using ISSR. In total, 2368 bands were amplified, resulting from 278 ISSR loci with 100% polymorphism at genus level. 31 species were distinguished based on ISSR fingerprinting. UPGMA showed that 31 *Dendrobium* species were grouped into six clusters, indicating the genus was polyphyletic with several well-supported lineages. The high polymorphism and reliable amplification across species demonstrated the utility of ISSR marker for species diagnosis and genetic diversity study of the genus *Dendrobium*. 
Chong Wang et al., (2008) investigated the genetic variation of 14 natural populations of *Gynostemma pentaphyllum* from China using ISSR markers. A total of 194 loci were detected and the percentage of polymorphic bands showed that the genetic diversity was high at the species level (96.39 %) but low at the population level (1.03 %). Nei’s analysis of gene diversity and the percentages of genetic variation among populations were 88.66 % and 88.94 % respectively. Based on the genetic data, effective conservation strategies were proposed for conserving this medicinal herb. Concerning the management of *G. pentaphyllum*, they suggested that *in situ* conservation can be an important and practical measure for maintaining the genetic diversity and that a possibly maximum number of populations can be conserved.

Thul et al., (2011) analyzed the genetic diversity among the different species of *Sida* using ISSR markers. For genetic fingerprint investigation, selected 10 ISSR primers generating reproducible banding patterns were used. Among the total of 63 amplicons, 62 were recorded as polymorphic, genetic similarity index deduced from ISSR profiles ranged from 12 to 51 %. Based on similarity index, *S. acuta* and *S. rhombifolia* found to be most similar (51 %). High number of species-specific bands played pivotal role to delineate species at genetic level. This report summarizes the genotypic diversity and the use of profiles for authentication of species of *Sida* complex.

Genetic diversity was studied in 33 individuals of *Gomortega Keule* from three populations in Cauquencs, a coastal mountain area (35° 58’ S - 72° 41’ W). Fifteen ISSR primers were used to determine the degree of similarity between populations while 70% was within. Nevertheless individuals were clearly clustered in a pattern which reflected a
narrow base of diversity. Three other species from the Laurels order were used in order to provide an external reference as to the degree of diversity. In addition, an external wild population from the native species, peumus boldus, was used to verify the utility the markers. It was shown that the primers are effective in quickly giving an estimate of the degree of diversity of a population, thus giving important topical information relevant to preserving endangered species, aspects of the conservation and management policy for the species in order to maintain the remaining populations and to preserve the genetic resources were discussed (Raul Herrera et al., 2005).

**Comparison on RAPD and ISSR makers**

RAPD and ISSR markers were used to assess the genetic diversity among 10 individuals of *Rehmannia glutinosa*. 17 RAPD primers and 10 ISSR primers, with polymorphic and informative patterns, were selected from a total of 80 RAPD ones and 44 ISSR ones to determine these individuals' genetic diversity. The number of effective loci, the percentage of polymorphic loci, Shannon's Information index (I) and effective number of alleles (Ne) is in turn 109, 61.58 %, 0.3135, 1.3641 for RAPD makers, and 79, 71.82 %, 0.3577 and 1.4037 for ISSR markers. The results revealed that RAPD and ISSR markers were suitable for assessment of germplasm genetic diversity of *R. glutinosa* and ISSR marker was superior to RAPD marker (Zhou et al., 2004).

Domyati et al., (2011) investigated the genetic diversity of some selected medicinal plants germplasam collected along the Western Red Sea coast of Sinai using RAPD, ISSR & AFLP technologies. The study showed that taxonomical locations can be
distinguished for each subspecies according to its molecular fingerprint but it cannot be recognized as a different subspecies.

Genetic diversity was evaluated among 14 cultivars of *Catharanthus roseus* using RAPD and ISSR markers. The RAPD primers resulted in the amplification of 56 bands, among which 46 (82%) bands were polymorphic. In the dendrogram constructed on the basis of both RAPD and ISSR data two clear clusters were obtained. In this study, it was found that RAPD analysis produced more polymorphic bands than the ISSR analysis. The correlation among different markers suggested that the correlation between RAPD and ISSR is lower, i.e., 0.57.

RAPD and ISSR were performed to assess the genetic diversity of the wild orchid *Rhynchostylis retusa*. Among the 35 primers tested 13 RAPD and 7 ISSR primers were selected for the analysis. In total, 74 RAPD and 30 ISSR fragments were generated. High level of polymorphism was recorded in RAPD (76.13%) than ISSR (62.6%). In case of RAPD, Nei’s average genetic identities value for different populations of *retusa* from 0.405 to 0.932, while for ISSR, it ranged from 0.733 to 0.933. The results of this study can be seen as starting point for future research on the population and evolutionary genetics of this species (Parab and Krishnan, 2008).

Genome fingerprinting in 21 *Camellia sinensis* genotypes was carried out using 7 ISSR and 12 RAPD primers. The genetic diversity overall groups (*Hr*) on an average was 0.38, diversity within populations (*Hs*) was 0.27 and genetic differentiation (*Gst*) between populations over all loci was 0.25. In the light of present results, it is wise to conserve the whole diverse populations of the tea germplasm rather than selected individuals from
different populations or only some elite tea clones. The samples should be collected from all the natural populations and develop methods for *ex situ* conservation of the genetic resources of the tea (*Roy* and *Chankraborty*, 2009).

RAPD and ISSR methods were used to detect the genetic diversity of 57 rice accessions which were introduced from 10 countries or areas. For RAPD markers 85 polymorphic bands were produced and percentage of polymorphic bands was 69.4 %. For ISSR marker, 34 polymorphic bands were generated. The result from the clustering analysis by UPGMA indicated that those accessions from the same geographical location were clustered into one group. The estimates of correlation coefficient of RAPD and ISSR based on the genetic similarity matrices were significantly correlated (*He et al.*, 2004).

*Behera et al.*, (2008) carried out genetic diversity studies in 29 accessions of *Momordica charantia* using RAPD and ISSR markers. RAPD primers yielded 208 amplicons of which 76 (36.5 %) were polymorphic providing an average of 2.6 amplicons per primer. ISSR primers provided a total of 6.3 amplicons per primer. The *M. charantia* accessions examined were genetically distinct and these differences provided for the development of strategies for genetic analyzed and crop improvement in this species.

*Dangi et al.*, (2004) reported the genetic diversity in both, *Trigonella foenum-graecum* and *Trigonella caerulea*. 17 accessions of *T. foenum-graecum* and 9 accessions of *T. caerulea* representing various countries were analyzed using ISSR and RAPD markers. Genetic diversity parameters (average number of alleles per polymorphic locus, percentage of polymorphism, average heterozygosity and marker index) were calculated for ISSR, RAPD and ISSR+RAPD approaches in both the species. Dendrograms were constructed
using UPGMA algorithm based on the similarity index values for both *T. foenum-graecum* and *T. caerulea*. The genetic similarity matrices generated by ISSR and RAPD markers in both species were highly correlated ($r = 0.78$ at $p = 0.001$ for *T. foenum-graecum* and $r = 0.98$ at $p = 0.001$ for *T. caerulea*), indicating congruence between these two systems.

**Wang et al., (2008)** analyzed the genetic diversity of wild *Rehmannia glutinosa* using RAPD and ISSR. An average of 16.00 and 19.08 bands were amplified by RAPD primers and ISSR primers respectively, and the percentage of polymorphic bands was 89.58% and 94.32% respectively. *R. glutinosa* from 55 accessions were categorized into 7 clusters by UPGMA method. A high level of genetic diversity was displayed at DNA level and genetic diversity coefficient of *R. glutinosa* from different production areas was 0.63-0.98, and ISSR marker can detect higher genetic diversity of *R. glutinosa* germplasms than RAPD marker.

**Fernando Fracaro** and **Sergio Echeverrigaray, (2006)** assessed the intra and inter population genetic variability of *Hesperozygis ringens* by means of RAPD and ISSR molecular markers. The work demonstrated that *H. ringens* populations are genetically structured, with low gene flow between populations and confirming the fragmentation. Populations from the two areas of occurrence are genetically different. Low intra population variability and heterozygosity were detected, indicating genetic drift and inbreeding. For this purpose it is essential to choose plants on progenitors that will allow the broadening of the genetic base of current populations in conservation areas.

**Yuan et al., (2009)** investigated genetic variability in *Saussurea involucrate* using RAPD and ISSR markers from Tianshan Mountain. Cluster analysis indicated that the
genetic similarity values calculated on the basis of RAPD and ISSR data among the accessions ranged from 0.823 to 0.995 respectively. Therefore, RAPD and ISSR markers are efficient tools in genetic variation assessment and quality control in plant tissue culture process.

**Environmental factors and genetic diversity**

Nianxi et al., (2006) studied the genetic diversity of *Stipa grandis* and its relationship with climatic variables was using the RAPD technique for 90 genes from five natural populations sampled in the Xilingol steppe, China. Sixteen oligonucleotides screened from 100 random primers were used to amplify 310 scorable RAPD loci, which were all polymorphic. By analyzing the RAPD data using POPGENE software, different geographic *S. grandis* populations were studied, which indicated a high level of genetic diversity. Using Pearson correlation analysis, significant (P<0.05) or highly significant (P<0.01) relationship were found between gene diversity indexes and temperature factors (10 cumulative temperature in a year, annual mean temperature and mean temperature in January). Mantel’s tests showed that there was no significant correlation between Nei’s unbiased genetic distance and the geographic distance of *S.grandis* populations (r=0.184, P=0.261). However, there were significant or highly significant correlations between Nei’s genetic distance and the several climatic divergences in pairwise *S.grandis* populations. All results indicated that natural selection resulting from variations in water and temperature was responsible for the adaptive eco-geographical differentiation indicated by the RAPD markers of different *S.grandis* populations, and that immigration and gene drift did not play an important role in affecting the differentiation of *S.grandis* populations.
Genetic risk assessment of 56 samples of the flower from nine main populations on Zhejiang (china) was carried out by using the RAPD analysis. This was to study the ecological characteristics, spatial distribution and genetic features of the seven-sun flower communities and establish a feasible conservation plan. Twenty-one primers screened from 50 yielded 119 RAPD bands with 72 polymorphic products and 60.50 % of total bands. The high level of population variation observed is in contrast to that expected for a primarily outcrossed woody perennial plant and suggests that there may be inbreeding. The analysis showed that the biologic characteristics and habitat fragmentation were the reasons of the great diversity conservation were proposed on the fragmented habitats based on its genetic structure and its biological characteristics on this study (Liu et al., 2007).

Kiambi et al., (2008) investigated the relationship between genetic diversity and eco-geographic variables in Oryza longistaminata. The study clearly established that there is a close relationship between genetic diversity and eco-geographic variables. The study also revealed that genetic diversity is a function of annual rainfall, and peak diversity occurs in intermediate rainfall areas reflecting the ‘Curvilinear theory’ of clinal relationship between the level of genetic diversity and rainfall.