

WEST AFRICAN JOURNAL OF APPLIED ECOLOGY

Volume 2

Editors

S. K. A. Danso

Ecological Laboratory, University of Ghana, Legon

and

M. K. Abekoe

Department of Soil Science, University of Ghana, Legon, Ghana

Editorial Board

T. W. Awadzi, Department of Geography and Resource Development, University of Ghana, Legon, Ghana

A. Tidiane Ba, Institute des Sciences de l'Environnement, Faculte des Sciences, Université Cheik Anta Diop, Dakar, Senegal

J. J. Baidu-Forson, United Nations University Institute for National Resources of Africa, University of Ghana, Legon, Ghana

H. Breuning-Madsen, Institute of Geography, University of Copenhagen, Denmark

A. Emechebe, Ahmadou Bello University, Zaria, Nigeria

E. Laing, Department of Botany, University of Ghana, Legon, Ghana

R. Lal, Department of Agricultural Engineering, Ohio State University, Columbus, USA

Y. Ntiamoa-Baidu, Department of Zoology, University of Ghana, Legon, Ghana

N. Sanginga, International Institute for Tropical Agriculture, Ibadan, Nigeria

Published by

Ecological Laboratory, University of Ghana, Legon

Sponsored by

Danida

2001

Isozyme Variation and Genetic Diversity at 3 Phosphoglucose-Isomerase (PGI) [Glucose-1-phosphate] Gene Loci in Nine Cowpea Accessions (*Vigna unguiculata* (L.) Walp) from Three Agroecological Zones

I. K. Asante and E. Laing

Department of Botany, University of Ghana, P. O. Box 55, Legon, Ghana

Abstract

Isozyme variation and genetic diversity in three loci of the phosphoglucose-isomerase [glucose-1-phosphate] gene loci were studied within nine accessions of cowpea [*Vigna unguiculata* (L.) Walp] landraces by means of starch gel electrophoresis. These nine accessions, namely 87/139, 89/142, 87/157 (Deciduous forest accessions), 87/30, 87/37, 87/55 (Guinea savanna accessions) and 87/77, 87/81, 87/83 (Sudan savanna accessions) were sampled from three agroecological zones. The three PGI loci *PGI2**, *PGI3** and *PGI4** are polymorphic. Results show that there was clinal trend in all the three enzyme loci, and the cowpea landraces studied showed ecogeographical racial differences in the incidence of genes for the phosphoglucose-isomerase enzyme. Genetic distances within Deciduous forest, Guinea savanna and Sudan savanna agroecological zones were 0.068, 0.048 and 0.128, respectively. Between Deciduous forest and Sudan savanna zones accessions genetic distance ranged from 0.030 to 0.234 with a mean genetic distance of 0.128 ± 0.020 , between Deciduous forest and Guinea savanna zones accession genetic distance ranged from 0.007 to 0.127 with a mean value of 0.053 ± 0.010 , while between Guinea savanna and Sudan savanna zones accessions genetic distance ranged from 0.052 to 0.139 with a mean value of 0.087 ± 0.011 . The observed pattern of allozyme distribution is explained by Neo-Darwinian evolutionary models, in which natural selection plays a predominant role.

Introduction

Isozymes are direct gene products and are the most widely used molecular markers by plant breeders. They have been used by several workers to identify biochemical species, as well as population and cultivar markers (Kephart, 1990). Among other advantages isozyme analysis is simple and low cost; isozymes have simple molecular basis of polymorphism and a reasonable genome coverage of 10 to 50 loci per species. The technique has been useful in the breeding of cultivated crops. By using isozyme analysis Gutierrez *et al.* (1998) determined genetic relationships among 24 collections of common bean (*Phaseolus vulgaris* L). Twenty-four collections, 21 of Andean origin and three from Central America were charac-

terized. Eight out of 22 isozyme systems showed good resolution. Six of the enzymes malate dehydrogenase (MDH), shikimate dehydrogenase (SKDM), ribulose-bisphosphate (Rubisco; RBCS), isocitrate dehydrogenase (IDH) and glutamate dehydrogenase (GDH) were polymorphic. The two others, glutamate oxalacetate transaminase (GOT) [aspartate aminotransferase] and endopeptidase (EP), were monomorphic.

Isozymes have also been useful in the study of *Vigna unguiculata* and the wild forms of the species (Panella & Gepts, 1992; Pasquet, 1993; Vaillancourt & Weeden, (1993). Danquah *et al.* (2000) applied isozyme markers to study genetic polymorphism in four accessions of sor-