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OPINION

Molecular marker-based conservation – An appraisal

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In the last two decades, researchers and planners have demonstrated the essential link between biodiversity and future food security. This is evidenced by the sudden increase of growth in the number of genetic resource conservation programmes all over the world from about 10 in 1972 to over 100 in 1992. Many of these programmes aim at looking into variations that occur within germplasm, based on mostly biochemical (isozymes), molecular (Restriction Fragment Length Polymorphisms, RFLPs; Random Amplified Polymorphic DNAs, RAPDs) and other data. The application of these techniques in conservation is the best spoken topic of the day. Unfortunately there has been very little attention paid to answer the question of how the variations are to be used and what kind of studies in evaluating the variations are relevant.

Generally, almost all germplasm conservation programmes aim at documenting variability both at inter and intra-specific levels. Data is gathered for as many accessions as possible and relationship patterns (dendrograms) will be constructed based on different statistical packages. Definitely we would expect variability and sensitive techniques like RAPDs will pick up differences between individuals also. This will not help much but add

on to the already confusing studies of biodiversity, especially genetic conservation.

What is often forgotten in these conservation programmes are the utilitarian aspects. Variations if not used are lost. But using variability is only a possibility if we understand where they will be useful. Our efforts on conservation will succeed only if we are to understand the characteristics of the population or species, dynamics of the ecosystem. Character-based selection and subsequent molecular analysis would greatly help us identify specific individuals and markers for characters. This will not only aid marker-aided selection but will also help us adopt suitable conservation strategies. But often variability data pertaining to individual differences will be of little use, except in telling us if there are variants. Variants identified as such cannot be used as it is difficult to relate it to performance.

Looking at genetic variability for conservation need to take into account the sampling methodology and account for characters of performance in the field. Recently we studied genetic variations in traditional rice germplasm tolerant to salinity, using molecular markers. Molecular variation, in relation to salt tolerance has helped us generate suitable methods based on the genetic distances

between varieties and variants within varieties, to recommend them in breeding programmes. Another point of interest to discuss is to evaluate the construction of dendrograms. Our experience shows that with different statistical packages, we can generate different dendrograms from the same data-set. So we should be careful to consider one analytical package that will be common and uniform to evaluate the results relating to genetic variability.

What is important in scientific research is not to generate data but to carefully plan an experiment using appropriate tools and discuss the results with the logic of its application. At least for conservation genetics the programmes will fail if we only look at generating variability data completely forgetting that characters are better manifestations of differences and more useful practically. Maybe that is where our farmer-breeders are more intelligent than us in selecting and breeding besides maintaining and using variability, through on-farm conservation.

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