Genetic diversity in agricultural plants

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**Introduction**

Crop plant diversification, whether it is anthropogenic (human) or innately, is essentially based on the population's genetic diversity. The degree of heterogeneity between or within species can be used to define diversity. All crop improvement systems are designed on the already-present intra- and inter-specific variations. If every member of the species had been the same, it's possible that there would be limited room for improvement in the way the plants performed across a range of qualities. Agricultural crops have been extensively examined for for its diversity and Natural variation present in and between crop species. And it is being employed in several crop improvement programs. But as going on, the natural variation among the individual of species is reducing as a result of (i) biased breeding techniques tha are focused to improve just very less numbers of traits (more precisely its yield and its economic yield components), (ii) More often use of few numbers of intentionally chosen lines and parents in variety development programmes. (iii) Selection and introduction of few exceptionally performing lines into many countries, that very often increases genetics likeliness between new developed crop cultivated varieties. Agricultural researchers have serious concern about decreasing genetic variability among the cultivated plant species. It will be difficult to further strengthen agricultural types with less genetic diversity. It will become challenge to break yield limitations and crop plant, and the breeders would not be able to keep up with the demands caused by and increasing population. Climate change and related unforeseen events make genetic diversity even more significant since it may be the source of several unique features that give tolerance to various biotic and abiotic pressures. Numerous major agriculturally significant phenomena, including as heterosis and transgressive segregation, are caused by genetic diversity. For the improvement of defects in commercial variations and the creation of new varieties, diverse lines are required. Therefore, the main objectives of any crop development programmes are to identify the genetically diverse lines if available or to create variations in the line and utilize it in the subsequent research programmes. To make sensible use of genetic diversity in this context, it is essential to have knowledge of all its facts, including the variables influencing genetic variability, various methods of analysis of diversity, their measurement, and the softwares used for statistical data analysis. Numerous articles and reviews have been written that focuses on important issues related to evolutionary divergence changes due to plant breeding, the assessment of genetic variations using molecular markers and statistical tools, and the conservation and use of genetic resources. In this review, an effort is being made to compile broadly applicable ideas in the field of crop plant genetic diversity, which could be absolutely critical for advancing understanding and constructive research.

**Understanding of diversity**

The core of the living domain is diversity. Even maternal siblings don't exactly resemble one another in any way. Variability is the difference in one or more characteristics of the organism. Genetic variety and variability are incorrectly conflated in everyday speech, which is incorrect. Genetic variation is the diversity in DNA/RNA sequences or gene alleles within a species' or population's gene pool. This exhibits itself in several phenotypic forms. In contrary, genetic diversification is used in broad sense that refers to all genetic diversity and richness within and across genotypes that are connected to a single species or between species. The amount of uniqueness of genes in a gene pool can be measured to determine genetic variety, but genetic variation cannot be counted and can only be anticipated to develop. Thus, genetic variability can be thought of as the foundation of genetic diversity. According to CBD, there are three levels of diversity (Figure 1). (i) The ecosystems diversity, which represents variation among various communities of species, is situated at the top of the hierarchy. (ii) The species diversity present within a community, also known as species richness. (iii) The genetic diversity that exhibited within various genotypes of the same species. This is brought on by various individuals developed different phenotypes caused by different alleles of the same gene. According to Swingland (2001), genetic variability is the variation in heritable characters that found in a population of a species. Variation in heritable characters may manifest as change in morphological, anatomy, physiological behaviour, or biochemical compositions.



**Figure 1** Hierarchy of diversity.

**Genetic diversity and its importance**

The underpinning for plant survival in nature and crop development is genetic diversification. Plant breeders are able to generate new and improved plant varieties with desirable characters (traits), preferably high yielding varieties, large seed size etc. with other attributes like disease and pest resistant varieties and photosensitivity in cultivars. Preferably natural genetic variability within crop species has been exploited since the beginning of agriculture to meet the food demand for subsistence. Later, the emphasis turned to producing extra food to feed expanding populations. To ensure that the people have balanced diet, the yield and quality characteristics of important food crops are currently being prioritised. Breeding of climatic adaptable varieties is becoming increasingly crucial as the environmental situation are changing lately. The presence of genetic variability, which may be founds in wild related species, breeding lines, closely related species and mutant lines, etc., that can act as a source of beneficial genes of desirable traits and help plant breeders to create varieties that are more tolerant to climatic changes. Breeding plants that are resilient to climatic changes demands the development of some peculiar characters *i.e.* resistant to new insect pests and diseases, withstand environmental stress etc. The genes of interest should be conserved in the form of cultivars and germplasm resources for future breeding programme. Because there are many genetic variations present within and between crop plant species, that breeders may choose superior genotypes as parents in hybridization programmes or to use directly as new varieties. To achieve heterosis and produce transgressive segregants, two parents must have genetic variability. Plant breeders can create plant cultivars for specific traits like qualitative traits enhancement and resistance to biotic and abiotic factors that affect plant yield, thanks to genetic diversity. Additionally, it makes it easier to generate new lines for non-traditional purposes such biofuel types of sorghum, maize, etc. Diversity is crucial for crop plants' ability to adapt to many habitats, particularly those with shifting climatic circumstances.

**Crop genetic diversity**

Genetic diversity is crucial for any crop enhancement programme and the creation and management of genetic diversity is central base to crop breeding. The multivariate analysis by means of Mahalanobis’s D2 statistic for estimating genetic divergence has been emphasized by many workers (Anand and Murty, 1968; Kole and Chakraborty, 2012; Gadi et al. 2020). The more diverse the parents, within overall limits of fitness, the greater are the chances of obtaining higher amount of heterotic expression in F1(Chakraborty and Bhattachraya, 2018; Sunny et al. 2022) and broad spectrum of variability in segregating generations (Anand and Murty, 1968, Singh et al, 2016a).

Genetic divergence was not associated to geographic differentiation, according to the genotype distribution pattern in the various clusters. Numerous genotypes those are geographically adjacent to one another fall into separate clusters, and vice versa. The propensity for such clustering to emerge notwithstanding borders of geography demonstrated that regional isolation was not the only factor causing variation in natural population (Rao et al., 1980). One explanation for the grouping of genotypes from various eco-geographical places into one cluster is the potential for free exchange of breeding materials. However, unidirectional selection used for a specific trait or a set of related traits in many locations may yield a comparable phenotype that can clump together into one cluster regardless of their location (Singh and Gupta, 1968). Different genotypes of common geographic origin may form distinct clusters due to their parentage, developmental features, history of selection, and various out-crossing rates (Arnold et al., 1996).

Crossing between the intra-cluster genotypes is most likely to lead to a significant amount of heterosis in the F1 generation and to produce a wide range of recombinants in the segregating generation, deciding to take genetic divergence, per se performance of genotypes, as well as cluster mean, into cognizance (Sunny et al. 2022).

PCA is a statistical method for locating and getting rid of duplicate genotypes with comparable traits (Singh et al., 2016b). It provides a precise indicator of genotypic differences and permits the natural classification of genotypes. One group may be allocated to each genotype in PCA, which is its main advantage (Singh et al., 2016b; Debnath et al. 2022). This test is also used to divide a large number of variables into significant components and determine how much each contributes to overall variation. Therefore, PCA was used to examine the connections among the various attributes and to highlight the features that co-segregated.

Induced mutagenesis, particularly using gamma (γ) irradiation, plays an important role in generating genetic variability in crops including cereals, pulses and oilseeds for desirable traits of economic importance and these variants were used further in cross breeding programme of several seed propagated crops (Chakraborty and Paul, 2012) and also meets up challenges including world food and nutritional security (Kant et al. 2020).

Hybridization is important tools for generation of genetic variability. As a result, information on genotypic and phenotypic variation, heritability, and genetic advance are crucial for the possibility of direct selection as well as the prediction of the inheritable nature of the traits. This will increase the success of transferring the desirable traits through hybridization. The F1 rice varieties with high grain yield, semi-dwarf to medium stature, high tillering behaviour, resistance to lodging, and pleasant aroma were selected by Sunny et al. (2022) after extensive research on aromatic rice.

**Forces affecting genetic diversity**

Natural recombination is the primary mechanism through which genetic variety is perpetuated. During meiosis, recombinations occur when homologous chromosomes cross throughout and establish new pairs. Plants' genetic diversity is driven by a range of environmental factors. Changes that happen in allelic frequency in a population and that impact on genetic diversity of the population are ongoing effects of evolutionary processes such as selection, migration, genetic drift and mutation. Some alleles become more common as a result of genetic manipulation during domestication, while others become less common. Therefore, domestication lessens genetic diversity relative to wild populations. Significantly influencing genetic diversity is natural selection too though. Selection that is both directional and stabilising tends to reduce genetic variety, while selection that is both asymmetric and disruptive tends to increase it. It has been suggested that mutation can significantly boost genetic diversity. Symptoms of qualitative mutation include dramatic alterations in structure and function at the molecular and cellular level. It's possible that mutation also causes many chromosomal abnormalities. Genetic variety is manifested in the form of phenotypic variation, which is brought about by smaller sub-lethal or non-lethal abnormalities. The method by which agricultural plants reproduce also has an impact on the species' overall genetic diversity. While outbreeding enhances genetic variety, inbreeding decreases it. Reduced genetic diversity occurs when uncommon alleles are lost caused by genetic drift. A species' genetic variation is influenced not only by the number of individuals but also by their geographic dispersal. The greater the geographical separation between people, the less likely it is that they have the same DNA. Use of several hybridization methods such as wide-hybridization, hybridization between incompatible types can increase genetic diversity. Conversely, hybridization within the same species has effects of inbreeding depressions.

**Diversity analysis techniques**

Morphological indicators, cytological indicators, biochemical indicators, and molecular characterization can all be used in a biodiversity analysis. As with their counterparts, morphological markers have continued to be used in biodiversity studies. These were all-natural variations of a single plant species. Ultimately, genetic diversity was measured in part by looking at cytological and biochemical variations within a species' genotypes. Since the emergence of genomic information, molecular markers have dominated efforts to quantify genetic differences.

1. **Indicators of morphology**

Germplasm lines, purelines, enhanced varieties, etc., are cultivated according to a predetermined experimental design for the intention of these analyses. Because morphological traits are so significant in deciding a plant's agronomic value and taxonomy classification, this process requires morphological characterization of numerous entries established in the field. Direct, low-cost, simple, and requiring no fancy equipment, morphological evaluations are a fantastic choice. However, it's costly because of the enormous amounts of land and human labourers needed over time. Their limitations in comparison to other methods include environmental sensitivity and subjective characterisation. These traits are typically dominant or recessive in nature, have a measurable biological impact, and render some physical variants impotent.

1. **Cytological indicators**

There are many researches have been done in cytological characteristic, such as chromosome size, centromere position, arm ratio, heterochromatin patterns, banding patterns etc. In maize, potato, lentil, radish, and other plants, several cytological traits have been used to evaluate genetic diversity of the species. However, due to their scarcity and low resolution, these have only a few applications in genetic diversity analysis.

1. **Biochemical indicators**

It comprises the segmentation of proteins or isozyme polymorphisms into specified banding patterns. Not the genes, but distinct alleles' products are reflected in the isozymes. These isozymes can be utilised as genetic markers to map other genes and can be transferred onto chromosomes. This methodology of evaluating variety is quick and only needs a small plant tissue sample for analysis. However, they are few in number, vulnerable to changes in the climate, and unable to be used to create a full genetic map.

1. **Molecular indicators**

This involves investigating genotypic variations at DNA/RNA level. Many types of molecular markers can be used for multiple reasons because of their unique features. They are usually categorized as PCR- and hybridization-based. New generations of markers based on platforms for sequences or arrays have recently been created. They can also be categorised based on their activity and expression as (i) neutral markers (ii) genetic markers and (iii) functional markers. In wheat, barley, apples, rice, pearl-millet, and other species, chloroplast microsatellites are used to measure genetic diversity at the intra-specific level. Contrarily, due to its quantitative scarcity, mitochondrial DNA from plants has been shown to be an inadequate tool for assessing genetic variation. Due to their great repeatability, superior genomic coverage, automation-friendliness, neutrality, and lack of environmental sensitivity, molecular markers are the method of choice for assessing genetic variation.

**Measures of genetic diversity**

1. **Genetic base**

Coefficient of Parentage or Coefficient of Correlation are terminology used to describe the genetic foundation of every crop. These are obtained by pedigree records of varieties that have been released and show how often a line appears in the commercial variations of a specific crop. Coefficient of Parentage is defined as the chance that alleles of two individuals are similar by descent. Less variability will be present in the segregating generations that arise from a cross between individuals with high Coefficient of Parentage, and vice versa. Coefficient of parentage values range from zero, where two cultivars have no genetic relationship at all, to one, where two cultivars share all of their alleles. Genotypes can be grouped into groups with a similar genealogy using the COP data matrix. The formula shown below (Falconer & Mackay, 1996) can be used to compute the coefficient of parentage (COP) or coefficient of correlation (rxy) for all pairwise combinations of genotypes.



Where fxy is a co-ancestry coefficient and Fx and Fy are the inbreeding coefficients of X and Y, respectively. For the purpose of calculating the coefficient of parentage, multiple algorithms were devised by Delannay *et al.,* Murphy *et al.,* and Cox *et al.* Another comparable metric is called "Relative Genetic Contribution (RGC)," which is calculated by dividing a selection's genetic make-up into notional percentages attributable to several ancestors. The average of the relative genetic contributions made by a certain ancestor to all kinds that have been published is used to assess the ancestor's mean genetic contribution. Cumulative relative genetic contributions are produced over time by adding up the mean relative genetic contributions throughout time. The assumptions behind the relative genetic contribution measurement are (i) the unrelatedness of forebears and (ii) the equally likely transfer of 50% of parental genes to the children.

Numerous crop studies have shown that the released cultivars of various crops in India have a limited genetic diversity. For instance, the lines IR-8 and TN-1 in rice, Bragg in soybeans, Spanish improved in groundnuts, Pb-7 in chickpeas and T-1 and T-190 in pigeonpeas all commonly showed up in commercial varieties of the aforementioned commodities that were made available in India. The genetic diversity and genetic basis are roughly estimated by the frequency of emergence of specific lines.

1. **Genetic separation**

Nei was the first to define genetic distance as the distinction between two things that can be explained by allelic variation. The term "extent of gene differences among populations that are quantified using numerical values" was later added to this definition (1987). A more thorough definition of genetic distance was offered by Beumont et al. as any quantitative measure of genetic difference calculated between genotype individuals or groups, either at the sequence or allele frequency level. Simply said, there is less genetic distance between genotypes that share a lot of genes. The most popular statistic technique to determine the genetic separation between individuals (genotypes or populations) from morphological data is the euclidean or straight-line measure of distance. In-depth descriptions of several genetic distance measurements have been provided by Mohammadi and Prasanna. The following definition of the Euclidean distance between two genotypes is mathematical:



Where, d (a, b) is the Euclidean distance between genotype a and b; *Xi* is the observation on *ith* phenotypic character, and *Yi* is the observation on *ith* phenotypic character.

Another measure of genetic diversity in inbred lines was developed by Smith *et al*. Which can be expressed as below:



Where, d (a, b) is the Euclidean distance between genotype a and b; *X1* and *X2*are the values for *ith*trait for inbred lines a and b and *Var X(i)* is the variance for *ith* trait over all inbred.

PCR amplification data of molecular markers are also be used to calculate genetic distance:



Where genotypes a and b's Euclidean distance, d (a, b), is the; Xai is the allele frequency for individual i; r is a constant determined by the coefficient used, and Xaj is the frequency of the allele a for individual j.

1. **Molecular variability**

When a locus/allele model may be utilised to evaluate molecular marker data, allelic diversity is used. In these circumstances, data is utilised to create a binary matrix for additional research. Polymorphic loci (p) percentage, the average number of alleles per locus (n), the average anticipated heterozygosity (H), and the content of polymorphism information can all be used to define allelic diversity (PIC). In terms of all loci, including polymorphic and monomorphic loci, the percentage of polymorphic loci (p) provides an estimation number of polymorphic loci.



Where Np is the number of polymorphic loci (polymorphic and monomorphic) and Nt is the total number of loci.

Mean number of alleles per locus (n) is represented as follows:



Where, n­­i is the number of alleles at ith locus and *k* is the number of loci.

Polymorphism information content (PIC) is an indirect estimate of number of alleles per locus. This can be expressed as below:



Where, Pi is the frequency of ith allele at any particular locus.

**Genetic diversity assessment with statistical methods**

For the evaluating the genetic diversity a species among various strains, variations, or entries, multivariate statistics are used. These methods can be used to evaluate genetic diversity since they have a very solid theoretical foundation and can provide the most accurate information about the actual genetic distances between genotypes. These methods can be used to evaluate genetic divergence, divide germplasm into groups, and choose diverse parents to produce transgressive segregants. Here are some examples of multivariate approaches in use:

1. **Analysis of metroglyphs**

Anderson created a semi-graphical method known as "Metroglyph analysis" for demonstrating genetic variability among several lines. With this approach, each genotype is represented by a circle (referred to as a glyph) with a defined radius and rays extending from its edge. Every variable has a specific place on the glyph. The index score of the variate is represented by the ray's length. This method makes use of a variety of trait variants such that the length of the rays on the glyph determines how much trait variation there is. The value of a genotype's index score is used to evaluate that genotype's performance.

1. **D2  Statistics**

Mahalanobis created this method, which is also known as the generalised distance. By grouping genotypes into various clusters, this approach minimises the amount of comparisons between genotypes. The crucial condensation method is used to convert correlated data into uncorrelated variables in order to determine D2 values. The Mahalanobis distance, in its most basic form, is a measurement of the separation between two locations in a space defined by two or more correlated variables. The Mahalanobis distances between the points in a normal two-dimensional scatterplot, for instance, would be the same as the Euclidean distance if there are two uncorrelated variables. In a 3-D display, we could also just use a ruler to measure the separations between points if there are three uncorrelated variables. We are no longer able to plot the distances for more than three variables. The Mahalanobis distance will sufficiently account for the correlations in those situations, but the simple Euclidean distance is not a suitable measurement.

1. **Cluster studies**

The study makes the assumption that the data are discontinuous. It shows the pattern of grouping of genotypes on the basis of genetic similarity between genotypes based on phenotypic characteristics. It is used to distinguish between distinct groups and put related lines or genomes in one group. It is based on the following techniques: (i) single linkages (SLCA), (ii) complete linkage (CLCA), (iii) weighted paired group method using arithmetic mean (WPGMA), (iv) single linkages (WPGMA), (v) weighted paired group method using centroid (UPGMC), and (vi) median linkage (MLCA). Comparing breeding materials employed in accordance with pedigrees and calculated findings found to be most consistent with recognised heterotic groupings, UPGMA and UPGMC provide more accurate grouping information than the other clusters.

1. **Principal component analysis (PCA)**

One way to describe principal components analysis (PCA) is as a data-reduction method that works with quantitative types of data. Multi-correlated data are converted by PCA into another set of uncorrelated variables for additional research. Eigen-values generation and mutually independent eigen-vectors (principal components), sorting data in descending order of variance size, is the basis of this method. These elements produce scatter plots of data that have the best characteristics for examining underlying variability and correlation. If X1, X2,..., Xn are the study's original data, then principal components can be described as:



With the condition such that a112 + a122+………..+ a1n2 = 1
Similarly other principal components can be defined as:



With the condition, ap12 + ap22+………..+ apn2 = 1

This method is merely a means to an end for additional investigation. No statistical model or original variate distribution assumptions are needed for this procedure. It is important to note that this analysis is not necessary when the initial variables are uncorrelated. When distinct variables have the same unit, this is most appropriate. Standardizing all the variables allows for the avoidance of the challenges presented by various scales. Each variable is standardised by dividing it by the estimated standard deviation. It has been noted that PCA use in genetic diversity investigations has increased recently.

1. **Principal coordinate analysis (PCoA)**

Schoenberg created another ordination technique that is somewhat akin to PCA. The Gower or Euclidean distances used to estimate the distances between all of the data points are matrices that the PCoA frequently discovers the eigen-values and eigen-vectors of. It creates a 2-D or 3-D scatter map of the samples with the least amount of distortion possible, with the distances between the samples in the plot reflecting their genetic distances. This has the drawbacks of being complex functions of the original variables and I not offering a direct connection between the components and the original variables.

1. **Canonical research**

It was Bartlett who initially proposed the concept of canonical analysis. By removing linear correlations between characters, it improves prediction by assuming additivity in all characters. The method to explain the relationships between two sets of variants was put out by Hotelling. Using the same variance-covariance matrix, Seal characterised it as "a process of differentiating as clearly as feasible between two or more multivariate normal universes." The benefit of this approach is that it is scale-neutral. Furthermore, when compared to PCA, group variable comparison is simpler.

1. **Factor evaluation**

On the basis of their shared variance or inter-correlations, this method breaks down large amounts of data into smaller, more manageable groups. It is predicated on the idea that correlated variables capture the same quality or trait. It is used to explain the covariance relationships between numerous variables in terms of a small number of fundamental random variables known as factors. The basic objective of factor analysis is to use the fewest available factors and the fewest possible variables within each factor to explain as much variance in a data set as possible. The elements with Eigen values larger than 1.0 are taken into consideration for analytical interpretation.

1. **Communication Analysis**

Similar to PCA in certain ways, correspondence analysis (CA) is an ordination technique that uses numbered or discrete data. It makes advantage of the Chi-square distance between the research objects. Correspondence analysis allows for comparison of relationships with counts of taxa or associations with counts of taxa. It has been discovered that several techniques for genetic diversity analysis produce comparable outcomes and may therefore be used interchangeably. Chandra analysed the results of the Metroglyph analysis and the Mahalanobis D2 distance and discovered a startling consistency in the grouping of flax genotypes. On the basis of this, he proposed using metroglyph analysis for preliminary grouping in several germplasms. Ariyo used factor, PCA, and canonical analysis to examine the degree of genetic variation in okra. She discovered that the results from factor and PCA were comparable.

**Software for analysing genetic diversity**

Software of many different kinds has been created to analyse genetic diversity. Multivariate statistics is the foundation of the majority of these programmes. The majority of PC-compatible software is freely accessible online. Various programmes are offered, according to Tanavar et al. Below is a brief description of some of the software:

**(i) SAS**

SAS provides the package for several multivariate methodologies. It includes cluster analysis, principal component analysis, correspondence analysis factor analysis, and canonical correlation, among other things. PROC PRINCOMP or PROC PRINQUAL can be used to do principal component analysis. You may do correspondence analysis, canonical correlation analysis, and factorial analysis, respectively, using PROC CANCORR, PROC CORRESP and PROC FACTOR.

**(ii) SPAR 3.0**

The Statistical Package for Agricultural Research was created by IASRI, New Delhi (SPAR). In addition to other modules, it has the ability to do multivariate statistics.

**(iii)  past**

Hammer *et al*. created this software for paleontological statistics. It is a no-cost, user-friendly, all-inclusive package. principal coordinates analysis, Parsimony analysis with cladogram plotting, detrended correspondence analysis, PCA, geometrical analysis, time-series analysis etc. are some of the functions present in PAST.

**(iv) Numerical Taxonomy System for personal computer (NTSYSpc)**

It is a well-known algorithm that has been applied in numerous scientific fields for analysing genetic diversity from molecular marker data. It uses a 0, 1 genotypic data matrix and is based on similarity indexes. It is employed in a number of applications, including principal coordinate analysis, principal component analysis, and cluster analysis.

**(v) Genetic Analysis in Excel (GenAlEx**)

It is an easy-to-use software that is based on Excel. It was created for use in diversity genetics investigations using multilocus markers, allozyme, AFLP, SSR, SNP and DNA sequencing data. It accepts three different types of data: codominant, dominant, and geographic. Marker index, haploid diversity by locus, frequency by locus, observed and expected heterozygosity, allelic patterns, fixation index, allele list, private alleles list, Shannon index, haploid diversity by population, haploid disequilibrium and pairwise Fst, Nei's genetic distance, PCA, etc. are all included in the GenALEx analysis.

**(vi) Popgene**

It is another another approachable tool for studying genetic variation in and within natural populations. It makes it possible to carry out intricate analyses, generate statistical data that is supported by science, and analyse the population genetic structure using the desired markers or features. It accepts codominant, dominant, and quantitative qualities as three different types of data. Polymorphic loci, Gene frequency, effective allele number, gene diversity, Shannon index, genetic distance, homozygosity test, F-statistics, gene flow (based on Nei coefficient), dendrogram (based on UPGMA and neighbour-joining method), neutrality, and neutrality are all included in the analysis

**(vii) Power marker**

It was created especially for the analysis of population genetics using SNP/ SSR data. Data setup is relatively simple and may be done by importing data from Excel or other formats. This software includes population structure, association analysis, phylogenetic analysis, and tools.

**Genetic diversity-related threats**

A sizable collections of valuable crop plant germplasms (roughly 6 million) are kept in gene banks around the world. Less than 1% of them have been used by breeders. This is a result of a biased approach to plant breeding that prioritises a small number of crucial features that affect yield at the expense of other qualities. Numerous other germplasm accessions with a variety of characteristics are still untapped. This causes agricultural types to have a limited genetic foundation, which increases their genetic fragility and can be disastrous in the face of shifting climatic conditions. A sizable area of land has been converted to monoculture as a result of increased mechanisation in agriculture. This has taken the place of many local types and landraces from farmers' fields, which are the genetic sources of many beneficial features. In addition, the potential for producing natural variety in the form of wild forms and wild relatives of crop plants has been diminished due to the degradation of natural habitats in the name of urbanisation and modernization. A few lines have been employed exclusively in the breeding of new varieties and hybrids due to the commercialization of agriculture, virtually to the exclusion of other lines. As a result, many cultivars now have plateaued yields and are more vulnerable to various biotic and abiotic stressors. The source of crucial genes, such as those for biotic and abiotic challenges, is genetic variety, which takes the shape of various landraces and germplasm

**Conclusion**

To feed the growing population on shrinking cultivable land, plant breeders face challenges. In this aspect, modern plant breeding has had some success. However, because of the limited genetic diversity of cultivated types in many crops, it has led to genetic fragility. Therefore, a large shift in plant breeding that focuses on a variety of genetic resources is required. Genetic variety is generally recognised as a distinct area that can contribute to the security and availability of food and nutrition for existing population. Determining what to protect and where to conserve it will be easier with a better grasp of genetic variety. Crop plant genetic diversity is the cornerstone for the long-term creation of new types. Therefore, it is necessary to use various statistical approaches to characterise the distinct genetic resources and use them in the breeding programme. For accurate characterisation of germplasm resources, morphological and molecular data are used. High throughput molecular marker technologies have made it possible to characterise more germplasms in a shorter amount of time and with less resources. To enable better interpretation, the analysis is based on statistical tools. D2 statistics and PCA are the most popular statistical methods for morphological data because of how simple they are to interpret. For the analysis of molecular diversity, PCoA is widely used. The main software programmes used are POWERMARKER and GenAlEX because to their great informativeness. The diversity shown by various analyses can also be used in interogression of alien genes for particular phenotypes, heterosis breeding, and transgressive breeding.

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