

**Supplemental Table 1. List of the genomic databases used in this study.**

Fungal species	Data source
<i>Alternaria brassicicola</i>	<a href="http://genome.jgi-psf.org/Altbr1/Altbr1.home.html">http://genome.jgi-psf.org/Altbr1/Altbr1.home.html</a>
<i>Botrytis cinerea</i>	<a href="http://www.broadinstitute.org/annotation/genome/botrytis_cinerea/Home.html">http://www.broadinstitute.org/annotation/genome/botrytis_cinerea/Home.html</a>
<i>Cochliobolus heterostrophus</i>	<a href="http://genome.jgi-psf.org/CocheC5_1/CocheC5_1.home.html">http://genome.jgi-psf.org/CocheC5_1/CocheC5_1.home.html</a>
<i>Cryphonectria parasitica</i>	<a href="http://genomeportal.jgi-psf.org/Crypa1/Crypa1.home.html">http://genomeportal.jgi-psf.org/Crypa1/Crypa1.home.html</a>
<i>Fusarium graminearum</i>	<a href="http://www.broadinstitute.org/annotation/genome/fusarium_graminearum/MultiHome.html">http://www.broadinstitute.org/annotation/genome/fusarium_graminearum/MultiHome.html</a>
<i>Fusarium oxysporum</i>	<a href="http://www.broadinstitute.org/annotation/genome/fusarium_graminearum/MultiHome.html">http://www.broadinstitute.org/annotation/genome/fusarium_graminearum/MultiHome.html</a>
<i>Fusarium verticillioides</i>	<a href="http://www.broadinstitute.org/annotation/genome/fusarium_graminearum/MultiHome.html">http://www.broadinstitute.org/annotation/genome/fusarium_graminearum/MultiHome.html</a>
<i>Heterobasidion annosum sensu lato</i>	<a href="http://genome.jgi-psf.org/cgi-bin/searchGM?db=Hetan2">http://genome.jgi-psf.org/cgi-bin/searchGM?db=Hetan2</a>
<i>Laccaria bicolor</i>	<a href="http://genome.jgi-psf.org/Lacbi1/Lacbi1.home.html">http://genome.jgi-psf.org/Lacbi1/Lacbi1.home.html</a>
<i>Magnaporthe oryzae</i>	<a href="http://www.broadinstitute.org/annotation/fungi/magnaporthe/">http://www.broadinstitute.org/annotation/fungi/magnaporthe/</a>
<i>Melampsora larici-populina</i>	<a href="http://genome.jgi-psf.org/Mellp1/Mellp1.home.html">http://genome.jgi-psf.org/Mellp1/Mellp1.home.html</a>
<i>Mycosphaerella fijiensis</i>	<a href="http://genome.jgi-psf.org/Mycfi1/Mycfi1.home.html">http://genome.jgi-psf.org/Mycfi1/Mycfi1.home.html</a>
<i>Mycosphaerella graminicola</i>	<a href="http://genome.jgi-psf.org/Mycgr3/Mycgr3.home.html">http://genome.jgi-psf.org/Mycgr3/Mycgr3.home.html</a>
<i>Mycosphaerella pini</i>	<a href="http://genome.jgi-psf.org/Dotse1/Dotse1.home.html">http://genome.jgi-psf.org/Dotse1/Dotse1.home.html</a>
<i>Mycosphaerella populinum</i>	<a href="http://genome.jgi-psf.org/Sepmu1/Sepmu1.home.html">http://genome.jgi-psf.org/Sepmu1/Sepmu1.home.html</a>
<i>Puccinia graminis-tritici</i>	<a href="http://www.broadinstitute.org/annotation/genome/puccinia_group/MultiHome.html">http://www.broadinstitute.org/annotation/genome/puccinia_group/MultiHome.html</a>
<i>Puccinia triticina</i>	<a href="http://www.broadinstitute.org/annotation/genome/puccinia_group/MultiHome.html">http://www.broadinstitute.org/annotation/genome/puccinia_group/MultiHome.html</a>
<i>Pyrenophora tritici-repentis</i>	<a href="http://genome.jgi-psf.org/Pyrtr1/Pyrtr1.home.html">http://genome.jgi-psf.org/Pyrtr1/Pyrtr1.home.html</a>
<i>Saccharomyces cerevisiae</i>	<a href="http://www.yeastgenome.org/">http://www.yeastgenome.org/</a>
<i>Sclerotinia sclerotiorum</i>	<a href="http://genome.jgi-psf.org/Sclsc1/Sclsc1.home.html">http://genome.jgi-psf.org/Sclsc1/Sclsc1.home.html</a>
<i>Stagonospora nodorum</i>	<a href="http://genome.jgi-psf.org/Stano1/Stano1.home.html">http://genome.jgi-psf.org/Stano1/Stano1.home.html</a>
<i>Trichoderma virens</i>	<a href="http://genome.jgi-psf.org/Trive1/Trive1.home.html">http://genome.jgi-psf.org/Trive1/Trive1.home.html</a>
<i>Tuber melanosporum</i>	<a href="http://www.genoscope.cns.fr/externe/GenomeBrowser/Tuber/">http://www.genoscope.cns.fr/externe/GenomeBrowser/Tuber/</a>
<i>Ustilago maydis</i>	<a href="http://genome.jgi-psf.org/Ustma1/Ustma1.home.html">http://genome.jgi-psf.org/Ustma1/Ustma1.home.html</a>
<i>Verticillium dahliae</i>	<a href="http://genome.jgi-psf.org/Verda1/Verda1.home.html">http://genome.jgi-psf.org/Verda1/Verda1.home.html</a>

**Supplemental References.**

1. **Amselem, J., et al.** (2011). Genomic analysis of the necrotrophic fungal pathogens *Sclerotinia sclerotiorum* and *Botrytis cinerea*. PLoS Genet. **7**: e1002230.
2. **Andrews, D.L., Egan, J.D., Mayorga, M.E., and Gold, S.E.** (2000). The *Ustilago maydis* *ubc4* and *ubc5* genes encode members of a MAP kinase cascade required for filamentous growth. Mol. Plant Microbe Interact. **13**: 781-786.
3. **Banuett, F., and Herskowitz, I.** (1994). Identification of Fuz7, a *Ustilago maydis* MEK/MAPKK homolog required for a-locus-dependent and -independent steps in the fungal life cycle. Genes Dev. **8**: 1367-1378.
4. **Brachmann, A., Schirawski, J., Müller, P., and Kahmann, R.** (2003). An unusual MAP kinase is required for efficient penetration of the plant surface by *Ustilago maydis*. EMBO J. **22**: 2199-2210.
5. **Brewster, J.L., de Valoir, T., Dwyer, N.D., Winter, E., and Gustin M.C.** (1993). An osmosensing signal transduction pathway in yeast. Science **259**:1760-1763.

6. **Bruno, K.S., Tenjo, F., Li, L., Hamer, J.E., and Xu, J.R.** (2004). Cellular localization and role of kinase activity of *PMK1* in *Magnaporthe grisea*. *Eukaryot. Cell* **3**: 1525-1532.
7. **Carbó, N., and Pérez-Martín, J.** (2010). Activation of the cell wall integrity pathway promotes escape from G2 in the fungus *Ustilago maydis*. *PLoS Genet.* **6**: e1001009.
8. **Cho, Y., Cramer, R.A., Jr., Kim, K.H., Davis, J., Mitchell, T.K., Figuli, P., Pryor, B.M., Lemasters, E., and Lawrence, C.B.** (2007). The *Fus3/Kss1* MAP kinase homolog *Amk1* regulates the expression of genes encoding hydrolytic enzymes in *Alternaria brassicicola*. *Fungal Genet. Biol.* **44**: 543-553.
9. **Choi, E.S., Chung, H.J., Kim, M.J., Park, S.M., Cha, B.J., Yang, M.S., and Kim, D.H.** (2005). Characterization of the ERK homologue CpMK2 from the chestnut blight fungus *Cryphonectria parasitica*. *Microbiology* **151**:1349-1358.
10. **Cousin, A., Mehrabi, R., Guilleroux, M., Dufresne, M., T, V.D.L., Waalwijk, C., Langin, T., and Kema, G.H.** (2006). The MAP kinase-encoding gene *MgFus3* of the non-appressorium phytopathogen *Mycosphaerella graminicola* is required for penetration and *in vitro* pycnidia formation. *Mol. Plant Pathol.* **7**: 269-278.
11. **Dean, R.A., et al.** (2005). The genome sequence of the rice blast fungus *Magnaporthe grisea*. *Nature* **434**: 980-986.
12. **Di Pietro, A., García-Maceira, F.I., Méglez, E., and Roncero, M.I.** (2001). A MAP kinase of the vascular wilt fungus *Fusarium oxysporum* is essential for root penetration and pathogenesis. *Mol. Microbiol.* **39**: 1140-1152.
13. **Di Stasio, M., Brefort, T., Mendoza-Mendoza, A., Münch, K., and Kahmann, R.** (2009). The dual specificity phosphatase Rok1 negatively regulates mating and pathogenicity in *Ustilago maydis*. *Mol. Microbiol.* **73**: 73-88.
14. **Dixon, K.P., Xu, J.R., Smirnoff, N., and Talbot, N.J.** (1999). Independent signaling pathways regulate cellular turgor during hyperosmotic stress and appressorium-mediated plant infection by *Magnaporthe grisea*. *Plant Cell* **11**: 2045-2058.
15. **Doeleman, G., Berndt, P., and Hahn, M.** (2006). Different signalling pathways involving a G $\alpha$  protein, cAMP and a MAP kinase control germination of *Botrytis cinerea* conidia. *Mol. Microbiol.* **59**: 821-835.
16. **Duplessis, S., et al.** (2011). Obligate biotrophy features unraveled by the genomic analysis of rust fungi. *Proc. Natl. Acad. Sci. USA* **108**: 9166-9171.

17. **Ebole, D.J., Jin, Y., Thon, M., Pan, H., Bhattachari, E., Thomas, T., and Dean, R.** (2004). Gene discovery and gene expression in the rice blast fungus, *Magnaporthe grisea*: Analysis of expressed sequence tags. *Mol. Plant Microbe Interact.* **17**: 1337-1347.
18. **Eliahu, N., Igbaria, A., Rose, M.S., Horwitz, B.A., and Lev, S.** (2007). Melanin biosynthesis in the maize pathogen *Cochliobolus heterostrophus* depends on two mitogen-activated protein kinases, Chk1 and Mps1, and the transcription factor Cmr1. *Eukaryot. Cell* **6**: 421-429.
19. **Errede, B., Gartner, A., Zhou, Z., Nasmyth, K., and Ammerer, G.** (1993). MAP kinase-related FUS3 from *S. cerevisiae* is activated by STE7 *in vitro*. *Nature* **362**: 261-264.
20. **Fujikawa, T., Kuga, Y., Yano, S., Yoshimi, A., Tachiki, T., Abe, K., and Nishimura, M.** (2009). Dynamics of cell wall components of *Magnaporthe grisea* during infectious structure development. *Mol. Microbiol.* **73**: 553-570.
21. **García-Pedrajas, M.D., Nadal, M., Böker, M., Gold, S.E., and Perlin, M.H.** (2008). Sending mixed signals: Redundancy vs. uniqueness of signaling components in the plant pathogen, *Ustilago maydis*. *Fungal Genet. Biol.* **45**: S22-30.
22. **Garrido, E., and Pérez-Martín, J.** (2003). The *crk1* gene encodes an Ime2-related protein that is required for morphogenesis in the plant pathogen *Ustilago maydis*. *Mol. Microbiol.* **47**: 729-743.
23. **Garrido, E., Voß, U., Müller, P., Castillo-Lluva, S., Kahmann, R., and Pérez-Martín, J.** (2004). The induction of sexual development and virulence in the smut fungus *Ustilago maydis* depends on Crk1, a novel MAPK protein. *Genes Dev.* **18**: 3117-3130.
24. **Gartner, A., Nasmyth, K., Ammerer, G.** (1992). Signal transduction in *Saccharomyces cerevisiae* requires tyrosine and threonine phosphorylation of FUS3 and KSS1. *Genes Dev.* **6**: 1280-1292.
25. **Hou, Z., Xue, C., Peng, Y., Katan, T., Kistler, H.C., and Xu, J.R.** (2002). A mitogen-activated protein kinase gene (*MGV1*) in *Fusarium graminearum* is required for female fertility, heterokaryon formation, and plant infection. *Mol. Plant Microbe Interact.* **15**: 1119-1127.
26. **Hu, G., Kamp, A., Lanning, R., Naik, S., and Bakkeren, G.** (2007). Complementation of *Ustilago maydis* MAPK mutants by a wheat leaf rust, *Puccinia triticina* homolog: Potential for functional analyses of rust genes. *Mol. Plant Microbe Interact.* **20**: 637-647.

27. Igbaria, A., Lev, S., Rose, M.S., Lee, B.N., Hadar, R., Degani, O., and Horwitz, B.A. (2008). Distinct and combined roles of the MAP kinases of *Cochliobolus heterostrophus* in virulence and stress responses. Mol. Plant Microbe Interact. **21**: 769-780.
28. Irie, K., Takase, M., Lee, K.S., Levin, D.E., Araki, H., Matsumoto, K., and Oshima, Y. (1993). *MKK1* and *MKK2*, which encode *Saccharomyces cerevisiae* mitogen-activated protein kinase-kinase homologs, function in the pathway mediated by protein kinase C. Mol. Cell Biol. **13**: 3076-3083.
29. Izumitsu, K., Yoshimi, A., Kubo, D., Morita, A., Saitoh, Y., and Tanaka, C. (2009). The MAPKK kinase ChSte11 regulates sexual/asexual development, melanization, pathogenicity, and adaptation to oxidative stress in *Cochliobolus heterostrophus*. Curr. Genet. **55**: 439-448.
30. Jenczmionka, N.J., Maier, F.J., Lösch, A.P., and Schäfer, W. (2003). Mating, conidiation and pathogenicity of *Fusarium graminearum*, the main causal agent of the head-blight disease of wheat, are regulated by the MAP kinase gpmk1. Curr. Genet. **43**: 87-95.
31. Jenczmionka, N.J., and Schäfer, W. (2005). The Gpmk1 MAP kinase of *Fusarium graminearum* regulates the induction of specific secreted enzymes. Curr. Genet. **47**: 29-36.
32. Jeon, J., Goh, J., Yoo, S., Chi, M.H., Choi, J., Rho, H.S., Park, J., Han, S.S., Kim, B.R., Park, S.Y., Kim, S., and Lee, Y.H. (2008). A putative MAP kinase kinase kinase, *MCK1*, is required for cell wall integrity and pathogenicity of the rice blast fungus, *Magnaporthe oryzae*. Mol. Plant Microbe Interact. **21**: 525-534.
33. Joubert, A., Bataille-Simoneau, N., Campion, C., Guillemette, T., Hudhomme, P., Iacomi-Vasilescu, B., Leroy, T., Pochon, S., Poupard, P., and Simoneau, P. (2011). Cell wall integrity and high osmolarity glycerol pathways are required for adaptation of *Alternaria brassicicola* to cell wall stress caused by brassicaceous indolic phytoalexins. Cell. Microbiol. **13**: 62-80.
34. Kaffarnik, F., Müller, P., Leibundgut, M., Kahmann, R., and Feldbrügge, M. (2003). PKA and MAPK phosphorylation of Prf1 allows promoter discrimination in *Ustilago maydis*. EMBO J. **22**: 5817-5826.
35. Klosterman, S.J., Martinez-Espinoza, A.D., Andrews, D.L., Seay, J.R., and Gold, S.E. (2008). Ubc2, an ortholog of the yeast Ste50p adaptor, possesses a basidiomycete-specific carboxy terminal extension essential for pathogenicity independent of pheromone response. Mol. Plant Microbe Interact. **21**: 110-121.

36. **Kominami, K., Sakata, Y., Sakai, M., and Yamashita, I.** (1993). Protein kinase activity associated with the *IME2* gene product, a meiotic inducer in the yeast *Saccharomyces cerevisiae*. *Biosci. Biotechnol. Biochem.* **57**: 1731-1735.
37. **Kramer, B., Thines, E., and Foster, A.J.** (2009). MAP kinase signalling pathway components and targets conserved between the distantly related plant pathogenic fungi *Mycosphaerella graminicola* and *Magnaporthe grisea*. *Fungal Genet. Biol.* **46**: 667-681.
38. **Krisak, L., Strich, R., Winters, R.S., Hall, J.P., Mallory, M.J., Kreitzer, D., Tuan, R.S., and Winter, E.** (1994). *SMK1*, a developmentally regulated MAP kinase, is required for spore wall assembly in *Saccharomyces cerevisiae*. *Genes Dev.* **8**: 2151-2161.
39. **Kulkarni, R.D., and Dean, R.A.** (2004). Identification of proteins that interact with two regulators of appressorium development, adenylate cyclase and cAMP-dependent protein kinase A, in the rice blast fungus *Magnaporthe grisea*. *Mol. Gen. Genomics* **270**: 497-508.
40. **Kumar, A., Scher, K., Mukherjee, M., Pardovitz-Kedmi, E., Sible, G.V., Singh, U.S., Kale, S.P., Mukherjee, P.K., and Horwitz, A.** (2010). Overlapping and distinct functions of two *Trichoderma virens* MAP kinases in cell-wall integrity, antagonistic properties and repression of conidiation. *Biochem. Biophys. Res. Commun.* **398**: 765-770.
41. **Lanver, D., Mendoza-Mendoza, A., Brachmann, A., and Kahmann, R.** (2010). Sho1 and Msb2-related proteins regulate appressorium development in the smut fungus *Ustilago maydis*. *Plant Cell* **22**: 2085-2101.
42. **Lee, K.S., Irie, K., Gotoh, Y., Watanabe, Y., Araki, H., Nishida, E., Matsumoto, K., and Levin, D.E.** (1993). A yeast mitogen-activated protein kinase homolog (Mpk1p) mediates signalling by protein kinase C. *Mol. Cell. Biol.* **13**: 3067-3075.
43. **Lee KS, and Levin DE.** (1992). Dominant mutations in a gene encoding a putative protein kinase (*BCK1*) bypass the requirement for a *Saccharomyces cerevisiae* protein kinase C homolog. *Mol. Cell. Biol.* **12**: 172-182.
44. **Lev, S., and Horwitz, B.A.** (2003). A mitogen-activated protein kinase pathway modulates the expression of two cellulase genes in *Cochliobolus heterostrophus* during plant infection. *Plant Cell* **15**: 835-844.
45. **Lev, S., Sharon, A., Hadar, R., Ma, H., and Horwitz, B.A.** (1999). A mitogen-activated protein kinase of the corn leaf pathogen *Cochliobolus heterostrophus* is involved in conidiation, appressorium formation, and pathogenicity: Diverse roles for mitogen-activated protein kinase homologs in foliar pathogens. *Proc. Natl. Acad. Sci. USA* **96**: 13542-13547.

46. **Lev, S., Tal, H., Rose, M.S., and Horwitz, B.A.** (2009). Signaling by the pathogenicity-related MAP kinase of *Cochliobolus heterostrophus* correlates with its local accumulation rather than phosphorylation. *Mol. Plant-Microbe Interact.* **22**: 1093-1103.
47. **Li, G., Zhou, X., Kong, L., Wang, Y., Zhang, H., Zhu, H., Mitchell, T.K., Dean, R.A., and Xu, J.R.** (2011). *MoSfl1* is important for virulence and heat tolerance in *Magnaporthe oryzae*. *PLoS One* **6**: e19951.
48. **Liu, W., Soulié, M.C., Perrino, C., and Fillinger, S.** (2011). The osmosensing signal transduction pathway from *Botrytis cinerea* regulates cell wall integrity and MAP kinase pathways control melanin biosynthesis with influence of light. *Fungal Genet. Biol.* **48**: 377-387.
49. **Liu, W., Zhou, X., Li, G., Li, L., Kong, L., Wang, C., Zhang, H., and Xu, J.R.** (2011). Multiple plant surface signals are sensed by different mechanisms in the rice blast fungus for appressorium formation. *PLoS Pathog.* **7**: e1001261.
50. **Ma, L.J., et al.** (2010). Comparative genomics reveals mobile pathogenicity chromosomes in *Fusarium*. *Nature* **464**: 367-373.
51. **Martin, F., et al.** (2008). The genome of *Laccaria bicolor* provides insights into mycorrhizal symbiosis. *Nature* **452**: 88-92.
52. **Martin, F., et al.** (2010). Périgord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. *Nature* **464**: 1033-1038.
53. **Mayorga, M.E., and Gold, S.E.** (1999). A MAP kinase encoded by the *ubc3* gene of *Ustilago maydis* is required for filamentous growth and full virulence. *Mol. Microbiol.* **34**: 485-497.
54. **Mayorga, M.E., and Gold, S.E.** (2001). The *ubc2* gene of *Ustilago maydis* encodes a putative novel adaptor protein required for filamentous growth, pheromone response and virulence. *Mol. Microbiol.* **41**: 1365-1379.
55. **Mehrabi, R., Ding, S., and Xu, J.R.** (2008). MADS-box transcription factor Mig1 is required for infectious growth in *Magnaporthe grisea*. *Eukaryot. Cell* **7**: 791-799.
56. **Mehrabi, R., Van der Lee, T., Waalwijk, C., and Gert, H.J.** (2006). *MgSlt2*, a cellular integrity MAP kinase gene of the fungal wheat pathogen *Mycosphaerella graminicola*, is dispensable for penetration but essential for invasive growth. *Mol. Plant Microbe Interact.* **19**: 389-398.

57. **Mehrabi, R., Zwiers, L.H., de Waard, M.A., and Kema, G.H.** (2006). *MgHog1* regulates dimorphism and pathogenicity in the fungal wheat pathogen *Mycosphaerella graminicola*. *Mol. Plant Microbe Interact.* **19:** 1262-1269.
58. **Mendoza-Mendoza, A., Eskova, A., Weise, C., Czajkowski, R., and Kahmann, R.** (2009). Hap2 regulates the pheromone response transcription factor *prf1* in *Ustilago maydis*. *Mol. Microbiol.* **72:** 683-698.
59. **Mendoza-Mendoza, A., Pozo, M.J., Grzegorski, D., Martínez, P., García, J.M., Olmedo-Monfil, V., Cortés, C., Kenerley, C., and Herrera-Estrella, A.** (2003). Enhanced biocontrol activity of *Trichoderma* through inactivation of a mitogen-activated protein kinase. *Proc. Natl. Acad. Sci. USA* **100:** 15965-15970.
60. **Mukherjee, P.K., Latha, J., Hadar, R., and Horwitz, B.A.** (2003). TmkA, a mitogen-activated protein kinase of *Trichoderma virens*, is involved in biocontrol properties and repression of conidiation in the dark. *Eukaryot. Cell* **2:** 446-455.
61. **Müller, P., Aichinger, C., Feldbrügge, M., and Kahmann, R.** (1999). The MAP kinase kpp2 regulates mating and pathogenic development in *Ustilago maydis*. *Mol. Microbiol.* **34:** 1007-1017.
62. **Müller, P., Weinzierl, G., Brachmann, A., Feldbrügge, M., and Kahmann, R.** (2003). Mating and pathogenic development of the smut fungus *Ustilago maydis* are regulated by one mitogen-activated protein kinase cascade. *Eukaryot. Cell* **2:** 1187-1199.
63. **Ochiai, N., Tokai, T., Nishiuchi, T., Takahashi-Ando, N., Fujimura, M., and Kimura, M.** (2007). Involvement of the osmosensor histidine kinase and osmotic stress-activated protein kinases in the regulation of secondary metabolism in *Fusarium graminearum*. *Biochem. Biophys. Res. Commun.* **363:** 639-644.
64. **Ortoneda, M., Guarro, J., Madrid, M.P., Caracuel, Z., Roncero, M.I., Mayayo, E., and Di Pietro, A.** (2004). *Fusarium oxysporum* as a multihost model for the genetic dissection of fungal virulence in plants and mammals. *Infect. Immun.* **72:** 1760-1766.
65. **Park, G., Xue, C., Zhao, X., Kim, Y., Orbach, M., and Xu, J.R.** (2006). Multiple upstream signals converge on the adaptor protein Mst50 in *Magnaporthe grisea*. *Plant Cell* **18:** 2822-2835.
66. **Park, G., Xue, C., Zheng, L., Lam, S., and Xu, J.R.** (2002). *MST12* regulates infectious growth but not appressorium formation in the rice blast fungus *Magnaporthe grisea*. *Mol. Plant Microbe Interact.* **15:** 183-192.
67. **Park, S.M., Choi, E.S., Kim, M.J., Cha, B.J., Yang, M.S., and Kim, D.H.** (2004). Characterization of HOG1 homologue, CpMK1, from *Cryphonectria parasitica* and

- evidence for hypovirus-mediated perturbation of its phosphorylation in response to hypertonic stress. *Mol. Microbiol.* **51**: 1267-1277.
68. **Pérez-Nadale, E., and Di Pietro, A.** (2011). The membrane mucin Msb2 regulates invasive growth and plant infection in *Fusarium oxysporum*. *Plant Cell* **23**: 1171-1185.
69. **Posas, F., Saito, H.** (1998). Activation of the yeast SSK2 MAP kinase kinase by the SSK1 two-component response regulator. *EMBO J.* **17**: 1385-1394.
70. **Prados Rosales, R.C., Di Pietro, A.** (2008). Vegetative hyphal fusion is not essential for plant infection by *Fusarium oxysporum*. *Eukaryot. Cell* **7**: 162-171.
71. **Ramamoorthy, V., Zhao, X., Snyder, A.K., Xu, J.R., and Shah, D.M.** (2007). Two mitogen-activated protein kinase signalling cascades mediate basal resistance to antifungal plant defensins in *Fusarium graminearum*. *Cell. Microbiol.* **9**: 1491-1506.
72. **Rauyaree, P., Ospina-Giraldo, M.D., Kang, S., Bhat, R.G., Subbarao, K.V., Grant, S.J., and Dobinson, K.F.** (2005). Mutations in VMK1, a mitogen-activated protein kinase gene, affect microsclerotia formation and pathogenicity in *Verticillium dahliae*. *Curr. Genet.* **48**: 109-116.
73. **Rhodes, N., Connell, L., and Errede B.** (1990). STE11 is a protein kinase required for cell-type-specific transcription and signal transduction in yeast. *Genes Dev.* **4**: 1862-1874.
74. **Rispail, N., and Di Pietro, A.** (2009). *Fusarium oxysporum* Ste12 controls invasive growth and virulence downstream of the Fmk1 MAPK cascade. *Mol. Plant-Microbe Interact.* **22**: 830-839.
75. **Rostagno, L., Prodi, A., and Turina, M.** (2010). Cpkk1, MAPKK of *Cryphonectria parasitica*, is necessary for virulence on chestnut. *Phytopathology* **100**: 1100-1110.
76. **Rui, O., and Hahn, M.** (2007). The Slt2-type MAP kinase Bmp3 of *Botrytis cinerea* is required for normal saprotrophic growth, conidiation, plant surface sensing and host tissue colonization. *Mol. Plant Pathol.* **8**: 173-184.
77. **Schamber, A., Leroch, M., Diwo, J., Mendgen, K., and Hahn, M.** (2010). The role of mitogen-activated protein (MAP) kinase signalling components and the Ste12 transcription factor in germination and pathogenicity of *Botrytis cinerea*. *Mol. Plant Pathol.* **11**: 105-119.
78. **Segmüller, N., Ellendorf, U., Tudzynski, B., and Tudzynski, P.** (2007). BcSAK1, a stress-activated mitogen-activated protein kinase, is involved in vegetative differentiation and pathogenicity in *Botrytis cinerea*. *Eukaryot. Cell* **6**: 211-221.

79. **Solomon, P.S., Waters, O.D., Simmonds, J., Cooper, R.M., and Oliver, R.P.** (2005). The *Mak2* MAP kinase signal transduction pathway is required for pathogenicity in *Stagonospora nodorum*. *Curr. Genet.* **48**: 60-68.
80. **Thines, E., Weber, R.W., and Talbot, N.J.** (2000). MAP kinase and protein kinase A-dependent mobilization of triacylglycerol and glycogen during appressorium turgor generation by *Magnaporthe grisea*. *Plant Cell* **12**: 1703-1718.
81. **Turina, M., Zhang, L., and Van Alfen, N.K.** (2006). Effect of *Cryphonectria hypovirus* 1 (CHV1) infection on Cpkk1, a mitogen-activated protein kinase kinase of the filamentous fungus *Cryphonectria parasitica*. *Fungal Genet. Biol.* **43**: 764-774.
82. **Urban, M., Mott, E., Farley, T., and Hammond-Kosack, K.** (2003). The *Fusarium graminearum* *MAP1* gene is essential for pathogenicity and development of perithecia. *Mol. Plant Pathol.* **4**: 347-359.
83. **Viterbo, A., Harel, M., Horwitz, B.A., Chet, I., and Mukherjee, P.K.** (2005). *Trichoderma* mitogen-activated protein kinase signaling is involved in induction of plant systemic resistance. *Appl. Environ. Microbiol.* **71**: 6241-6246.
84. **Xu, J.R., and Hamer, J.E.** (1996). MAP kinase and cAMP signaling regulate infection structure formation and pathogenic growth in the rice blast fungus *Magnaporthe grisea*. *Genes Dev.* **10**: 2696-2706.
85. **Xu, J.R., Staiger, C.J., and Hamer, J.E.** (1998). Inactivation of the mitogen-activated protein kinase Mps1 from the rice blast fungus prevents penetration of host cells but allows activation of plant defense responses. *Proc. Natl. Acad. Sci. USA* **95**: 12713-12718.
86. **Xue, C., Park, G., Choi, W., Zheng, L., Dean, R.A., and Xu, J.R.** (2002). Two novel fungal virulence genes specifically expressed in appressoria of the rice blast fungus. *Plant Cell* **14**: 2107-2119.
87. **Yan, L., Yang, Q., Sundin, G.W., Li, H., and Ma, Z.** (2005). The mitogen-activated protein kinase kinase BOS5 is involved in regulating vegetative differentiation and virulence in *Botrytis cinerea*. *Fungal Genet. Biol.* **47**: 753-760.
88. **Yoshimi, A., Kojima, K., Takano, Y., and Tanaka, C.** (2005). Group III histidine kinase is a positive regulator of Hog1-type mitogen-activated protein kinase in filamentous fungi. *Eukaryot. Cell* **4**: 1820-1828.
89. **Zhang, H., Xue, C., Kong, L., Li, G., and Xu, J.R.** (2011). A Pmk1-interacting gene is involved in appressorium differentiation and plant infection in *Magnaporthe oryzae*. *Eukaryot. Cell* **10**: 1062-1070.

90. **Zhao, X., Kim, Y., Park, G., and Xu, J.R.** (2005). A mitogen-activated protein kinase cascade regulating infection-related morphogenesis in *Magnaporthe grisea*. *Plant Cell* **17**: 1317-1329.
91. **Zhao, X., and Xu, J.R.** (2007). A highly conserved MAPK-docking site in Mst7 is essential for Pmk1 activation in *Magnaporthe grisea*. *Mol. Microbiol.* **63**: 881-894.
92. **Zheng, L., Campbell, M., Murphy, J., Lam, S., and Xu, J.R.** (2000). The *BMP1* gene is essential for pathogenicity in the gray mold fungus *Botrytis cinerea*. *Mol. Plant Microbe Interact.* **13**: 724-732.