بسم الله الرحمن الرحيم

شبكة المعلومـــــات الجامعية

التوثيق الالكتروني والميكروفيلم

شبكة المعلومات الجامعية

جامعة عين شمس

التوثيق الالكتروني والميكروفيلم

﴿ قـــســـم ﴾

نقسم بالله العظيم أن المادة التي تم توثيقها وتسجيلها
علي هذه الأفلام قد اعدت دون آية تغيرات

يجب أن

تحفظ هذه الأفلام بعيداً عن الغبار

في درجة حرارة من 15 – 20 مئوية ورطوبة نسبية من 20-40 %

To be kept away from dust in dry cool place of
15 – 25c and relative humidity 20-40 %

بعض الوثائق الأصلية تالفة

بالرسالة صفحات

لم ترد بالأصـــل

UTILIZATION OF MODERN GENETIC TECHINQUES IN IMPROVEMENT OF EGYPTIAN RICE VARIETIES

BY

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CONTENTS

INTRODUCTION

A) DNA fingerprinting

Genetic diversity is the basis for species survival. The relentless process of recombination and gene mutation guarantees a continuous input of new variants, while equally relentless processes of environmental adaptation and random drift the shape of the distribution of genetic diversity in time and space (**Brown *et al.*, 1989**). Without genetic variation, any diverse changes in the environment would doom the species to extinction in its natural habitat. The degree of variability in the local populations therefore is a balance between the two opposing forces; one that creates variability and the other that leads to its dissolution (**Smith *et al.*, 1992**). However, a different situation is occurring in human-directed crop improvement. Modern plant breeding manipulated genetic diversity of domesticated species and made it suitable for modern agricultural production systems. In such processes, agronomically useful traits are fixed within cultivars through selective breeding, thus increasing the chance of producing homogeneity within species genotype.

Genetic improvement of crops by man can be regarded as directed evolution acting on the existing genetic variability in the germplasm. The genetic component of crops today is based on landraces, slightly improved the obsolete varieties, breeders' lines and wild species. Recently, numerous studies claimed that the genetic base of a number of major agricultural crop species is restricted since the improved varieties had less genetic variability than their parental landraces. It was found that genetic basis of the elite varieties limited the use of exotic germplasm. In addition, problems of industrialization, population expansion, agricultural land conversion and modernization of agriculture are among the contributory factors to narrowing selection standards for improved

cultivars. Concern over the potential vulnerability of major crops due to lack of diversity has prompted increase effort in analysis and characterization of variability in many breeding programs.

In spite of the relative richness of the genetic variability in the rice gene pool, utilization of these germplasms had been limited to only adaptable genotypes. Rice breeders preferably make crosses between elite germplasms proven for their outstanding performance or the progenitor of superior cultivars. This contributed to the existence of a small number of genotypes being recycled, making modern rice varieties genetically related. During the past three decades, rice production was dramatically altered because of the development of the fertilizer- responsive and small statured cultivars. From then on most of the rice lands; particularly irrigated areas were planted with improved semi-dwarf varieties. In Asia, many rice varieties are tailored to local conditions, but the great majority shares a common dwarfing of parents. Methods of estimating genetic distance have been expanded from Mendelian analysis of discrete morphological and cytological variants to statistical analysis of quantitative variation, then to biochemical assay and finally to molecular assay (**Brown *et al.*, 1989**). Molecular markers provide a good estimate of genetic relationships among genotypes. These markers can be detected easily throughout plant genomes. They provided discrete data that are less ambiguous than many other types of data, and which can be used in statistical analysis (**Thormann *et al.*, 1994**). Recently, PCR-based molecular marker dependent methods have been established (**Saiki *et al.*, 1985, Mullis and Faloona, 1987**) such as Sequence Tagged Sites (STSs) (**Olson *et al.*,1989**), Random Amplified Polymorphic DNA (RAPD) (**Williams *et al.*, 1990**), DNA Amplification Fingerprinting (DAF) (**Caetano-Anolles *et al.*, 1991**), microsatellite (**Litt and Luty, 1989**) and

PCR- based RFLP (PBR) **(Williams *et al.*, 1991; Ghareyazie *et al.*, 1995).** The PCR technique provides a simpler, safer and less expensive means of genome assay. Many major genes of agricultural importance in rice have been mapped with molecular markers. Which have laid down the foundation for Marker-Assisted Selection (MAS) in rice breeding using STS which is linked to target genes **(Zheng *et al.*, 1997).**

B- The Wide Compatibility Gene(s):

The extent of heterosis depends on the degree to which parental lines are related. Hybrids between distantly related high yielding varieties are most promising. Indica and Japonica rices are genetically diverse. Therefore, Indica/Japonica hybrids show strong heterosis for various traits, including total dry matter, tillers number, spikelet number and 1000-grain weight. However, heterosis for yield is difficult to be attained in these hybrids because of sterility, **(Butany *et al.*, 1961; Jennings, 1966; Ikehashi, 1982).**

In inbred rice programs, crosses between Indica and Japonica groups varieties have been studied by plant breeders. In tropical Asia, Korea, Japan and Egypt for further improvement of yield, cold tolerance, grain quality and adaptability to adverse soil conditions with varying degrees of success. However, crosses between Indica and Japonica varieties generally showed low fertility in F_1 and segregated in a wide range of semi- sterile plants in F_2 and subsequent generations, which limited the recovery of certain recombination. If there is any means to solve such problem, rice breeding involving Indica/Japonica crosses would become more efficient.

Several researchers have reported that certain rice varieties produce fertile F1 hybrids when crossed with Indica or Japonica lines

(Terao and Mdusima, 1939; Jennings, 1966 and Heu, 1967). Such varieties were designated as Wide Compatible Varieties (WCVs) **(Ikehashi and Araki 1986).** WCVs provide a bridging mechanism between Indica and Japonica varieties in rice improvement.

The genetic basis of F1 sterility and WCV were due to multiple alleles locus (S_5) located between 'C^+' (chromogen for apiculus color) and Wx (waxy endosperm) loci in chromosome 6 **(Ikehashi and Araki 1986).** An interaction of two alleles out of three i.e., S_5^i from Indica and S_5^j from Japonica were found to confer female gamete abortion, which was expressed as semi-sterility of the panicle. Female gametes carrying S_5^j were aborted in the genotype of S_5^i / S_5^j, while a neutral allele S_5^n did not cause the abortion in heterozygotes of S_5^i / S_5^n and S_5^j / S_5^n. The donor parent of S_5^n was termed as (WCV), where S_5^n is the allele which overcomes Indica/Japonica hybrid sterility **(Araki *et al.*, 1988).**

Ikehashi and Yanagihara (1991) showed that the S_5^n allele of Bulu variety, Ketan Nangka did not cause hybrid sterility in either S_5^i or S_5^j. If the S_5^n gene was substituted for S_5^i or S_5^j in a parental line, the line became compatible with both Indica and Japonica. The S_5^n gene was successfully incorporated into Norin PL9 from Ketan Nangka (**Araki *et al.*, 1988**). The allele of S_5^n has also been incorporated into Japonica types and successfully utilized for obtaining Indica- Japonica hybrids **(Araki *et al.*, 1988; Ikehashi and Yanagihara 1991).)** Thus, the WC S_5^n gene is expected to contribute to the hybrid rice-breeding program, by means of their broad capabilities of overcoming sterility problems

The objectives of this study are:

1- To study the degree of similarity of Egyptian - bred varieties and lines