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MOLECULAR DETECTION OF VIRULENCE GENES (*PILB* AND *SID*) IN *PSEUDOMONAS SYRINGAE* PV. *LACHRYMANS* ISOLATED FROM CUCUMBER LEAVES

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ABSTRACT : *Pseudomonas syringae* pv. *lachrymans* possessed a lot of factors that play an important role in the development of parasitism and growth stages of the pathogen on plant host and consider a quantitative measure of plant disease. Therefore, this study was conducted to investigate some genes responsible for the virulence factors (*pilB* and *Sid*) in isolates of *P. syringae*pv. *lachrymans* that caused angular spot disease on cucumber leaves in different areas of Najaf province. The results showed that the *pilB* and *Sid* genes were amplified in fifty-two isolates of *P. syringae* pv. *lachrymans*, forty-five isolates contained*pilB* gene which responsible for adhesion factors through the emergence of binds in a molecular size of 586 base pairs on agarose gel after electrophoresis. Also forty-five isolates contained *Sid* gene, which responsible for the siderophore factor through the emergence of binds in a molecular size of 572 base pairs on agarose gel.

Key words : *Pseudomonas syringae*, virulence, *pilB*, *Sid,* angular spot disease.

INTRODUCTION

P. syringae pv. *Lachrymans* is one of the Gram negative that caused angular spot disease on cucumber leaves, causing significantlosses in green houses rating from 19% to 32% in Najaf province (Saba *et al*, 2019). *P. syringae* possesses a lot of virulence factors, which are a measure of the degree of damage in planthost or a quantitative measure of the pathogenicity. This status was controlled by genes inherited by the pathogen that evolve through natural selection andinteraction with host resistance genes (Sharif, 2012). Through signals, the host and the *P. syringae* cells can be connected to coordinate the gene expression which is necessary for infection on the plant host. Where the presence of signals, *P. syringae* can be transition from the saprophytic to the parasite stage by disrupting the process of saprophytic behavior such as movement and stimulating activities that required for the infection, the production of polysaccharides, enzymes and the release of other effectivecontrolled in a manner depends on the density of the number of *P. syringae* cells in planttissues (O'Brien *et al*, 2011a). The adhesion of *P. syringae* to host cell surfaces is an important mechanism for causing infection by producing virulence factors. The *pilB* gene is responsible for adhesion, which was an important step in the progression of the parasitism. Adhesion to the cell surface can occur by producing a high molecular weight sugars that promote virulence, bimolecular formation and adhesion to the cell surface (Schmid *et al*, 2015). After the adhesion of the host cells was achieved, thebiochemical effect occurs between *P. syringae* and host cells, which respond quickly to changes through associating them with small particle signals and synchronizing them to activities of a large number of cells (Mathesius *et al*, 2003). *P. Syringae*is a pathogen that produces a large amount of Siderophore, it is iron chelated compound responsible for the *Sid* gene, where iron absorption systems were very complex (Wensing *et al*, 2010). The production of siderophore considered an important factor in the virulence of *P. syringae* that supported in the evolution of *P. syringae* parasitism on cucumber plants (Thakur, 2017). The aim of this study was to investigate some genes that responsible for virulence factors (*pilB* and *Sid*) in isolates of *P. syringae* pv. *lachrymans* for the first time in Iraq.

MATERIALS AND METHODS

Leaf samples (Seventy four leaves) were collected randomly and placed in plastic bags with proper labeling andbrought directly to phytopathology laboratory thenkept in the refrigerator at 4 ± 1°C until used for subsequent studies.