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5- SUMMARY

The present study aimed to evaluate the genetic diversity among some genotypes that belong to different rice types, using different tools of genetic diversity assessment. Subsequently, to determine the suitable breeding programme for improvement the important studied traits. For this purposes, 72 rice genotypes belong to species (*Oryza sativa* L.) were investigated. These genotypes represent three different types of rice, which were collected from the Genetic Stock of Rice Research and Training Center (RRTC), Sakha, Kafr El-Sheikh, Egypt. These types were including Temperate Japonica, Indica and Tropical Japonica. Each one of these types contained 24 rice genotypes. Two kinds of evaluation were used; the first one was field experiment in order to evaluate some quantitative & qualitative agronomic traits at the Research Farm of Rice Research and Training Center (RRTC) during the two successive growing seasons 2014 and 2015. While, the second was molecular assessment at Laboratories of Genetics Department, Faculty of Agriculture, Kafr El-Sheikh University.

The obtained results could be summarized in the following points:

- Highly significant mean square estimates were recorded between and within all the rice genotypes that belong to the three types used. These significant variations suggested the existence of some sort of genetic variability which might reflect their different wide genetic backgrounds.
- The most desirable rice genotypes belong to Temperate Japonica Type for days to 50% heading, grain yield as well as for most of the economic

traits were namely, IR 82187-17-3-3, SUWEON 349, 96002-TR 1741-1-2-2-1, GZ 7769-2-1-1-2, Sakha 104 and Sakha 105. With reference to Indica Type, GZ 1368, IR 60 and Giza 178 were found to be the best rice genotypes for most of the studied traits, particularly grain yield/plant. Concerning, Tropical Japonica Type, the results clearly revealed that rice genotypes namely IR65600-129-1-1-2, IR 69093-41-2-3-2 ,IR69853-70-3-1-1, IR68011-15-1-1 and IR681-28-3-2-2 were the superior rice varieties for the most important traits such as earliness, grain yield and its components traits.

- The results concluded that high estimates of genotypic and phenotypic coefficients of variability were observed for grain length, 1000-grain weight, panicle exertion%, grain shape, grain elongation% and gelatinization temperature, indicating that both additive and dominance gene action were played remarkable roll in the inheritance of these mentioned traits under the three studied types.
- High estimates of broad sense heritability coupled with high genetic advance were recorded for days to 50% heading, plant height, number of filled grains/panicle and grain elongation% traits under the three types, indicating the important of selection in early generation to improve such traits in any rice breeding program.
- Both genotypic and phenotypic correlation coefficients were significant or highly significant in positive direction between grain yield/plant and each of panicle excretion%, number of panicles/plant, number of filled grains/panicle, 1000-grain weight, fertility % and milling %, while it was non-significant positively correlated with each of days to 50% heading,

panicle length, hulling%, head rice%, grain elongation% and amylose content%, implied that selection for these traits not effective in improving grain yield in rice in respect to the three types of genotypes. However, the genotypic correlation coefficient was close or little higher than the corresponding values of phenotypic correlation coefficient for most of pairs studied traits, indicating that these traits were mainly controlled by genetic factors, while the environmental factors play minor role in the expression of these traits.

- The first and the second types of genotypes (Temperate Japonica and Indica) were divided into the same number of major clusters equal to ten clusters. While, the third type (Tropical japonica) comprised into 11 major clusters.
- The results indicated that the parental lines which selected from the three types were Temperate Japonica clusters viz., I, II, III, IV, VI, VII and X, Indica clusters viz. I, IV, VII and VIII and Tropical Japonica clusters viz., VI, VII, IX and XI and these parental lines could be used in a hybridization programme. The crossing between superior genotypes of above diverse cluster pairs as well as between different types may provide desirable transgressive segregants for developing high yielding varieties of rice.
- Out of twelve ISJ markers used in this study only eight primers amplified and generated polymorphic alleles (ISJ 1, ISJ 3, ISJ 5, ISJ 6, ISJ 7, ISJ 9, ISJ 10 and ISJ 11) in all types (Temperate Japonica, Indica and Tropical Japonica). The sizes of amplified fragments were ranged from 300 to 2000 bp with respect to the three types. However, the amplifications products

were scored 38, 60 and 44 polymorphic bands for Temperate Japonica, Indica and Tropical japonica types, respectively.

- The morphological and ISJ markers data illustrated two dendograms with six major clusters in the both types (Indica and Tropical Japonica) while, five major clusters in Temperate Japonica type were found, that were not completely corresponding; however, there were some concordances between them.
- Finally in conclusion, from all the previous results it could be concluded that, the presence of genetic difference between the studied genotypes with respect all studied traits and these genotypes are stable in their behaviour with different environmental conditions with respect to most of studied traits. In addition, high heritability coupled with high genetic advance was observed for most of studied traits, suggesting the effectiveness of selection in early generation to improve these traits. Furthermore, due to most of morphological traits are strongly associated with molecular markers (ISJ), it could be use the simple morphological traits as marker for selection in the early generation during the applied breeding programme. In addition, molecular markers have the potential to detect genetic diversity and to aid the management of plant genetic resources.