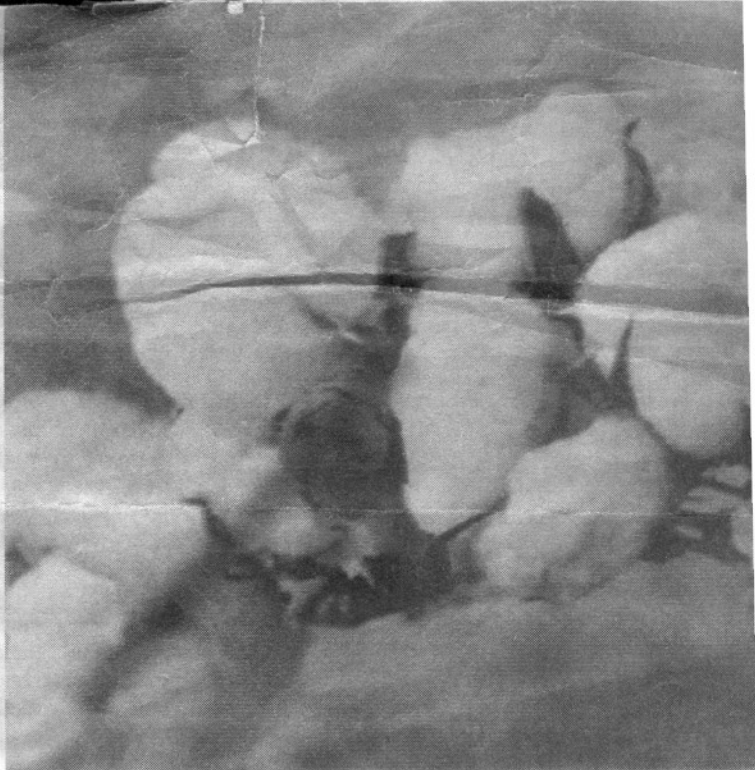


says that bio-technology has found new methods to overcome pests, which harm the production of Cotton

Within the last 100 years the world has seen the rise of genetics as a scientific discipline. In crop

sciences, sequencing genetic material (genomics) has been promoted using *Arabidopsis* as a model plant. *Arabidopsis* is a weed of mustard family that is found all over the world. It is easy to grow and use for genetic experiments and it has one of the smallest genomes (140 million base pairs). Similarly, in crop plants, the study of genomes at DNA level will open new horizons in conservation of plant biodiversity and their genetic enhancement. Moreover, it will accelerate the utilisation of candidate genes available at these gene banks through plant genetic engineering without barriers across plant species or other living kingdoms. The study has an edge over the traditional methods in that it has unlimited gene pool, is more precise and delivers the product in a shorter time.

Cotton is the most important textile fibre crop of Pakistan. The cotton production is seriously hampered by the infestation of diseases and insect pests. Among diseases, recent epidemic of cotton leaf curl virus disease (CLCD) is a major threat to the cotton crop in Pakistan. The CLCD was first observed during 1967 from Multan area and remained in low intensities until 1987. By the early 1990s, the CLCD had become the major limitation to cotton production in Pakistan and has now spread both south into the Sindh region and across the border into the states of Punjab and Rajasthan in India. The symptoms caused by the CLCD are leaf curling, darkened veins, vein swelling and galls which frequently develop into cup shaped leaf like structures on the under sides of leaf. It has been reported that CLCD is associated with a whitefly-transmitted geminivirus. Epidemics of the CLCD compelled to devise new strategies in cotton breeding programs in the country. The national R and D programmes though started late (1994) enabled



A hope for sustained production

us to recover the losses made by the CLCD.

The estimation of genetic diversity, is one of the potential buffers to control the outbreak of any natural disaster in advance and allows populations to adapt to changes in climate and other local environmental conditions. The recent epidemic of CLCD in Pakistan was also caused by lack of genetic diversity. The genetic similarity among the local elite cotton cultivars released prior to CLCD (1994) epidemics was in the range of 81.5 per cent to 93.41 per cent, which was declared alarming. A study was planned at National Institute for Biotechnology and Genetic Engineering (NIBGE), Faisalabad on the assumption that most of the newly released disease resistant cotton cultivars of Pakistan have been developed by crossing exotic resistant cotton

genotypes followed by selection of superior plant types, making a relatively small gene pool for all cotton cultivars. A total of 20 different newly released cultivated cotton varieties were selected to estimate the genetic diversity. A narrow genetic similarity (82-95 per cent) was found among the cotton cultivars on the basis of DNA fingerprinting technology. The close genetic kinships are quite alarming and may impede further plant improvement. This information about genetic relatedness will be helpful for cotton breeders to avoid any chance of elite germplasm becoming genetically uniform and endangering long-term productivity gains.

On long term basis, genetic control is inexpensive and a durable strategy to overcome the problem of any epidemics. The

visible or measurable traits, called the phenotype. This process is difficult, slow and costly. As a shortcut, plant breeders now use marker-assisted selection (MAS). To help identify specific genes, scientists use what are called molecular markers. The markers are a string or sequence of nucleic acid which makes up a segment of DNA. The markers are near the DNA sequence of the desired gene. Since the markers and the genes are close together on the same chromosome, they tend to stay together as each generation of plants is produced. This is called genetic linkage. This linkage helps scientists to predict whether a plant will have a desired gene. If researchers can find the marker for the gene, it means the gene itself is present. As scientists learn where each of the markers occurs on a chromosome, and how close it is to a specific gene, they can create a map of the markers and genes on specific chromosomes. The

MAS reduced five years (almost half time period) to release these varieties. Thus for the sake of expediency, a total of three DNA markers against the CLCD were detected with the application of modern tool of biotechnology. These DNA markers could be used by national breeding centres to predict resistant plant types. Application of the MAS has several other advantages. Firstly, it does not require the isolation of the targeted gene, which often takes years and considerable resources to accomplish. Secondly, most of the gene constructs such as those commonly used in many transformation studies are now covered by intellectual property right (IPR), hence are not freely available for varietal development. Thirdly, the progeny developed by MAS in general does not suffer from adverse effects such as over- or under expression and transgene silencing, which are now fre-

The second major threat to cotton production is the infestation of insect pests. Among these, chewing and sucking pests are very serious. Many control measures have been reported to check or at least keep the damage below threshold level, which includes varietal non-preference for pests (presence or absence of nectars, hairiness, leaf size, shape etc.), cultivation practices, biological control, management of beneficial insects etc. collectively referred as Integrated Pest Management (IPM). The modern tool of biotechnology such as recombinant DNA (rDNA) technology can overcome the barrier of linkage drags of conventional breeding. For the purpose, gene isolation is the way before the commencement of rDNA technology. Gene(s) could be isolated through map-based cloning which needs DNA markers at both side of the gene of interest. In the present studies, a DNA marker linked with velvet hairiness and a DNA marker linked with extrafloral nectarilessness trait was detected. For the isolation of genes, additional DNA markers are needed to saturate the region around the genes. For this purpose, with the help of new robust biotechnological tool such as Bioinformatics are needed to expedite the process of finding new DNA markers linked with the genes of interest. Thus, additional funds must be allocated to undertake cutting edge technology to effectively face the serious challenge of feeding the rapidly growing world population in the next millennium.

This work was part of on going project of cotton biotechnology conducted in Plant Biotechnology Division, NIBGE Faisalabad, Pakistan. All these efforts and R and D at other cotton research centres are expected to put Pakistan again on top of the cotton producing countries. In this regard government should also seriously consider the approval of insect resistant Bt cotton in the country. Experts say the new technology would change the cotton production trend. It would increase quality cotton production and bring down the cost of production. The study reported here laid the foundation of cotton genomics study in the country. ■

—The writer works in the National Institute for Biotechnology and Genetic Engineering (NIBGE) Faisalabad



application of biotechnology have considerably shortened the time to release a variety. For instance, rice varieties Cadet and Jacinto was developed with the application of

quently reported with transgenic plants. The performance of the progeny resulting from MAS is therefore much more predictable than those from transformation.

*Agriculture
The Nation
19.5.02*

genetic control of different traits is controlled by heritable units called genes, composed of genetic material, the DNA. All of the plant's genes together make up its genome. Some traits, like flower colour, may be controlled by only one gene. But other more complex characteristics, like crop yield or starch content, may be influenced by many genes called quantitative trait loci (QTLs). At the commencement of the present studies and till now, reports on the number of gene(s) against the disease are scanty. A systematic study was performed at NIBGE to understand the number and role of various genes in developing resistance against the disease. We found that three genes control the disease without any role of extrachromosomal inheritance.

Traditionally, plant breeders have selected plants based on their