

This figure shows a relation tree of *gapA* barcode of Moroccan populations and other *Pectobacterium* and *Dickeya* strains (sequences were collected from NCBI database). The alignment was generated using ClustalW; the evolutionary history was inferred using the Neighbor-Joining method and the evolutionary distances were computed using the Maximum Composite Likelihood method. Phylogenetic analyses were conducted using MEGA7 software.

