Traditional and molecular evaluations of some local and introduced cucumber cultivars with special reference to downy mildew resistance genes

by

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B.Sc. (Horticulture), Zagazig University 1980
M.Sc. (Vegetable Crops), Cairo University 1985

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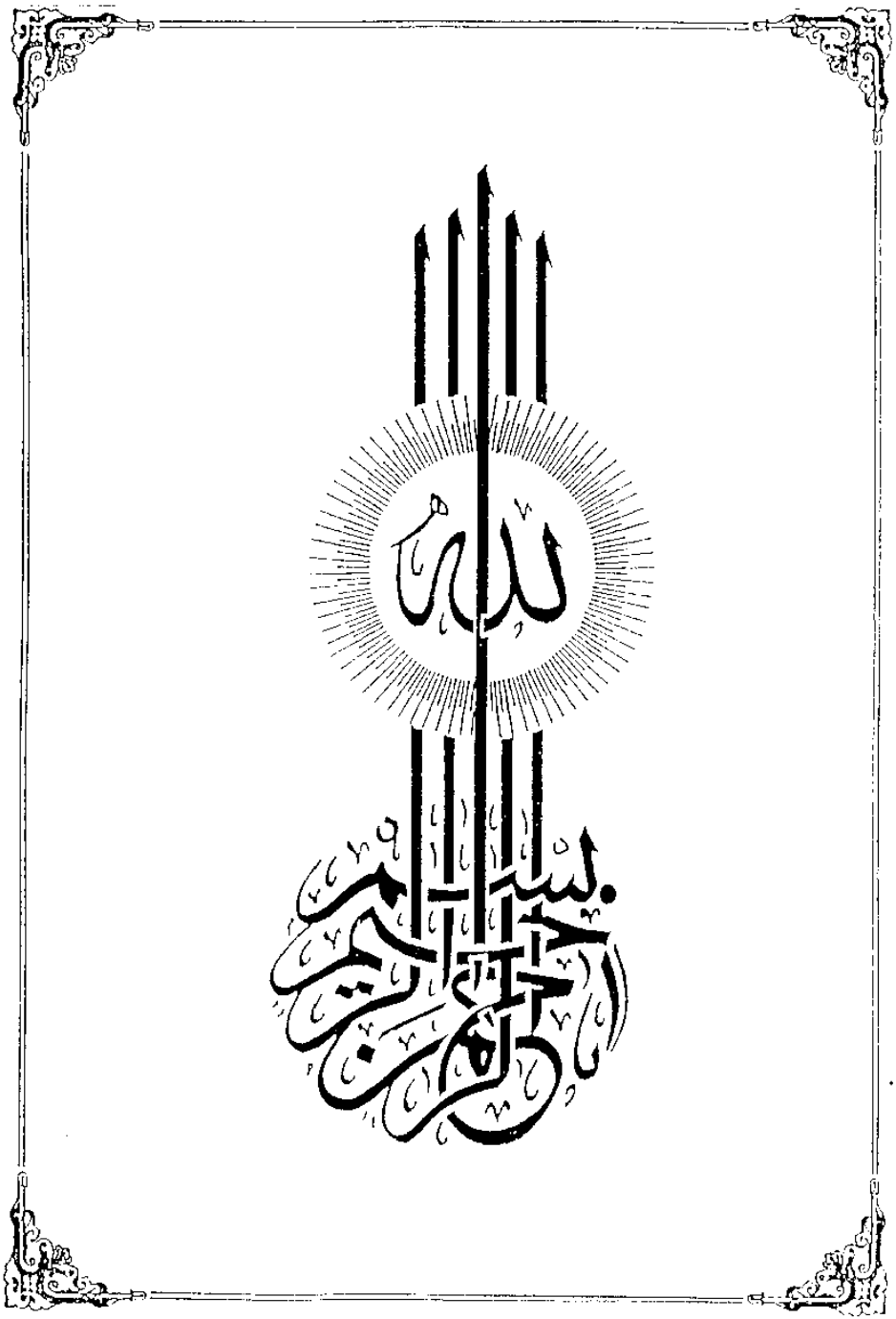

APPROVAL SHEET

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ABSTRACT

EL SAYED IMAM EL ATTAR." Traditional and molecular evaluation of some local and introduced cucumber cultivars with special reference to downy - mildew resistance genes " . Unpublished Doctor of Philosophy dissertation. Ain Shams University, 1997 .

Morphological and molecular analyses were employed to identify markers linked to the major downy mildew resistance genes in diverse sources of cucumber (*Cucumis sativus* L.). Studying the inheritance of resistance, genetic analysis of resistance and development of the RFLP and RAPD genetic maps of downy mildew resistance genes in cucumber were conducted. Inoculation was made by two physiological pathotypes of *Pseudoperonospora cubensis* (path. I = isolated from cucumber & path. II = isolated from melon). However, out of forty two cultigenes that were tested with both races, the selected genotypes that used in this study were. PI 432870(R), PI 432877(S), PI 357857(S), PI 426169(R), PI 426170(R), PI 422182(R), PI 197088(R), GY 14(R), ST8(S) and Beit alpha type(S). The morphological analysis revealed that the inheritance of resistance in the cross Beit alpha xPI 197088 (S x R) is expressed in two loci *dm*1 and *dm*2 corresponding to pathotype I and pathotype II. The *dm*1 locus is conditioned by one major recessive gene and one minor gene whereas, the *dm*2 locus is controlled by one single recessive gene. Infection level of the susceptible genotype (Beit alpha) significantly differed according to the used pathotype. Conversely, the resistant genotype (PI 197088) mean was not affected by pathotypes. The genetic analysis of resistance gave more role for genetics towards this trait and proved the effectiveness of the selection in the improvement for the resistance to downy mildew. The molecular analysis showed that the RFLP map of *dm* in a wide cross (GY14 x PI 183967) was relatively less efficient to detect polymorphisms among the cultivated selected lines. However , the Bc1P2 families of the cross GY14 x PI 197088 (R x R) showed segregating mode when tested with pathotypes I & II. The use of RAPD screening showed that out of 470 arbitrary

10-mer primer, only six RAPD markers (0.013%) were segregating in F2 families of both crosses. In the cross Beit alpha x PI 197088 the markers that represented the linked donor chromosome segment to *dm*1 (AA09, AC19 and AM13) gave a map length of 7.3 cM as compared to the map length of *dm*2 with polymorphic markers (AC19, AM13 and AN01) linked to the target gene 63.6 cM. In the cross GY14 x PI 197088 the chromosome segment was about 24.8 cM linked to *dm*1 locus and may enable us to compensate for the lack of polymorphisms in RFLP map. The *dm*2 introgressed region was 99.7 cM with no clear-cut trend, supporting the need for more evaluation in this region. As for PCR aided-markers, of 22 primers potentially polymorphic, but when tested with one single line DNA template of Beit alpha, PI 197088 and their F2 family examined with pathotypes I&II and no infection III, only one RAPD (AN01) was polymorphic with path. II and Beit alpha. The other RAPDs were monomorphic in all cases, giving bias of the divergence of fungal pathotypes and their resistance loci *dm*1 & *dm*2 in the same specific genomic DNA. These gained RAPDs should be cloned and sequenced for future research as probes for multidisease resistance to downy mildew or for transgenic plants and transformation of these genes to a single line.

Key words: *Cucumis sativus* L., downy mildew (*P. cubensis* pathotypes), genetic analysis, RFLP, RAPD markers, genetic map

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Finally, I produce this work purely at the most merciful God for the soul of my late mother.

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