Identification of association between microsatellite markers and Downy mildew resistance in elite maize inbred lines in Thailand

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Association study is an alternative to linkage mapping in traditional biparental populations which relied on the variation and extent of linkage disequilibrium contrast with variation in the two parents of the mapping population. The objective of this research was investigating genetic diversity within germplasm of maize inbred lines in Thailand and identifies SSR markers associated with downy mildew resistance.

1. Screening resistance/susceptible maize inbred line to artificial infection

Sixty maize inbred lines from public and private sectors were screened to the spreader-row technique for field inoculation at two locations (NCSR, NFR). Percentage disease is determined by the ratio of the total number of plants with systemic infection to the total number of plants multiplied by 100 at NCSR (a) and NFR (b) (Fig. 1) . The analysis of variance show significant variation among entries. There was a significant location effect as well as a significant entry by location effect. The analysis of variance results were used to measure broad sense heritability. The value was 0.50.

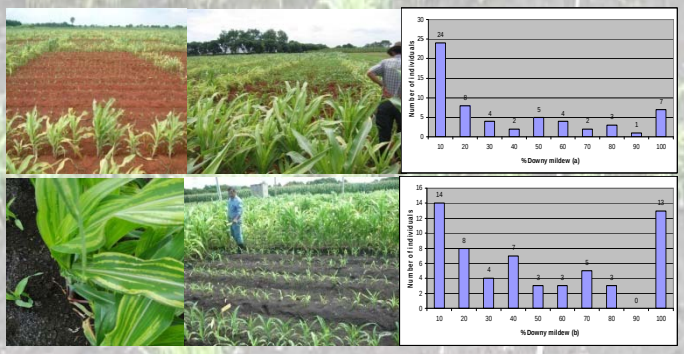

Fig. 1 Comparison of distribution of % Downy mildew for individual maize inbred lines at NCSR (a) and NFR (b)

2. Identified grouping of genetic diversity within germplasm of maize inbred lines by using SSR markers

All of 48 SSR markers produced a total of 489 alleles among 60 entries (Fig.2) . A dendrogram (Fig.3) was generating using the UPGMA algorithm with GD matrix that all of the entries could be group in to three clusters.

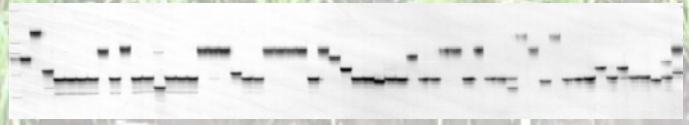

Fig.2 A silver-stained polyacrylamide gel (6%) at the umc1014 locus among 60 maize inberd lines

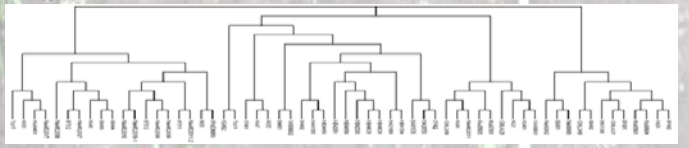

Fig.3 Dendrogram representing the relationship among the 60 maize inbred lines as revealed by Neighbor joining tree analysis based on Nei (1983) using PowerMarker 3.25 program

3. Population structure analysis

Population structure was estimated using the software program STRUCTURE (Pritchard and Wen 2007). The number of subpopulation (K) was difficult to determine the optimal number of subgroups (Fig.4) and Fig.5 , since the posterior or probabilities for the number of clusters increased steadily.

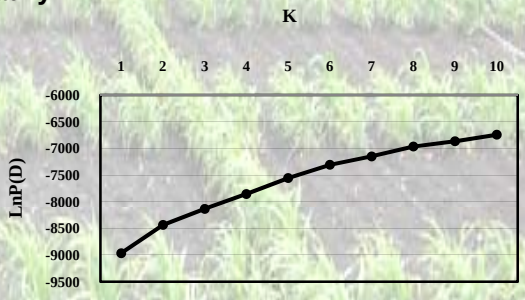

Fig.4 Plot of the average logarithm of the probability of data, Ln *(PD)*, averaged over the replicates

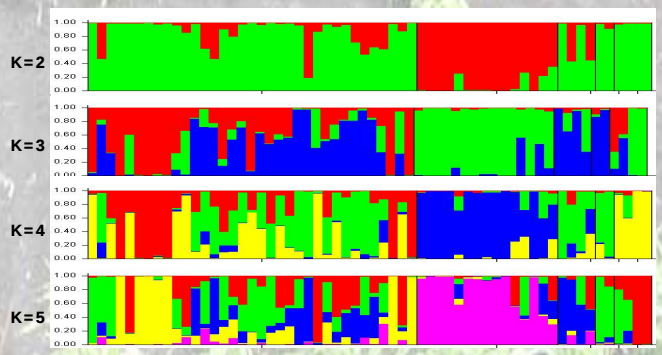

Fig.5 Estimated population structure of maize inbred lines in Thailand. Each individuals is represented by a thin vertical bar plot, that can be partitioned into K colored segment, representing a single individual estimated membership to the K cluster.

4. Association between Downy mildew resistance and SSR markers

Association analysis was carried out with the TASSEL 2.1 software program (Buckler et al. 2007). Three significant SSR/trait associations were detected with the Q GLM model over 2 locations. These marker loci could explain 38.25–70.93% of the total variation.

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