Supplementary Information

The *Riemerella anatipestifer AS87_01735* gene encodes a nicotinamidase (PncA), an important virulence factor

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Running title: Characterization of *R. anatipestifer* PncA

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A

Percent Identity

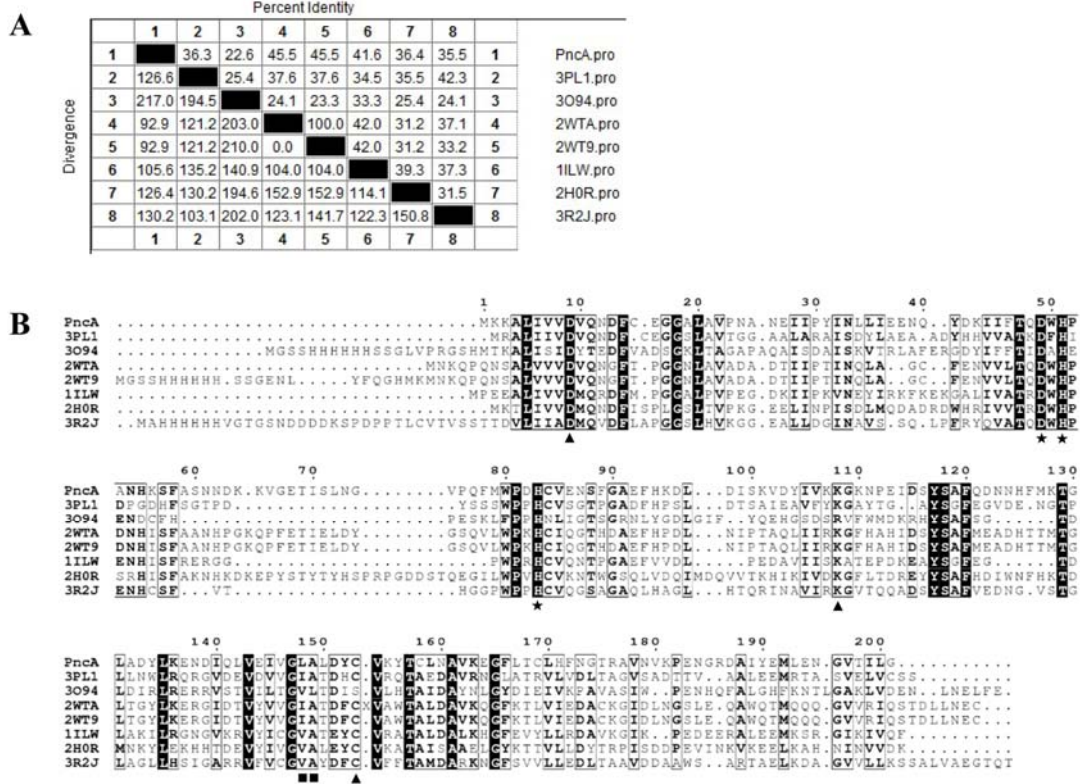|	1	2	3	4	5	6	7	8		
1		36.3	22.6	45.5	45.5	41.6	36.4	35.5	1	PncA.pro
2	126.6		25.4	37.6	37.6	34.5	35.5	42.3	2	3PL1.pro
3	217.0	194.5		24.1	23.3	33.3	25.4	24.1	3	3O94.pro
4	92.9	121.2	203.0		100.0	42.0	31.2	37.1	4	2WTA.pro
5	92.9	121.2	210.0	0.0		42.0	31.2	33.2	5	2WT9.pro
6	105.6	135.2	140.9	104.0	104.0		39.3	37.3	6	1ILW.pro
7	126.4	130.2	194.6	152.9	152.9	114.1		31.5	7	2H0R.pro
8	130.2	103.1	202.0	123.1	141.7	122.3	150.8		8	3R2J.pro
	1	2	3	4	5	6	7	8		

Divergence

B

Figure S1. Amino acid sequence alignment for *R. anatipestifer* nicotinamidase (PncA) and other known nicotinamidases. The crystallized nicotinamidase sequences [*Mycobacterium tuberculosis* (pdb3PL1), *Streptococcus pneumoniae* (pdb3O94), *Acinetobacter baumanii* (pdb2WTA, 2WT9), *Pyrococcus horikoshii* (pdb1ILW), *Sacharomyces cerevisiae* (pdb2H0R), *Leishmania infantum* (pdb3R2J)] were retrieved from Uniprot database and later aligned with Clustal W algorithm in the MegAlign program from the DNASTAR Lasergene suite.(A) Percent identity and divergence analysis. (B) Multiple sequence alignment. Strictly conserved residues in all sequences are boxed in black. Residues involed in catalysis and metal binding are indicated by black triangle (D9, K108 and C153) and black asterisk (D49, H51 and H83), respectively. The residues forming the conserved cis-peptide bond are indicted byblack square (L148 and A149). The figure was made using Espript (http://espript.ibcp.fr).