

Large-scale identification of lysine acetylated proteins in vegetative hyphae of the rice blast fungus

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Table S1 Gene annotation of acetylated proteins in *Magnaporthe. oryzae*

Table S2 Clusters in protein-protein interaction network

Table S3 List of acetylated proteins potentially involved in vegetative hyphal growth and pathogenicity

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Disrupted genes	Mutant ID	Vegetative hyphal growth	Pathogenicity	Annotation
MGG_07200	0421D1	slow	reduced virulence	plasma membrane ATPase
MGG_09901	0100B2	slow	reduced virulence	NAD dependent epimerase/dehydratase
MGG_09991	0236D1	slow	reduced virulence	phosphatidylinositol transfer protein SFH5
MGG_03310	0424D5	slow	reduced virulence	T-complex protein 1 subunit eta
MGG_01062	0082C3	slow	reduced virulence	autophagy-related protein 8
MGG_01061	0082C3	slow	reduced virulence	coproporphyrinogen III oxidase
MGG_00450	0137A2	slow	reduced virulence	phosphoenolpyruvate carboxykinase
MGG_09531	0090D1	slow	reduced virulence	rho-GTPase-activating protein 8
MGG_06204	0249A4	slow	reduced virulence	alpha/beta hydrolase family
MGG_09212	0129C3	slow	reduced virulence	nitroreductase
MGG_04140	0128A4	slow	reduced virulence	mitochondrial NADH dehydrogenase
MGG_02927	0249B2	slow	reduced virulence	putative importin-beta domain-containing protein
MGG_12268	0076D1	slow	wild type	transcription elongation factor spt-5
MGG_08065	0076D1	slow	wild type	WD domain-containing protein
MGG_01712	0135B6	slow	wild type	isocitrate dehydrogenase subunit 2
MGG_08661	0069A4	slow	wild type	acyl-CoA dehydrogenase family member 11