**Supplementary table 4**: Pathogen proteins summarized from eligible studies in the systematic review.

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|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Protein** | **Function** | **Accumulation** | **Region** | **Authors** |
| MpNEP1 | Induction of necrosis and ethylene synthesis | ↑ | Biotrophic and saprotrophic mycelium | Garcia et al. 2007\*\* |
| MpNEP2 | Induction of necrosis and ethylene synthesis | ↑ |
| Aldo-keto reductase | Stress response | ↑ | Mycelium | Pierre et al. 2017\*\* |
| Malate dehydrogenase | Metabolism enzyme | ↑ |
| Phosphoglycerate kinase | Metabolism enzyme | ↑ |
| NAD-dependent epimerase/dehydratase | Metabolism enzyme | ↑ |
| 1-Cys peroxiredoxin | Peroxide decomposers | ↑ |
| Acetyl-acetyltransferase | NA | ↑ |
| Aspartate aminotransferase | NA | ↑ |
| Pleurotolysin B homologue | NA | ↑ |
| Erylysin B | NA | ↑ |
| Glyceraldehyde-3-phosphate dehydrogenase | Metabolism enzyme | ↑ |
| Heat-shock protein hss1 | Stress response | ↑ |
| Enolase | Metabolism enzyme | ↑ |
| Nitrilase | Auxin biosynthesis and cyanide detoxification | ↑ |
| Mannitol-1-phosphate dehydrogenase | Mannitol biosynthesis | ↑ |
| MPER\_00772 | Unknown function | ↑ |
| NAD-dependent formate dehydrogenase | Methanol catabolism | ↑ |
| Putative anhydrolase | NA | ↑ |
| ATP binding cassete | Fungal pathogenicity | ↑ |
| PR-1 | Fungal pathogenicity | ↑ |
| Initial translation factor | Metabolism and energy | ↓ | Basidiospores | Mares et al. 2017\*\* |
| Nucleoside diphosphate kinase | Metabolism and energy | ↓ |
| Small ribosomal subunit | Metabolism and energy | ↓ |
| 60S ribosomal protein | Metabolism and energy | ↓ |
| Serine protease inhibitor | Metabolism and energy | ↓ |
| Nucleoside triphosphate hydrolase | Metabolism and energy | ↑ |
| Large ribosomal subunit | Metabolism and energy | ↑ |
| Translation elongation factor 1α | Metabolism and energy | ↑ |
| Folding protein | Metabolism and energy | ↑ |
| Heat shock protein (HSP70) | Metabolism and energy | ↑ |
| Binding immunoglobulin protein (BiP) | Metabolism and energy | ↑ |
| ATP synthase | Metabolism and energy | ↑ |
| Glyceraldehyde-3-phosphate dehydrogenase | Metabolism and energy | ↓ |
| Valosin contain protein (VCP) | Cell cycle regulation | ↑ |
| Kinesin | Cell cycle regulation | ↑ |
| Septin | Primary hypha septation | ↑ |
| Oxidorredutase | Stress response and anti-oxidation | ↑ |
| Ascorbate peroxidase | Stress response and anti-oxidation | ↑ |
| Catalase | Stress response and anti-oxidation | ↑ |
| Superoxide dismutase | Stress response and anti-oxidation | ↑ |
| Peptidyl-prolyl cis-trans isomerase | Fungal pathogenicity | ↑ |
| Transcription factor FapR | Fungal pathogenicity | ↑ |
| Polyketide synthase | Fungal pathogenicity | ↑ |
| MpPR-1 | Neutralization of plant defenses, antimicrobial activity to avoid competitors and fruiting body physiology | NA | Dikaryotic mycelium | Teixeira et al. 2012\*\* |
| MpAtg8p | Autophagy | NA | *In sílico* | Pereira et al. 2013\*\* |
| Reverse transcriptase (RT-Like) | Transposition of transposable elements | ↑ | NA | Pereira et al. 2007\*\* |
| Acyl-CoA binding protein (ACBP) | Intracellular acyl-CoA transporter | ↑ | *In sílico* | Monzani et al. 2010\*\* |
| Glyceraldehyde-3-phosphate dehydrogenase (MpGAPDH) | Fungal pathogenicity and glucose biosynthesis | ↑ | *In sílico* | Lima et al. 2009\*\* |
| Lanosterol 14α-demethylase (ERG11) | Ergosterol biosynthesis | ↑ | Mycelium | Ceita et al. 2014\*\* |
| Putative effector | Catabolic process | DA | Mycelium | Barbosa et al. 2018\*\* |
| Putative effector | Cell wall organization or biogenesis | DA |
| Putative effector | Cellular metabolic process | DA |
| Putative effector | Cellular process | DA |
| Putative effector | Establishment of localization | DA |
| Putative effector | Localization, single-organism process | DA |
| Putative effector | Metabolic process | DA |
| Putative effector | Multi-organism process | DA |
| Putative effector | Nitrogen compound metabolic process | DA |
| Putative effector | Organic substance metabolic process | DA |
| Putative effector | Pathogenesis | DA |
| Putative effector | Primary metabolic process | DA |
| Putative effector | Response to stress | DA |
| Putative effector | Single-organism cellular process | DA |
| Putative effector | Single-organism metabolic process | DA |
| Putative effector | Carbohydrate binding | DA |
| Putative effector | Heterocyclic compound binding | DA |
| Putative effector | Hydrolase activity | DA |
| Putative effector | Ion binding | DA |
| Putative effector | Lyase activity | DA |
| Putative effector | Organic cyclic compound binding | DA |
| Putative effector | Oxidoreductase activity | DA |
| Putative effector | Pattern binding | DA |
| Putative effector | Peroxidase activity | DA |
| Putative effector | Structural constituent of cell wall | DA |
| Putative effector | Cell periphery | DA |
| Putative effector | External encapsulating structure | DA |
| Putative effector | Intrinsic component of membrane | DA |
| Metal-dependent hydrolase (MDH) | Fungal pathogenicity | NA | NA | Tibúrcio et al. 2009\*\* |
| Necrosis-inducing proteins (NEPs) | Fungal pathogenicity | NA |
| Mannitol 1-phosphate 5-dehydrogenase(MPDH) | Fungal pathogenicity | NA |
| Thaumatin-like proteins (TLPs) | Fungal pathogenicity | NA | Basidiospores | Franco et al. 2015\*\* |
| Cerato-platanin (CP) | Necrosis inducing | NA | Saprotrophic mycelium | Zaparoli et al. 2009\*\* |
| Pyridoxal-dependent decarboxylase | Indoleacetic acid metabolism and synthesis (AIA) | ↑ | Necrotrophic mycelium and basiodiocarps | Gomes et al. 2021\*\* |
| Decarboxyl L-amino acids | Indoleacetic acid metabolism and synthesis (AIA) | ↑ |
| Nitrilase | Indoleacetic acid metabolism and synthesis (AIA) | ↑ |
| NAD-dependent aldehyde dehydrogenase | Indoleacetic acid metabolism and synthesis (AIA) | ↑ |
| RAB GDP dissociation inhibitor | Cell proliferation | ↑ |
| homocysteine methylase (HCM) | Methionine metabolism | ↑ |
| Alanine dehydrogenase | Pigment biosynthesis | ↑ |
| Hypothetical protein (gi|238614130) | Possible specificity for fungal division | ↑ |
| GDI | Regulation | ↓ |
| SEC4 | Signaling processes/regulation of vesicle transport and autophagy | ↑ |
| RAS | Signaling processes/regulation of vesicle transport and autophagy | ↑ |
| Ciclophyilin | Protein folding and trafficking, apoptosis, signal reception, alteration of gene expression, ROS detoxification | ↑ |
| Glycine-rich RNA binding protein 1 (GRP1) | Stress response | ↑ |
| Ciclophyilin (CYT450) | Stress response | ↑ |
| Agglutinins | Response to stress and nutrient deficiency | ↑ |
| Glyceraldehyde-3-P dehydrogenase (GAPDH) | Glucose biosynthesis | ↑ |
| aldo-keto reductase (AKR) | Stress response | ↑ |
| Tyrosine phosphatases (TYP) | Osmotic and oxidative stress response | ↑ |
| Linoleate diol synthase | Lipid biosynthesis | ↑ |
| Leukotriene-A4 hydrolase | Lipid biosynthesis | ↑ |
| 3-ketoacyl-coA-thiolase | Lipid biosynthesis | ↑ |
| Phosphatidylserine decarboxylase (PSD) | Phospholipid synthesis | ↑ |
| Δ-1-pyrroline-5-carboxylate dehydrogenase (P5Cdh | Sporulation and virulence | ↑ |
| N-acetyl-gamma-glutamyl phosphate reductase(ARGC) | Synthesis of ornithine precursors | ↑ |
| Arginase | Synthesis of ornithine precursors | ↑ |
| Rubber elongation factor protein (REF) | Latex biosynthesis | ↑ |
| Heat shock proteins (HSP) | Protein synthesis and folding, transport of proteins across the membrane, protein disassembly and protein degradation | ↑ |
| pleurotolysin PriA | Basidiocarp formation | ↑ |
| ATP synthase | Energy metabolism | ↑ | Basidiospores | Mares et al. 2020\*\* |
| Binding immunoglobulin protein (BiP) | Energy metabolism | ↑ |
| alcohol dehydrogenase (ADH) | Energy metabolism | ↑ |
| Polyketide cyclase | Fungal pathogenicity | ↑ |
| Glycoside hydrolase | Carbohydrate metabolism | ↑ |
| Major facilitator superfamily (MFS) | Resistance | ↑ |
| Catalase A | Anti-oxidation | ↑ |
| Cerato-platanins (MpCP1) | Fungus-host interaction (hyphae growth, fruiting body formation and substrate adhesion) | DA | Basidiospores | Barsottini et al. 2013\*\* |
| Cerato-platanins (MpCP2) | Fungus-host interaction (hyphae growth, fruiting body formation and substrate adhesion) | DA |
| Cerato-platanins (MpCP3) | Fungus-host interaction (hyphae growth, fruiting body formation and substrate adhesion) | DA |
| Cerato-platanins (MpCP4) | Fungus-host interaction (hyphae growth, fruiting body formation and substrate adhesion) | DA |
| Cerato-platanins (MpCP5) | Fungus-host interaction (hyphae growth, fruiting body formation and substrate adhesion) | DA |
| MpPR-1 (pathogenesis-related 1) | Fungal pathogenicity (lipid transport) | ↑ | NA | Darwiche et al. 2017\*\* |
| Glyceraldehyde-3-phosphate dehydrogenase | Oxidoreductase | ↑ | Hypha | Silva et al. 2013\*\* |
| Heat shock protein HSS1 | Stress response | ↑ |
| Eukaryotic translation initiation factor 5A-1 | Protein biosynthesis | ↑ |
| 14-3-3 protein homolog | Stress response | ↑ |
| ATP synthase subunit beta | Transport | ↑ |
| Protein disulfide-isomerase 1 | Cell redox homeostasis | ↑ |
| 78-kDa glucose-regulated protein homolog  Cobalamin synthase | Stress response  Zinc ion binding | ↑  ↑ |
| Thiazole synthase | Suicide enzyme; stress response and in DNA damage tolerance | ↑ |
| Malate dehydrogenase | Oxidoreductase | ↑ |
| Acetyl-CoA acetyltransferase | Ergosterol biosynthetic process | ↑ |
| ATP synthase subunit alpha, mitochondrial | ATP catabolic process | ↑ |
| Phosphoglycerate kinase | Phosphoprotein | ↑ |
| S-adenosylmethionine synthase 2 | One-carbon metabolism | ↑ |
| Glyceraldehyde-3-phosphate dehydrogenase | Oxidoreductase | ↑ |
| Chaperone protein DnaK | Stress response | ↑ |
| ATP-dependent protease ATPase subunit HslU (heat shock) | Stress response | ↑ |
| Pyruvate kinase | Carbohydrate metabolism | ↑ |
| Autophagy-related protein 18 | Autophagy | ↑ |
| Ubiquitin-conjugating enzyme | Postreplication repair | ↑ |
| Transaldolase | Pentose-phosphate shunt (stress response) | ↑ |
| Probable phosphoketolase | Stress response | ↓ |
| Glyceraldehyde-3-phosphate dehydrogenase | Oxidoreductase | ↓ |
| GTP-binding nuclear protein | Autophagy | ↓ |
| Dihydroxy-acid dehydratase, mitochondrial | Amino acid biosynthesis | ↓ |
| Cell division control protein 48 | Cell cycle; Autophagy | ↓ |
| 60S ribosomal protein L6 | Cytoplasmic translation | ↓ |
| Malate dehydrogenase, mitochondrial | Oxidoreductase | ↓ |
| Catalase | Oxidoreductase | ↓ |
| 6-Phosphogluconate dehydrogenase,decarboxylating 1 | Oxidoreductase | ↓ |
| 5-Methyltetrahydropteroyltriglutamate | Stress response | ↓ |
| Chaperone protein ClpB | Stress response | ↓ |
| Heat shock protein 82 | Stress response | ↓ |
| Heat shock protein 90-2 | Stress response | ↓ |
| Heat shock protein HSS1 | Stress response | ↓ |
| Heat shock cognate 90-kDa protein | Stress response | ↓ |
| Heat shock protein Hsp88 | Stress response | ↓ |
| Thiazole synthase | Stress response | ↓ |
| 40S ribosomal protein | Ribosome biogenesis | ↓ |
| Nucleoside diphosphate kinase | Response to DNA damage stimulus | ↓ |
| Nucleoside diphosphate kinase Ndk1 | Repair of UV radiation- and etoposide-induced DNA damage | ↓ |
| Proteasome component PRE6 | Proteasomal ubiquitin-dependent protein catabolic process; regulation of mitotic cell cycle | ↓ |
| UPF0107 protein TSIB\_1943 | Phosphorylation | ↓ |
| Alanine--tRNA ligase, mitochondrial | Protein biosynthesis | ↓ |
| V-type proton ATPase subunit B | Phosphoprotein | ↓ |
| Mitochondrial-processing peptidase subunit beta | Phosphoprotein | ↓ |
| Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B | Protein biosynthesis | ↓ |
| ATP-dependent RNA helicase fal1 | rRNA processing | ↓ |
| Adenosylhomocysteinase | Phosphoprotein | ↓ |
| Asparagine synthetase [glutamine-hydrolyzing] 1 | Phosphoprotein | ↓ |
| SWI5-dependent HO expression protein 3 | Transport | ↓ |
| Paxillin-B | Zinc ion binding | ↓ |
| \*RPS1 | Protein synthesis or degradation | NA | Non-germinated basidiospores | Mares et al. 2016\*\* |
| \*UM00868.1 | Protein synthesis or degradation |
| \* UM05990.1 | Protein synthesis or degradation |
| \* RPS0 | Protein synthesis or degradation |
| \* UM03578.1 | Protein synthesis or degradation |
| \* UM01318.1 | Protein synthesis or degradation |
| \* UM04986.1 | Protein synthesis or degradation |
| \* UM04971.1 | Cellular metabolism |
| \* UM04562.1 | Cellular metabolism |
| \* UM02461.1 | Cellular metabolism |
| \* UM00595.1 | Cellular metabolism |
| \* UM02562.1 | Cellular metabolism |
| \* Tef1 | Cellular metabolism |
| \* UM05993.1 | Mitochondrial protein |
| \* UM05090.1 | Ion transport |
| \* UM04871.1 | Ion transport |
| \* UM03951.1 | Ion transport |
| \* UM00621.1 | Ion transport |
| \* UM03356.1 | Ion transport |
| \* UM03527.1 | Ion transport |
| \* UM04971.1 | Ion transport |
| \* UM04562 .1 | Ion transport |
| \* UM00595.1 | Ion transport |
| \* UM02462.1 | Ion transport |
| \* UM01672.1 | Cytoskeleton regulation and organization |
| \* UM0068.1 | Cytoskeleton regulation and organization |
| \* UM00403.1 | Cytoskeleton regulation and organization |
| \* UM05379.1 | Cytoskeleton regulation and organization |
| \* UM05918.1 | Cytoskeleton regulation and organization |
| \* UM06453.1 | Cytoskeleton regulation and organization |
| \* UM04507.1 | Cytoskeleton regulation and organization |
| \* UM02715.1 | Sporulation, reproduction and cell differentiation |
| \* UM028991.1 | Sporulation, reproduction and cell differentiation |
| \* UM03449.1 | Sporulation, reproduction and cell differentiation |
| \* UM03734.1 | Sporulation, reproduction and cell differentiation |
| \* UM06217.1 | Sporulation, reproduction and cell differentiation |
| \* CDC42 | Sporulation, reproduction and cell differentiation |
| \*UAC1 | Sporulation, reproduction and cell differentiation |
| \* KPP6 | Sporulation, reproduction and cell differentiation |
| \* RPB1 | Transcription |
| \* UM03988.1 | Transcription |
| \* UM00157.1 | Pyruvate kinase (transcription) |
| \* UM02776.1 | Nucleoside diphosphate kinase (transcription) |
| \* UM06156.1 | Transcription |
| \* UM06331.1 | Transcription |
| \* UM05334.1 | Transcription |
| \* UM03058.1 | Transcription |
| \* UM02324.1 | Transcription |
| \* UM04722.1 | Transcription |
| \* UM02903.1 | Transcription |

NA: not assigned

DA: differentially accumulated em diferentes condições experimentais dos estudos analisados.

\*Orthologous proteins of *Ustilagos maydis* in *Moniliophthora perniciosa* through System Biology.

\*\*References available at:<https://github.com/ArianaSantos/Santos-et-al.2022_systematic-review.git>