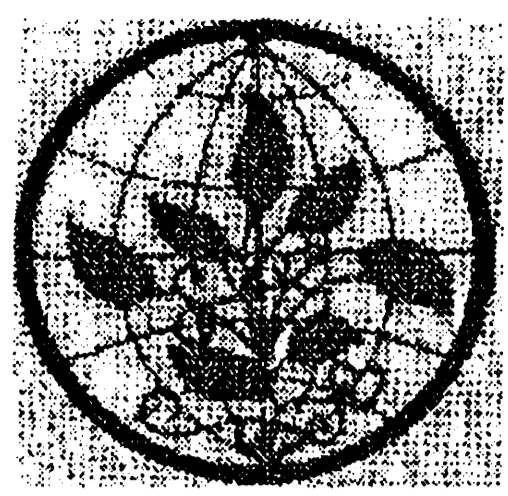


MASTER NEGATIVE NUMBER: 09296.72

Arunachalam, V., Prabhu, K. V. and Sujata, V.
Efficiency of Isozymes Markers in Genetic
Differentiation of Brassicas.

*In: Proc. 2nd International Crop Science
Congress, November 17-24, 1996, New Delhi.
New Delhi, India: Oxford & IBH Publishing
Co., Abstract No. P7-018, pp. 191.*

Record no. E-27



2nd International Crop Science Congress

CROP PRODUCTIVITY AND SUSTAINABILITY- SHAPING THE FUTURE

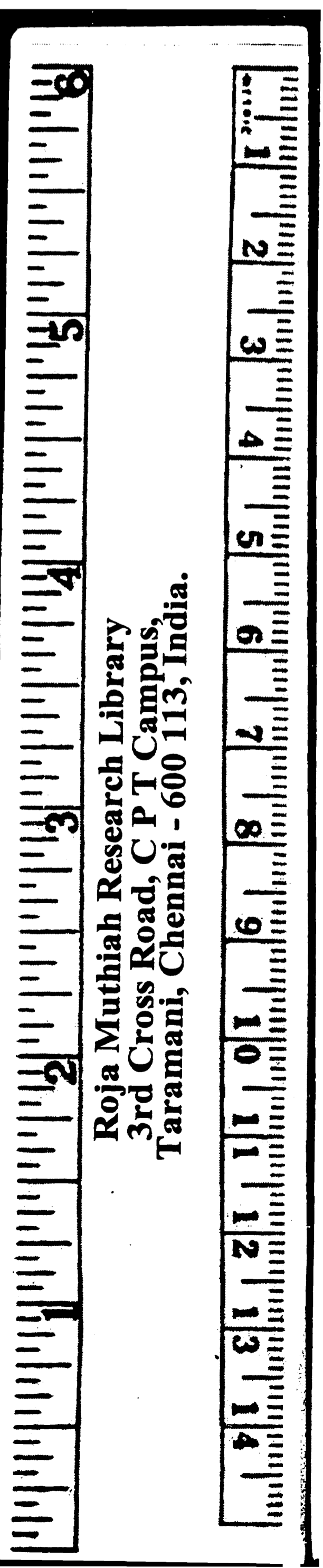
17-24 November, 1996, New Delhi, India

ABSTRACTS OF POSTER SESSIONS

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EFFICIENCY OF ISOZYME MARKERS IN GENETIC DIFFERENTIATION OF BRASSICAS

K.V. Prabhu, V. Sujata and V. Arunachalam, Division of Genetics, Indian Agricultural Research Institute, New Delhi 110 012, India

Plant breeding has the major components (i) choice of parents to produce heterotic F_1 S and (ii) progeny profile containing transgressive segregants. Intervarietal genetic divergence provides one method of characterising parents. Earlier work has shown that this could be efficiently done on the multivariate distance statistic (D^2). Methods have been developed to order intervarietal divergence into 4 different groups; 2 belonging to 'High' (H1 and H2) and 2 belonging to 'low' (L1 and L2) categories based on the distribution D^2 values. It was conceptually shown that H x L crosses generate high frequency of desirable heterosis. Any method that could delineate the 4 groups with high efficiency without the need to generate field data upto harvest would be useful in resources efficient breeding strategy. Isozyme marker traits (IST) – Number of bands, relative absorption, standard error (relative absorption), relative mobility and standard error (relative mobility) identified earlier qualify to rank as QTs. It is shown that the grouping based on divergence using IST has a high commonality with the base grouping defined by 6 QTs identified by stepwise multiple regression. Using experimental data on QTs identified by stepwise multiple regression. Using experimental data on QTs and ISTs on enzymes, esterase, anodal peroxidase and cathodal peroxidase the efficiency of IST genetic differentiation has been illustrated in brassica.

