ABSTRACT

CLASSIFICATION OF GENETIC DIVERSITY IN MAIZE GERMPLASM BY PHENOTYPIC CHARACTERISTICS AND DNA FINGERPRINTING

BY

SARAYUT TREERAT

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Chairman : Asst. Prof. Prawit Puddhanon

Department/Faculty : Agronomy/Faculty of Agricultural Production

Seventeen S_1lines of corn (*Zea mays*) were classified by using RAPD technique with 6 primers. Sixty-eight bands were found in the DNA profiles. All DNA bands were scattered between 512-1200 bp and polymorphic DNAs; OPF20a-1050 and OPF20b-600 were clearly visible. All DNA bands were later grouped by UPGMA method using NTSYS-pc V 2.02e analysis software. As a result, six groups of genetic similarities ranking from 1.00 to 0.727 were obtained as follow:

Group 1 : high similarlity at 1.000 with seven 7 lines : G10, G39, G42, G52, G44, G40 and G41

Group 2 : similarity at 0.909 with two lines : G24 and G32

Group 3 : similarity at 0.889 with two lines : G27 and G35

Group 4 : similarity at 0.875 with four lines : G3, G26, G20 and G34

Group 5 : similarity at 0.833 with one line : G19

Group 6 : least similarity at 0.727 with one line : G28

The experiment on the phenotypic characteristics of S_2 lines in corn was conducted at Maejo University, Chiang Mai during the dry season in 2000. The experiment which included 36 varieties, was carried out in a 6x6 double lattice design with statistical analysis and cluster analysis on phenotypic characteristics divided into two categories. The first category consisted of 11 quantitative traits such as ear diameter, ear length, number of row per ear, 100 grain weight, ear number per plant, plant height, ear height,

tasseling date, silking date, shelling percentage and yield characteristics. As a result, of the differentiation at 50 linkage distance (Squared Euclidean distance) 5 groups were obtained. In particular, numbers of Group A, namely : G39, G40 and G42 were matched with Group1 through DNA Fingerprinting. As for the second category which consisted of quantitative traits such as grain color, 8 groups were formed at 1.2 linkage distance. Moreover, some members of Group 1B : G24, G29 and G30 were also matched with those Group 3A in quantitative traits.

It is suggested that conservation and classification of plant germplasm could be performed on phenotypic characteristics simultaneously until there are no differences in the traits, then DNA classification could be employed.