

**PATHOLOGICAL AND MOLECULAR STUDIES
ON LATE BLIGHT DISEASE IN TOMATO
CAUSED BY *Phytophthora infestans***

By

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APPROVAL SHEET

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ABSTRACT

Our results demonstrated that all Egyptian *P. infestans* isolates were identified as A1 mating type except only one isolate EG_9 was self-fertile (SF), however the majority of Japanese isolates were A2 mating type. Additionally, based on PCR-RFLP approach all Egyptian isolates were the Ia mt-DNA haplotype, whereas the Japanese isolates were IIa. Genome-wide SSR analysis of *P. infestans* populations revealed that 45 alleles were detected using 16 microsatellite markers. According to presence or absence of *P. infestans* effector genes AVR1 was absent in all tested samples, however AVR4 effector gene was present in all isolates. Intriguingly, 996 high-quality SNPs marker were detected using double-digest restriction site-associated DNA sequencing (ddRAD-Seq) technology. Interestingly, the comparative genomics of *P. infestans* populations showed that the copy number variation (CNV) percent ranged from 0.4 to 12.5 %. The highest late blight resistance was detected in *S. habrochaites* accessions LA1777, LA1352, LA2855, LA1347, LA1718 and LA1295, with disease severities ranging from 4.5 to 13.5 %. Two quantitative trait loci on chromosomes 12 and 6 for resistance to an aggressive two Egyptian isolates of *P. infestans* EG_11 and EG_12, respectively, were identified. Whole-genome resequencing analysis revealed that two genes with missense mutations, Solyc06g071810.1 and Solyc06g083640.3, were considered to be potential candidates for disease resistance.

Key words: Tomato, late blight, resistance genes, genetic markers, wild species.

DEDICATION

I dedicate this work to my parents, my brothers and my sisters for all the support they lovely offered during my post-graduate studies.

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