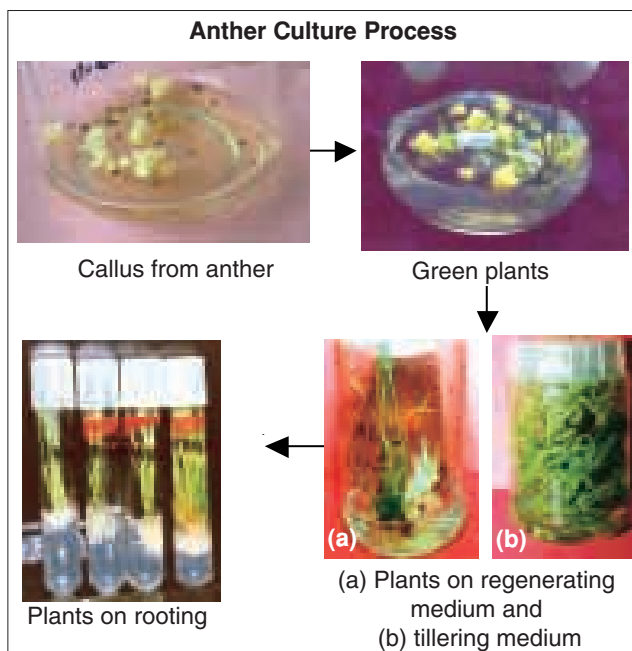


6. The Role and Use of Biotechnology

WARDA started using biotechnology tools in early 1990 with the establishment of an anther-culture laboratory. Anther-culture enabled researchers to overcome the fertility problems associated with interspecific crosses between *Oryza glaberrima* and *O. sativa*, and to rapidly fix these lines (known as

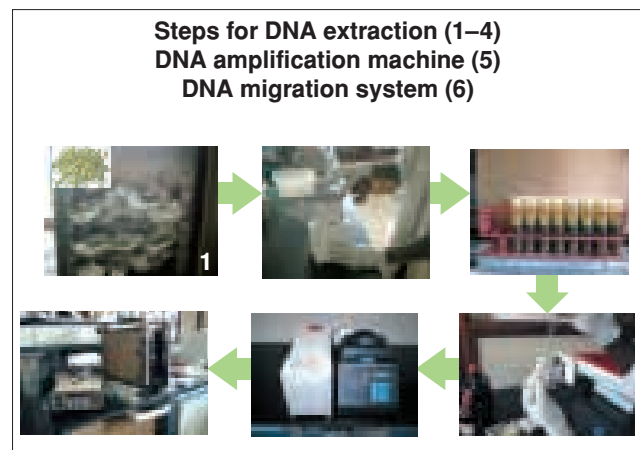
institutions to characterize pathogen strains using serological and molecular tools.

The efficiency of marker-assisted selection (MAS) for the transfer of the major rice genes is now widely recognized. Work at WARDA determined that PCR-based markers—simple sequence repeat, express sequence tag, cleaved amplified polymorphism sequence—are necessary to develop an MAS system. WARDA has also used mapped molecular markers called microsatellites to characterize alien variation in lines derived from interspecific crosses (NERICA lines). Graphical genotyping of all lines showed introgression of *O. glaberrima* alleles in all NERICAs. On average, the introgressed segments were not small (mean size of 20 cM) and were randomly distributed on the 12 chromosomes, indicating that recombination occurred frequently and that there was no genome-wide barrier to recombination during meiosis. The mean of *O. glaberrima* alleles across all NERICA lines analyzed was 12%. The maximum level of heterozygosity was low (1.5%) showing that the NERICA lines were fixed in almost all parts of the genome.



NERICAs). Facilities to undertake molecular-marker studies based on polymerase chain reaction (PCR) were added later. These markers were applied in breeding to assist in the development of lines combining high yield potential with stress tolerance.

Antibodies were developed and made available to NARS partners for detecting RYMV in rice plants. Collaboration was developed with advanced



Genetic studies and mapping showed that RYMV resistance in the variety Gigante (*O. sativa* subsp. *indica*) is based on a single recessive gene on chromosome 4. Fine mapping identified three microsatellite markers close to the RYMV resistance gene (2 cM), potentially allowing for easy transfer of the resistance from Gigante into other genetic backgrounds by MAS. To create high-yielding popular varieties resistant to RYMV, the RYMV resistance gene was transferred into three widely grown *O. sativa* varieties. F₁ hybrids and BC₁F₁ plants were developed, and MAS allowed the selection of BC₁F₁ resistant plants to develop BC₂F₁ progenies.

In the medium term, WARDA's goal is to have an autonomous biotechnology laboratory undertaking a wide range of applied research. Specifically it is anticipated that such a laboratory will:

- characterize disease and pest population structures and develop methods for rapid selection of disease and pest resistance;
- improve the understanding of the genetic control of resistance to pests and diseases, and determine whether distinct sources could be combined to obtain more durable resistance;
- develop near-isogenic lines (NILs) from advanced lines to determine the genomic function of introgressed regions;
- evaluate the genetic-resources collection of WARDA with a view to detecting duplicates, ensuring a representative core collection, facilitating evaluation, and complementing the seed genebank with a molecular genebank;
- undertake a wider range of biotechnological research with advanced institutes to improve the understanding of the genetic basis of resistance to complex abiotic constraints such as drought and salinity;
- work with national partners to help develop appropriate strategy and methodology for risk assessment of genetically modified organisms (GMOs);



- provide training in plant biotechnology to students and NARS personnel, and act as a bridge between advanced laboratories in the North and biotechnology laboratories in Africa.

The Rockefeller Foundation and the Government of Japan have been supporting the development of biotechnology capacity at WARDA.

Further reading

Albar, L., M.-N. Ndjiondjop, Z. Essibak, A. Berger, A. Pinel, M. Jones, D. Fargette and A. Ghesquière, 2003. Fine genetic mapping of a gene required for rice yellow mottle virus cell-to-cell movement. *Theoretical and Applied Genetics* (107): 371–378.

Chipili, J., S. Sreenivasaprasad, A.E. Brown, N.J. Talbot, M. Holderness, Y. Sere, S.K. Nutsugah, J. Twumasi and K. Dartey, 2001. Characterisation of the blast pathogen populations at rice screening sites in West Africa. In: S. Sreenivasaprasad and R. Johnson (ed.) *Major Fungal Diseases of Rice, Recent Advances*, pp. 9–20.

Lorieux, M., M.-N. Ndjiondjop and A. Ghesquière, 2000. A first interspecific *Oryza sativa* × *O. glaberrima* microsatellite-based genetic linkage map. *Theoretical and Applied Genetics* 100 (3–4): 593–601.

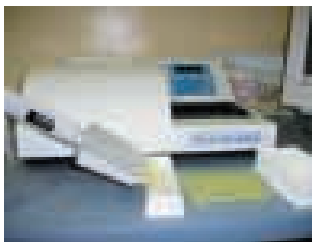
Ndjiondjop, M.-N., C. Brugidou, S. Zang, D. Fargette, A. Ghesquière and C. Fauquet, 2001. High resistance to rice yellow mottle virus (RYMV) in two cultivated rice cultivars is correlated to the failure of cell-to-cell movement. *Physiology and Molecular Plant Pathology* 59: 309–316.

Nguessan, P., A. Pinel, M.L. Caruana, R. Frutos, A. Sy, A. Ghesquière and D. Fargette, 2000. Evidence of the presence of two serotypes of rice yellow mottle sobemovirus in Côte d'Ivoire. *European Journal of Plant Pathology* 106: 167–178.

Nguessan, P., A. Pinel, A.A. Sy, A. Ghesquière and D. Fargette, 2001. Distribution, pathogenicity and interactions of two strains of rice yellow mottle virus in forest and savanna zones of West Africa. *Plant Disease* 85: 59–64.

Pinstrup-Andersen, P. and M.J. Cohen, 2000. Biotechnology and the CGIAR. Paper prepared for presentation at the international conference on Sustainable Agriculture in the Next Millennium – The Impact of Modern Biotechnology on Developing Countries, sponsored by Friends of Earth Europe, Oxfam Solidarity Belgium, and the Dag Hammarskjold Foundation, Brussels, Belgium, 28–31 May 2000.

ELISA reader



Training NARS on ELISA

