CBN-VI

Sixth International Scientific Meeting of the Cassava Biotechnology Network

8-14 March 2004 CIAT, Cali, Colombia

Adding Value to a Small-Farmer Crop

Abstracts

International Scientific Meeting of the Cassava Biotechnology Network (6, 2004, Cali, Colombia). Abstacts. Cali, CO: Centro Internacional de Agricultura Tropical (CIAT). 2004. p. 208

Descriptores AGROVOC:

1. Biotecnología vegetal. 2. Redes de investigación. 3. Subproductos. 4. Mercadeo. 5. Análisis de costos y beneficios. 6. Recursos genéticos vegetales. 7. Fitomejoramiento. 8. Variación genética. 9. Resistencia genética. 10. Conservación del germoplasma. 11. Cultivos alimenticios. 12. Estrés. 13. Tecnología postcosecha. 14. Tapioca. 15. Cultivo de tejidos. 16. Transformación genética. 17. Marcadores genéticos. 18. Transferencia de tecnología. 19. Países en desarrollo. 20. Africa. 21. Asia. 22. Colombia. 23. América Latina.

Descriptores Locales

1. Agrobiodiversidad. 2. Investigación participativa. 3. Técnicas moleculares.

Categoría de Materia AGRIS:F30 Genética vegetal y Fitomejoramiento.
A50 Investigación Agrícola

AGROVOC Descriptors:

1. Plant biotechnology. 2. Research networks. 3. Byproducts. 4. Marketing. 5. Cost benefit analysis. 6. Plant genetic resources. 7. Plant breeding. 8. Genetic variation. 9. Genetic resistance. 10. Germplasm conservation. 11. Food crops. 12. Stress. 13. Postharvest technology. 14. Tapioca. 15. Tissue culture. 16. Genetic transformation. 17. Genetic markers. 18. Technology transfer. 19. Developing countries. 20. Africa. 21. Asia. 22. Colombia. 23. Latin America.

Local Descriptors

1. Agrobiodiversity. 2. Participatory research. 3. Molecular techniques.

AGRIS Subject Categories: F30 Plant genetics and Breeding.
A50 Agricultural research.

Clasificación LC.: SB 211 .C3 I58

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Development of a diversity array technology (DArT) chip for cassava

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Genetic resources, mostly held by small farmers represent a critical resource for the future productivity and stability of production of the crop. How to evaluate and use in a systematic manner the vast amount of variability present in cassava is still a challenge to most cassava breeding programs. Genotyping micro-array technologies offer the highest throughput available up to date. One of them diversity array technology, DArT ™ (CAMBIA), is sequence-independent (low-input) and allows the fingerprint of an individual's genome based on a high number of polymorphic sites spread over the genome. These screening procedures should allow testing of thousands of individual samples in a speedy manner. Plant materials used for the generation of the DArT chip was chosen to represent a broad as possible diversity of the cultivar, a few genotype of its wild progenitors and 2 wild species were included to capture a large number of polymorphic fragments. They include 14 accessions from Brazil, 14 from Colombia, 4 from Guatemala, 2 each from Nigeria, Cuba, and Ecuador, Peru and Thailand respectively. Others include, one accession each from Argentina, Bolivia, Costa rica, Fiji islands, Indonesia, Mexico, Panama, Venezuela, and USA. Six and 2 improved varieties were included from CIAT and IITA respectively. Three enzyme combinations, /PstI/BstNI, PstI/ApoI, and PstI/TaqI) were tested in a preliminary experiment to determine the best enzyme combination,the library from PstI/BstNI gave the largest number of polymorphic clones (132), followed by *Taq*I (112) and ApoI (69). In total, 313 candidate polymorphic clones were obtained in the preliminary experiment. Libray expansion yielded 440 polymorphic clones (14.3%), for the PstI/TaqI array, and 554 polymorphic clones (18.0%) for the PstI/BstNI array, both consistent with the polymorphism frequency in the smaller in the preliminary experiment. A dendrogram was drawn for the 80 cassava samples based on analysis with the polymorphic clones fromm both arrays. There were differences between the two dendrograms obtained, inspection of the data suggests that the BstNI array contains a higher proportion of clones derived from repetitive sequences than PstI/TaqI array. Typing using repetitive sequences introduces a bias in genetic diversity analysis due to over-representation. The PstI/TaqI array does not show a high proportion of clones with repeated sequences and can be used as a routine genotyping tool for genetic diversity analysis.