```
A10             MSQKLTTNRKFEKGRPLPKFGEWDVNDPASAEGFTVIFNKARDEKKTGGKPESPGKVDPN 60
G16             MSQKLTTNRKFEKGRPLPKFGEWDVNDPASAEGFTVIFNKARDEKKTGGKPESPGKVDPN 60
a4              MSQKLTTNRKFEKGRPLPKFGEWDVNDPASAEGFTVIFNKARDEKKTGGKPESPGKVDPN 60
                ************************************************************

A10             IRHGGGVDPGTGRPSSESFRFTCKSQFNAYAQKHKHGARIEVLDSGHPKLPTEKAAKWEN 120
G16             IRHGGGVDPGTGRPSSESFRFTCKSQFNAYAQKHKHGARIEVLDSGHPKLPTEKAAKWEN 120
a4              IRHGGGVDPGTGRPSS-------------------------------VRLWSPQASVKE- 88
                ****************                                :* : :*:  *

A10             LGSTGTDKRCRYEKRPYGSTSDPLLRLLHQRLQETIYITKRLRKKLCLRGAREL 174
G16             LGSTGTDKRCRYEKRPYGSTSDPLLRLLHQRLQETIYITKRLRKKLCLRGAREL 174
a4              -----------------GSEVGKLGELWHR--QALLTRKKALWIDL-------- 115
                                 **  . * .* *:  *  :  .* *  .*
```

Red： RIN4， pathogenic type III effector avirulence factor Avr cleavage site

Fig. S4 Amino acid sequence alignment of predicted ORFs of A10, a4 and G16. Alignment was performed using ClastalW 2.1.