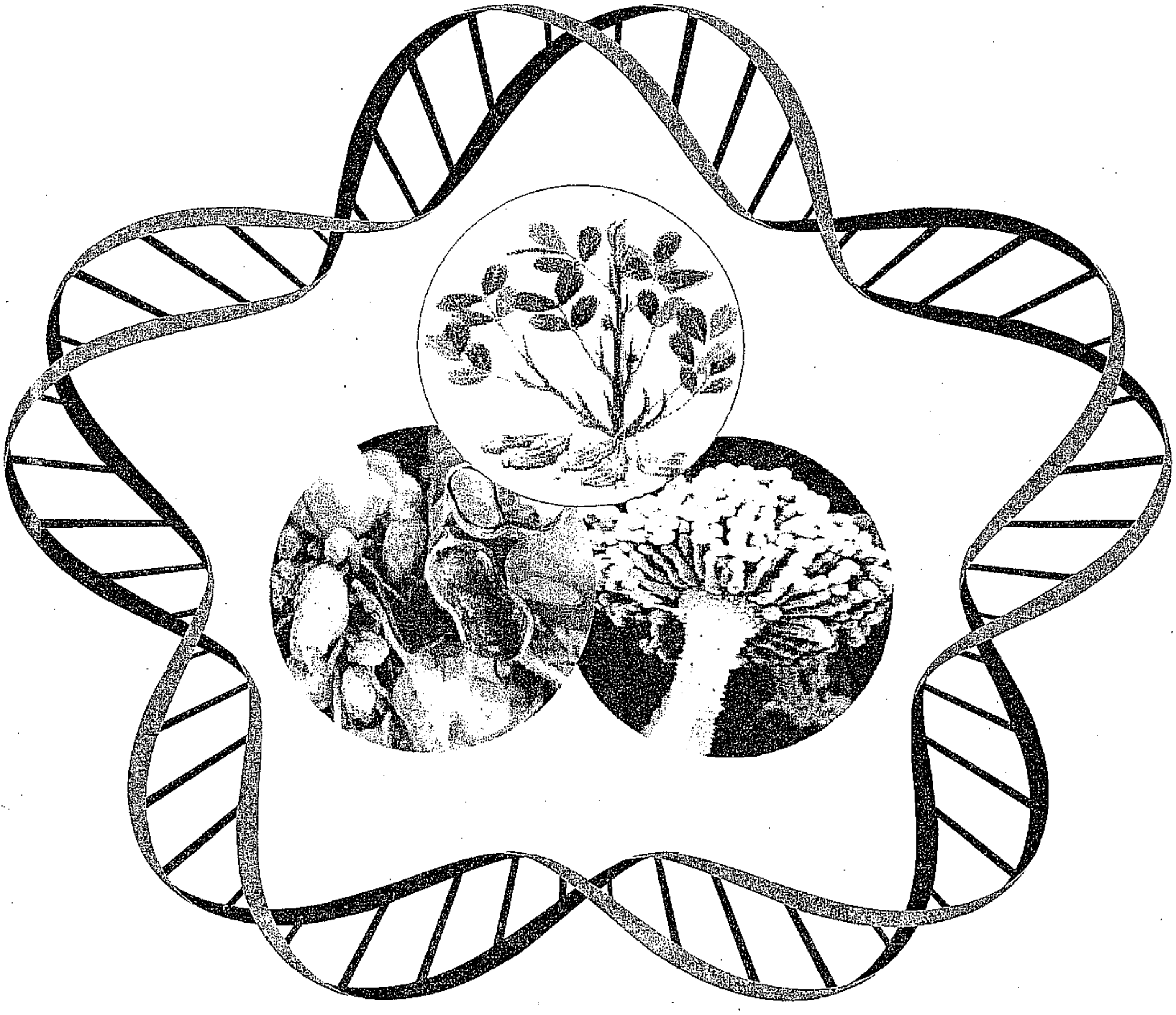
GROUNDNUT AFLATOXIN
Management & Genomics



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SSR and AFLP Markers for Resistance to Bacterial Wilt in Groundnut (*Arachis hypogaea* L)

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Bacterial wilt (BW) caused by *Ralstonia solanacearum* has been an important biotic constraint to groundnut production in several Asian and African countries. Infection in late growth stage by *R.solanacearum* may also increase aflatoxin contamination. Genetic enhancement for host plant resistance has been well proven as the most feasible approach for controlling bacterial wilt. In the past three decades, extensive efforts have been made on breeding for BW resistance in China and released resistant cultivars have played a unique role in reducing wilting in farmers' fields. However, the current BW-resistant cultivars are still less desirable due to their low yield potential, poor seed quality and resistance or tolerance to other constraints such as drought and foliar diseases. It is believed that selection of BW resistance in natural disease nursery may reduce useful genetic combinations especially in early segregating generations. Molecular markers linked to BW resistance genes would facilitate more efficient pyramiding of genes related to resistance with other important traits. In this paper, we report the results of SSR and AFLP markers for BW resistance.

Two mapping populations were developed by using resistant and susceptible groundnut lines. The recombinant inbred lines (RILs, F_6) derived from a cross of Yuanza 9102 and Chico was detected by SSR approach with 354 primers. Totally, 45 SSR markers which could reveal the polymorphism among the population were identified. Based on the results of resistance evaluation in F_6 and F_7 RILs and DNA markers identified, a genetic map including 8 linkage groups covering a map distance of 603.9 cM containing 29 markers (28 SSR markers and 1 phenotypic marker) and 17 unique markers were developed. Two SSR markers, 7G02 and PM137 were identified as linked to BW resistance and mapped on linkage group 1. The distances between the two markers and resistant genes were 10.9 cM and 13.8 cM respectively. Two AFLP markers (P1M58 and P3M59) linked with the resistance were identified in the RILs derived from "Zhonghua 5 × Yuanza 9102 ". The genetic distances between the P1M58 and P3M59 and the resistance were 13.93 cM and 8.73 cM respectively. High yielding breeding lines with high level BW resistance and extra high oil content have been selected from the RILs.