Abstract

Potato is vulnerable to many pathogenic agents such as viruses, bacteria and fungi. Brown rot disease caused by ***Ralstonia solanacearum*** is a devastative disease in terms of great loss and considerable effects on potato industry in Egypt. These losses result not only from pathogen broad geographical distribution and extensive host range, but also from the limited means of protection currently available. It has been postulated that, ***R. solanacearum*** may shift between two different physiological states, one adapted for saprophytic survival (avirulent) and the other for pathogenesis (wild-type), **(Denny *et al.*, 1994).** This phenotype conversion (PC) is probably coordinated with a complex array of transcription factors and many signal transduction elements. In this study, phenotypic and genotypic differences between virulent and a virulent ***R. solanacearum*** isolates were investigated at DNA and protein levels. Ten local isolates (Rso-$_{H1}$, Rso-$_{H2}$, EGY-MS $_{2003}$, Rso-$_{H4}$, Rso-$_{H5}$, Rso-$_{A1}$, Rso-$_{A3}$, Rso-$_{Tv}$, Rso-$_{Tav}$ and Rso-$_{N6}$) were collected from different geographic locations (Alexandria, Behera, El- Minia, Gharbia, Giza and Menofia) and analyzed. First, the grouping of these isolates into different biovars and races were determined based on biochemical & pathogenicty tests, respectively. Second, phenotypic characterization for cellular & membrane binding proteins were examined on SDS-PAGE. In addition, specific PCR was used to detect virulent genes such as exopolysaccharide (*eps*) & pectin methyl esterase (*pme*). Genetic analysis for one isolate, EGY-MS2003, using sequence analysis of 16S/23S rRNA Intragenic Spacer (ITS) and flanking regions and ARDRA typing (Amplified Ribosomal DNA Restriction Analysis) was conducted. Results revealed that, isolates under investigation

were phenotypically & genotypically comparable although, their pathogenicty index in potato & tomato were significantly different. Further, a 1.27 kb ITS segment was amplified and its nucleotide sequence was determined (accession number AY 383556). Sequence features of the ITS revealed the presence of $tRNA^{Ala}$ and $tRNA^{Ile}$. Blast search indicated a closest match (96%) with ***R. solanacearum*** strain GMI1000 (accession # AL 646073). Nucleotide differences were generally centered in the spacer between 23S rDNA and $tRNA^{Ala}$ and between $tRNA^{Ala}$ and $tRNA^{Ile}$. Restriction DNA analysis of the ITS revealed a unique ARDRA pattern of EGY–MS2003 that significantly different form the four ARDRA types a, b, c, and d proposed by **(Timms-Wilson *et al.*, 2001).** Accordingly, the new ARDRA type "e" was proposed.

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