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Adaptation to the Host Environment by Plant-Pathogenic Fungi
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Supplemental Table 2: transcription factors of plant-pathogenic fungi required for the ability to cause disease

Reference	TF	gene	TF type	*species*	host	virulence phenotype	other knock-out/knock-down phenotype	notes
(65)	AP1	AaAP1	bZIP	*Alternaria alternata*	tangerine, rough lemon	Non-pathogenic to rough lemon. When inoculated through wound sites, the mutants failed to incite any lesions.	Affects drug resistance. Mutantswere hypersensitive to H2O2 and ROS-generating oxidants, showed reduced vegetative growth, were less effective in detoxifying H2O2, and yet were unaltered in conidial formation or toxin production.	
(131)	AP1	BAP1	bZIP	*Borytis cinerea*	bean & soft fruit	virulence not affected in single mutant, but further reduced in bap1 skn7 double mutants	Pivotal regulator of ROS detoxification in vitro.	In planta analyses revealed that the Bap1 target genes were not expressed 2 days postinoculation although H2O2 was detectable.
(61; 112)	AP1	ChAP1	bZIP	*Cochliobolus heterostrophus*	maize	virulence not affected in single mutant, but reduced in ChAP1 skn7 double mutants	decreased resistance to oxidative stress. reduced expression of oxidative stress responsive genes; this effect is enhanced in ChAP1 skn7 double mutants.	Both proteins are predicted to work together in a complex and regulate oxidative stress. Antioxidant gene expression is impaired in both mutants and almost completely absent in the double mutant.
(120)	AP1	CgAP1	bZIP	*Colletotricum gloeosporioides*	poplar	obviously reduced	enhanced sensitivity to ROS, no growth or conidiation phenotype. Regulates ROS related genes	expression induced by ROS
(84; 85)	AP1	FgAP1	bZIP	*Fusarium graminearum*	wheat	no effect	affects oxidative stress & DON biosynthesis	
(42)	AP1	MoAP1	bZIP	*Magnaporthe oryzae*	rice and barley	required for pathogenicity	The bZIP transcription factor MoAP1 mediates the oxidative stress response and is critical for pathogenicity of the rice blast fungus Magnaporthe oryzae.	
(144)	AP1	MfAP1	bZIP	*Monilinia fructicola*	Rosaceae	smaller lesions on rose and peach petals in both KO and OE mutants	oxidative response altered expression of ROS and virulence related genes	upregulated upon infection

(83)	AP1	UmYAP1	bZIP	*Ustilago maydis*	maize	required for virulence	H2O2 resistance	
(113)	AreA/NIT2	NRF1	GATA	*Cladosporium fulvum*	tomato	reduced virulence, delayed colonization of the plant.	impaired growth on various nirogen sources, altered expression of several effector genes in vitro, reduced expression of Avr9 in planta.	Expression of diverse effectors is affected by nitrogen source in vitro. Deletion of Avr9 does not affect virulence, implying that NRF1 has additional virulence targets.
(50)	AREA/NIT2	Nir1	GATA	*Colletotrichum acutatum*	broad range fruit & flowers	impaired, but rescued by inoculation in presence of preferred nitrogen source		expression increased during appressorium production stage
(95)	AREA/NIT2	CLNR1	GATA	*Colletotrichum lindemuthianum*	bean	non pathogenic on leafs: rare lesions never extend. On petiole and stem, rare lesions may extend into watersoaked spots. On petiole and stem penetration and biotrophic phase are wild-type like, but establishment of necrotrophic phase is impaired.	unable to use a wide array of nitrogen sources, except aspartate, asparagine and alanine.	KO can be transcomplemented with AreA from Aspergillus nidulans
(39)	AreA/NIT2	AreA	GATA	*Fusarium graminearum*	wheat	reduced virulence	Reduced TRI gene expression and DON production, reduced vegetative growth, reduced conidiation, (defective response to non-favourable nitrogen sources) defective utilization of nitrate and glutamate.Deleyed maturation of ascospores, that can be rescued by addition of urea to the medium	AreA physically interacts with Tri10.
(25)	AREA/NIT2	FNR1	GATA	*Fusarium oxysporum*	tomato	reduced pathogenicity	growth impaired with NO3-, hypoxanthine or uric acid as a nitrogen source, but not on NH4+.	Fungal avirulence was not affected by the Fnr1 disruption as determined by normal resistance of the cultivar Motelle containing the I2 gene to this mutant.

(36)	AREA/ NIT2	NUT1	GATA	*Magnaporthe oryzae*	rice and barley	The infection efficiency of nut1- transformants on susceptible rice plants was similar to that of the parental strain, although lesions were reduced in size.	failed growth on a variety of nitrogen sources, but glutamate, proline and alanine could still be utilized.
(51)	AREA/ NIT2	NIT2	GATA	*Ustilago maydis*	maize	strongly compromised virulence	a major, but not the exclusive, positive regulator of nitrogen utilization. By transcriptome analysis of sporidia grown on artificial media devoid of favored nitrogen sources, we show that only a subset of nitrogen-responsive genes are regulated by Nit2, including the Gal4-like transcription factor Ton1 (a target of Nit2). Ustilagic acid biosynthesis is not under the control of Nit2, while nitrogen starvation-induced filamentous growth is largely dependent on functional Nit2. nit2 deletion mutants show the delayed initiation of filamentous growth on maize leaves
(90)	ART1	ART1	Zn2Cys6	*Fusarium graminearum*	wheat	reduced pathogenicity on flowering wheat heads.	Defect in starch hydrolysis and mycotoxin production. FgArt1 deletion resulted in impairment of germination in starch liquid medium and impaired starch hydrolysis as a result of significantly reduced α-amylase gene expression. The deletion strain was unable to produce trichothecenes and exhibited low Tri5 and Tri6 expression levels,

(90)	ART1	ART1	Zn2Cys6	*Fusarium verticilioides*	maize	reduced colonization of maize kernels	Defects in starch hydrolysis, no detectable level of fumonisin B1. Fum1 and Fum12 expression levels were undetectable in the deletion strain.	However, when the FvArt1-deleted F.□verticillioides strain was complemented with FgArt1, the resulting strain was unable to recover the production of fumonisin B1, although FgArt1 expression and starch hydrolysis were induced.
(22)	ART1	MoCOD1	Zn2Cys6	*Magnaporthe oryzae*	rice and barley	reduced lesions and delayed invasive growth.	reduced number of conidia and conidiophores. Decreased conidial germination and unable to make appressoria.	Homologs in other fungi characterized as regulators of b-glucosidase, maltase and a-amylase.
(74)	ASD4	ASD4	GATA	*Magnaporthe oryzae*	rice and barley	non-pathogenic	Δasd4 strains were impaired in nitrogen source utilization. TOR signaling is perturbed in Δasd4 mutant. KO has increased glutamine levels and reduced appressoria formation. Glutamine affects the TOR pathway, and this is the mechanism by which appressoria formation is reduced.	ATG8 is an autophagy gene whose expression was repressed in Δasd4 mutant.Autophagy is importnat for virulence and is affected by the TOR pathway. Lack of appressoria can be rescued by gln1 deletion or rapamycin treatment, both affacting the TOR pathway. However, resulting appressoria fail to penetrate.
(122)	ATF1	BcATF1	bZIP (ATF1/CREB)	*Botrytis cinerea*	bean & soft fruit	increased colonization efficiency	impaired conidia production and sclerotia formation, extremely vigorous growth in axenic culture, increased levels of SM	
(54; 130)	ATF1	FgAtf1	bZIP (ATF1/CREB)	*Fusarium graminearum*	wheat and maize	strongly reduced virulence. Constitutive expression results in hypervirulence on wheat maize and *Brachypodium distachyon*	more sensitive to osmotic stress, less sensitive to oxidative stress, delayed sexual reproduction, increased DON production in vitro, but reduced during infection.	Activated via the MAPK FgOS-2. Appears to intercat with FgOs-2 under osmotic stress conditions. Overexpression of FgAtf1 almost conpletely rescues the FgOS-2 knock-out phenotype. ΔFgskn7ΔFgatf1 double mutant has defects in various stresses and conidiation
(43)	ATF1	MoATF1	bZIP (ATF1/CREB)	*Magnaporthe oryzae*	rice and barley	necessary for full virulence	The basic leucine zipper transcription factor Moatf1 mediates oxidative stress responses and is necessary for full virulence of the rice blast fungus Magnaporthe oryzae	
(18; 117)	BDTF1	BDTF1	GAL4-like Zn2Cys6	*Alternaria brassicicola*	cabbage	essential for full virulence	essential for detoxification of brassinin (an antifungal indolyl compound produced by brassica sp.) and possibly its derivatives.	

(35)	BIZ1	BIZ1	C2H2	*Ustilago maydis*	maize	non-pathogenic impaired appressorium formation and proliferation of in plant tissue. Deletion mutants arrest growth after plant penetration.	When grown in liquid culture, the deletion strains showed no obvious phenotypic alterations with respect to morphology and cell cycle profile or growth properties in various media. Higher frequency of filaments carrying more than two nuclei, suggesting a defect in the ability to arrest mitosis.	biz1 expression is strictly dependent on the presence of an active bE/bW heterodimer. BIZ1 is not expressed in vitro and expressed at all stages during pathogenic development. BIZ1 overexpression downregulates the mitotic cyclin Clb1, leading to cell cycle arrest.
(139)	CDTF1	MoCDTF 1		*Magnaporthe oryzae*	rice and barley	non-pathogenic	important in vegetative growth and colony pigmentation. Deletion completely blocks production of asexual and sexual spores. KO is easy wettable. required for appressorium formation from mycelium.	required for efficient hyphal growth, melanization and hydrophobicity. No conidiophores in the mutants, indicating that the defect in conidiation of the mutants is associated with lack of conidiophore formation rather than subsequent conidiogenesis.
(28)	CLTA1	CLTA1	GAL4-like Zn2Cys6	*Colletotrichum lindemuthianum*	bean	Penetration and biotrophic stage as wild-type, but unable to form necrotrophic hyphae.	not determined	
(128)	CMR1	CMR1	C2H2 and Zn2Cys6	*Colletotrichum lagenarium*	cucumber	not determined	defect in mycelial melanization, but not in appressorial melanization.	
(29)	CMR1	CMR1	C2H2 and Zn2Cys6	*Cochliobolus heterostrophus*	maize	no effect	mutants that lacked dark pigmentation and acquired an orange-pink color. In cmr1 deletion strains the expression of putative scytalone dehydratase (SCD1) and hydroxynaphthalene reductase (BRN1 and BRN2) genes involved in melanin biosynthesis was undetectable	CMR1 gene was transcribed in both sense and antisense directions, apparently producing mRNA as well as a long noncoding RNA transcript.
(128)	CMR1	PIG1	C2H2 and Zn2Cys6	*Magnaporthe oryzae*	rice and barley	no effect	lack of pigmentation in culture	
(33)	CMR1	CMRA		*Alternaria alternata*	citrus	not determined	white colonies due to the lack of melanin. In addition, hyphal diameter and spore morphology were changed in the mutant and	

							the number of spores reduced.	
(20)	CMR1	AMR1	C2H2	*Alternaria brassicicola*	cabbage	deletion mutant shows increased virulence	reduced melanin biosynthesis, improved pectin usage, more sensitive to UV and glucanase digestion, increased secretion of a pink non-phytotoxic pigment.	Homolog of CMR1, a transcription factor that regulates melanin biosynthesis in several fungi.
(141)	COM1	COM1	HLH	*Magnaporthe oryzae*	rice and barley	Significantly reduced in virulence. Defective in appressorium turgor generation, penetration, and infectious growth.	Aberrant conidial shape (slender) and reduced conidiation.	
(104)	CON7	Con7-1	C2H2	*Fusarium oxysporum*	tomato	non pathogenic. Regulates genes involved in host-pathogen interactions (CHECK which ones!)	altered morphogenesis incl. Cell wall structure, polar growth, hyphal branching, conidiation. Regulates genes involved inmorphogenesi and development, signal perception and transduction, primary and secondary metabolism.	homolog of Mo Con7 gene, two identical non-functional homologs (Con7-2) encoded on one of the accesory chromosomes. WAAR IS DE PAPER MET Mo CON&???
(89)	CON7	CON7	C2H2	*Magnaporthe oryzae*	rice	non-pathogenic	Misformed conidia and germtubes. Unable to form appressoria. Reduced vegetative growth rate. Abberrant cell wall. Regulates genes involved in biosynthesis or remodelling of the fungal cell wall, or the signalling systems controlling pathogenic development.	
(126)	CON7	VTA2	C2H2	*Verticillium albo-atrum*	tomato	not determined	reduced in growth rate and early formation of microsclerotia. Defect in conidiation and increased sensitivity to H2O2.	

(126)	CON7	VTA2	C2H2	*Verticillium dahliae*	tomato	yes, required for systemic colonization of plant roots	reduced in growth rate and showed early formation of microsclerotia. Defect in conidiation. Increased sensitivity to H2O2. Overexpression inhibits microsclerotia formation.	Regulates CDP1 expression, coding for a Pth11-like protein
(126)	CON7	VTA2	C2H2	*Verticillium longisporum*	oilseed rape	required for virulence	increased sensitivity to H2O2. Overexpression inhibits microsclerotia formation.	
(153)	COS1	COS1	C2H2	*Magnaporthe oryzae*	barley and rice	Increased pathogenicity of mycelium on unwounded leafs.	complete loss of conidiation. No conidiophore stalk.	DNA sequence analysis of promoter regions of those of COS1-dependent genes showed enrichment in the DNA sequence AAAAGAAA (A4GA3), the putative COS1-binding motif. Gel shift experiments showed that COS1 binds to DNA elements with A4GA3 motif. These suggest that many of the COS1-dependent transcripts may be regulated directly by COS1 binding.
(108)	CPC1	CPC1	bZIP	*Fusarium fujikuroi*	rice	not determined	Sensitive to amino acid synthesis inhibitors. Cpc1 regulates expression of amino acid biosynthesis genes.	The deletion of glnA, encoding the glutamine synthetase (GS), had led to the down-regulation of genes involved in secondary metabolism and up-regulation of cpc1. Cpc1 does not repress SM production, suggesting that Cpc1 is not responsible for the GS-dependent down-regulation of secondary metabolism and that its role is focused on the activation of amino acid biosynthesis in response to the amino acid status of the cell. Cross-pathway control is repressed by nitrogen limitation in an AreA-dependent manner.
(123)	CPC1	Cpc1	bZIP	*Vericillium dahliae*	tomato	strongly reduced symptoms	sensitive to amino acid starvation.	
(123)	CPC1	Cpc1	bZIP	*Verticillium longisporum*	cruciferous crops like Brassica napus	significantly fewer symptoms	silencing of the two Cpc1 isogenes (VlPC1-1 and VlPC1-2) rsults in high amino acid starvation sensitivity	silencing

(31)	CpcA	CPCA	bZIP	*Leptospaeria maculans*	canola	not determined	Sir repressive circumstances (aa starvation) failed to repress SirP and sir Z expression in a c CPCA silenced strain.	
(109)	CRZ1	BcCRZ1	zinc finger	*Botrytis cinerea*	bean & soft fruit	full virulence on bean	Calcineurin-responsive zinc finger transcription factor CRZ1 of Botrytis cinerea is required for growth, development, and full virulence on bean plants	
(21; 147)	CRZ1	MoCRZ1	zinc finger	*Magnaporthe oryzae*	rice and barley	required for pathogenicity	a calcineurin-responsive transcription factor, controls growth and development	
(149)	CRZ1	PdCrz1	zinc finger	*Penicillium digitatum*	citrus (postharvest)	reduced virulence	conidiation, cell wall integrity, Ca++ and H2O2 sensitivity and DMI resistance. Reduced expression of 3 cell wall synthase genes and 2 P-type ATPase genes.	calcineurin response
(46)	CRZ1	VpCRZ1	zinc finger	*Valsa pyri*	pear and apple	impaired pathogenicity	lost the ability to form fruiting bodies, enhanced pigment deposition and increased resistance against cell wall preturbing agents.	Congo red resistance genes and chitin synthetase genes are upregulated in the KO. CRZ1 localizes to the nucleus in a Ca++ dependant manner.
(137)	CRZ1	VdCRZ1	zinc finger	*Vericillium dahliae*	tomato	delayed symptomson smoke tree	microsclerotia development and melanin accumulation impaired, hypersensitive to high Ca++ and cell wall preturbing agents	
(62)	CTF1	Ctf1alpha	zinc finger	*Fusarium solani f.sp. pisi*	pea	reduced	loss of expression of lipases and cutinases on inducive substrates	Activated upon perception of cutin monomers (produced by a low expressed cutinase). Regulates high expression of an inducible cutinase.
(135)	DEP6	DEP6		*Alternaria brassicicola*	cabbage	small but significant reduction	Impaired in the production of depudecin, an eleven carbonlinear polyketide, and an inhibitor of HDAC	the depudecin cluster contains 6 genes. Predicted functions DEP5: polyketide synthase, DEP6: TF, DEP2, DEP4: monooxygenase, DEP3 Major facilitator transporter, DEP1: unknown function. DEP6 is required for expression of DEP1-5.

(96)	DUO1	MoDUO1		*Magnaporthe oryzae*	rice	significantly attenuated virulence	Affects the formation pattern of conidiophores and conidial morphology, such as abnormal nucleic numbers in conidia and delayed extension of infectious hyphae.	DUO1 is a major component of the Dam1 complex. Proteomics-based investigation revealed that the expression of four mitosis- related proteins is shut down in the MoDUO1 mutant, suggesting that MoDuo1 may have a function in mitosis.
(56; 151)	EBR1	EBR1	Zn2Cys6	*Fusarium graminearum*	wheat	reduced virulence	Enhanced hyphal branching, reducedconidiation	FoEBR1 can complement the Fgebr1 deletion mutant
(56)	EBR1	EBR1	Zn2Cys6	*Fusarium oxysporum*	tomato	minor decrease in pathogenicity	impaierd growth	RNAseq of Fgebr1 and Foebr1 deletion mutants shows EBR1 controlsa different set of genesin each fungus.
(22)	EBR1	MoCOD2	Zn2Cys6	*Magnaporthe oryzae*	rice	restricted to the first invaded cell. Strong plant response at the site of infection.	Reduced number of conidia and conidiophores. Elongated germtubes, similar to cpka and Mohox7 deletion mutants. Sensitivity to ROS unaltered.	
(114)	FHS1	FHS1	Zn2Cys6	*Fusarium graminearum*	wheat	reduced pathogenicity. Able to infect the inoculated spikelet; but no spread into neighbouring spikelets.	Hypersensitive to hydroxyurea and defective in mitotic cell division: more nuclei per cell. Defects in perithecia production, perithecia neither matured nor produced ascospores. Accumulation of DNA damage.	High proportions of genes included in “Cell rescue, defense and virulence”, “Metabolism”, “Cellular transport”, “Interaction with the environment”, and “Energy” were highly up-regulated or down-regulated in the *fhs1* deletion mutant compared with the other groups
(94)	FKH1	FKH1	FH	*Magnaporthe oryzae*	rice and barley	Reduced virulence.	Reduced mycelial growth and conidial germination, abnormal septation and stress response.	
(32)	FKH1	SsFKH1	FH	*Sclerotinia sclerotiorum*	flowers & vegetables	Disease assays demonstrated that pathogenicity in RNAi-silenced strains was significantly compromised with the development of a smaller infection lesion on tomato leaves	slow hyphal growth and sclerotial developmental defects. In addition, the expression levels of a set of putative melanin biosynthesis-related laccase genes and a polyketide synthase-encoding gene were significantly down-regulated in silenced strains.	silencing
(52)	FOW2	FOW2	Zn2Cys6	*Fusarium oxysporum f.sp. melonis and f.sp. lycopersici*	melon or tomato	complete loss of pathogenicity	no effect on vegetative growth or conidiation	

(146)	FOX1	FOX1	FH	*Ustilago maydis*	maize	reduced virulence and impaired tumor development.	The Δfox1 hyphae induces plant defence responses (accumulation of H2O2 in and around infected cells and encasement of proliferating hyphae in a cellulose-containing matrix). The phenotype can be attributed to the fox1-dependent deregulation of several effector genes that are linked to pathogenic development and host defense suppression.	Exclusively expressed during biotrophic development. Regulates genes encoding proteins involved in sugar processing and transport and genes coding for secreted proteins in planta, but not when expressed *in vitro*.The plant-specific expression of fox1 is independent from the b-mating-type locus. The bE/bW heterodimer is neither sufficient to induce fox1 expression in axenic culture nor required for fox1 expression during in planta growth. Because ectopic expression of Fox1 in axenic culture has no influence on the gene expression profile, we have to assume that, in addition to its transcriptional regulation, Fox1 is regulated via either posttranslational modifications or the interaction with cofactors present only under the specific developmental or environmental conditions within the host plant.
(87; 129)	FTF	FTF1 & FTF2	Zn2Cys6	*Fusarium oxysporum*	pea (f.sp. pisii) and tomato (f.sp. lycopersici)	reduced virulence of FTF2 knock-out, reduced virulence when entire gene family partially silenced	none reported	Expression upregulated in planta. Ftf1 and Ftf2 can bind to a motif found in the promoter of effector genes and induce their expression. This required SGE1.
(101)	FUG	FUG1		*Fusarium verticilioides*	maize	impaired maize kernel colonization	impaired fumonisin biosynthesis, increased sensitivity to benzoxazolinone and H2O2	Protein localizes to the nucleus, can bind DNA and has a domainof unknown function associated with previously characterized TFs. The KO differentially expressed genes in sec metabolism and mycelial development in the kernel environment.
(103)	FUM21	FUM21	Zn2Cys6	*Fusarium fujikuroi*	rice	not determined	regulates fumonisin biosynthesis. Both AreA and AreB are critical for the action of Fum21 and efficient fumonisin production in F. fujikuroi	
(103)	FUM21	FUM21	Zn2Cys6	*Fusarium verticilioides*	maize	Required for pathogenicity	regulates fumonisin biosynthesis. Maize supplements induce fumonisin production in F.	

							verticillioides, but not in F. fujikuroi	
(57)	Hac	AbHacA	bZIP	*Alternaria brassicicola*	cabbage	non pathogenic	Unf.Prot. Resp. impaired secretion and cell wall defects, increased in vitro susceptibility to antimicrobial plant metabolites	
(44; 47)	Hac	CIB1	bZIP	*Ustilago maydis*	maize	non pathogenic.	Regulator of the unfolded protein response. Required for the expression of some effector genes. required for resistance to ER stress-inducing agents.	Interacts with Clp1 and stabilizes Clp1.
(100)	HAP complex	FvHAP2, FvHAP3, FvHAP5		*Fusarium verticilioides*	maize	single KO of any of the genes resulted in impaired infection and colonization of maize stalks.	single KO of any of the genes resulted in reduced radial growth and conidiation, altered colony morphology, derepression of pigmentation, hypersensitivity to osmotic and oxidative stress.	
(69)	HAPX	HapX	bZIP	*Fusarium oxysporum*	tomato	reduced capacity to invade and kill tomato plants.	KO shows derepression of genes involved in iron consuming pathways and reduced growth under iron-depleted conditions.	HapX contributes to iron competition of *F.oxysporum* in the rhizosphere.
(2)	HOX	HOX8	homeobox	*Botrytis cinerea*	bean & soft fruit	abnormal infection cushions, colonization efficiency compromised		
(58)	HOX	MoHOX7	homeobox	*Magnaporthe oryzae*	rice and barley	ΔMohox7: non-pathogenic, defect in appressoria formation.	ΔMohox7: unable to form appressoria.	systematic deletion of all homeobox TFs: ΔMohox3 & ΔMohox5: no phenotype detected. ΔMohox1: reduction in hyphal growth & increased melanin pigmentation. ΔMohox2: asexual reproduction completely abolished, but still fully pathogenic. ΔMohox4: significant reduced conidium size. ΔMohox6: significant reduced hyphal growth.
(110)	LTF1	BcLTF1	GATA	*Botrytis cinerea*	bean & soft fruit	yes	light response, stricholactone blind? (Belmondo 2016 curr genet)	homologs in other fungi

(115)	MANY	SYSTEMATIC ANALYSIS OF 657 TFs	various	*Fusarium graminearum*	wheat	61 TFs are required for virulence, and of those 7 TFs have no pleiotropic phenotypes.	Six major phenotypic categories including mycelial growth, sexual development, conidia production, virulence, toxin production, and stress responses. A substantial fraction of the mutants (26%, 170/657) displayed clearly visible mutant phenotypes, with 73% (124/170) of these mutants exhibiting multiple mutant phenotypes and 27% (46/170) with single mutant phenotype .	There are 709 putative TFs in the genome. Mutations causing defects in perithicia development frequently affect multiple other phenotypes.
(71)	MANY	SYSTEMATIC ANALYSIS OF 104 TFs	Zn2Cys6	*Magnaporthe oryzae*	rice and barley	8 genes were involved in pathogenicity, of which 5 in barley and 7 in rice.	A substantial fraction of the mutants (58.7%, 61/104) clearly displayed visible phenotypes. 27 genes were involved in mycelial growth, 25 genes in conidial production, 12 TF genes in conidial germination and 10 TF genes in appressorium formation.	There are 163 putative Zn2Cys6 TFs in the genome
(10)	MANY	SYSTEMATIC ANALYSIS OF 47 TFs	C2H2	*Magnaporthe oryzae*	rice and barley	22 TFs are involved in pathogenicity	44 genes are involved in any of the tested functions. Growth (20 genes), conidiation (28 genes), appressorium formation (4 genes)	
(133)	MeaB	MeaB	bZIP	*Fusarium fujikuroi*	rice	not determined	regulates bik expression together with AreA	
(70)	MeaB	MeaB	bZIP	*Fusarium oxysporum*	tomato	Increased pathogenicity on tomato plants supplemented with ammonium rather than nitrate		proposed that a conserved nitrogen-responsive pathway might operate via TOR and MeaB to control virulence. Ammonium represses virulence related functions and this can be restored by Gln synthetase inhibitors, TOR protein kinase inhibitors or MeaB deletion

(12)	MedA	Med1		*Ustilago maydis*	maize	reduced virulence	mating, pheromone response. med1 is required for in vitro mating and filamentation. Δmed1 mutants are reduced in expression of the transcription factor prf1, the pheromeone receptor pra1 and the a1 pheromone mfa1	
(150)	MEF2-type MADS box	BcMADS 1	MADS box	*Botrytis cinerea*	apple fruit	required for the full virulence potential	indispensable for sclerotia production	BcMADS1may influence sclerotia formation (which is darkness dependant) by regulating the expression of light responsive genes. BcMADS1 regulates protein levels of BcSEC14 and BcSEC31 (both associated with vescicle transport). Single KOs of BcSEC14 and BcSEC31 are also impaired in virulence and protein secretion. The virulence defect o the BcMADS1 KO may be caused by a defect in protein secretion.
(92)	MEF2-type MADS box	Fmt2	MADS box	*Fusarium verticilioides*	maize	no effect	decreased vegetative growth and FB1 production when compared to the wild-type. Fmt2 did not display a change in PKS gene expression. Significantly, the deletion of MADS2 in the MAT1-2 genotype led to strains that failed to produce perithecia and ascospores when crossed with the MAT1-1 wild-type strain.	

(75)	MEF2-type MADS box	MIG1	MADS box	*Magnaporthe oryzae*	rice and barley	nonpathogenic and failed to infect rice leaves through wounds. Appressoria formed by the mig1 mutant developed penetration pegs and primary infectious hyphae, but further differentiation of the secondary infectious hyphae inside live plant cells was blocked. However, the mig1 mutant formed infectious hypha-like structures in heat-killed plant cells or cellophane membranes.	The mig1 mutant was reduced in aerial hyphal growth and conidiation but had no defect in growth rate and cell wall integrity. The mig1 deletion mutant had a normal growth rate and formed melanized appressoria.	MIG1 interacts with MPS1 (MAPK)
(99)	MEF2-type MADS box	SsMADS	MADS box	*Sclerotinia sclerotiorum*	tomato	reduced virulence	reduced growth	
(26)	MYB1	MoMYB1	Myb	*Magnaporthe oryzae*	rice and barley	tissue specific	vegetative growth, conidiogenisis and cell wall biosynthesis	
(66)	MYT2	Myt2	Myb	*Fusarium graminearum*	wheat	overexpression results in reduced virulence	deletion results in a larger perithicium and overexpression in a smaller perithicium. Overexpression also affects vegetative growth, conidia production and mycotoxin production.	thought to primarily be a perithicium size regulator.

(59)	MYT3	MYT3	Myb	*Fusarium graminearum*	wheat	reduced pathogenicity	Deletion of MYT3 resulted in impairment of conidiation, germination, and vegetative growth compared to the wild type. the Dmyt3 strain grew poorly on nitrogen-limited media; however, the mutant grew robustly on minimal media supplemented with ammonium.Significant reductions in trichothecene production and transcript levels of trichothecene biosynthetic genes.	
(27)	Ndt80	UNH1	Ndt80-like	*Ustilago maydis*	maize	very late stage: teliospore formation.	plays a role in sexual development, tumor maturation, teliospore developmentand meiotic completion. OE mutants have abnormal pigmentation	Unh1, an Ustilago maydis Ndt80-like protein, controls completion of tumor maturation, teliospore development, and meiosis.
(23)	NUC2	VdNUC-2		*Vericillium dahliae*	tomato	reduced virulence	under Pi starvation: reduced growth compared to WT, reduced conidiation and resistance to H2O2.	
(20)	PacC	AbPacC	zinc finger	*Alternaria brassicicola*	cabbage	non pathogenic	non reported	
(143)	PacC	PacC	zinc finger	*Colletotrichum acutatum*	citrus	required for virulence	hypersensitive to a wide range of compounds, but more tolerant to CWDE. Lower chitin cell wall content and lower cellulase, cutinase, xylanase and catalase activity, but increased pecteolytic activity.	increased expression of endo-polygalacturonases and cellulases. Expression of cutinase abolished.
(82)	PacC	PAC1	zinc finger	*Colletotricum gloeosporioides*	avocado	dramatically reduced virulence	reduction of pectate lyase PELB transcript, delayed PL secretion on normal medium, but increase on glucose, sucrose and fructose	PELB is regulated by a multi-factor regulation, including pH and sugar.

(76; 115)	PacC	PAC1	zinc finger	*Fusarium graminearum*	wheat	not reqiured for pathogenicity	reduced development under neutral and alkaline pH, increased sensitivity to H2O2, earlier Tri gene induction and toxin accumulation at acidic pH. A strain expressing the FgPac1c constitutively active form of Pac1 exhibited a strongly repressed Tri gene expression and reduced toxin accumulation at acidic pH.	
(11)	PacC	PacC	zinc finger	*Fusarium oxysporum*	tomato	KO is more virulent and a dominant activating allelereduces virulence.	poor growth at alkaline pH, increased acid protease activity and higher levels of aid-expressed polygalacturonase genes.	Binds to the consensus motif GCCAAG elevated in alkaline conditions
(60)	PacC	MoPACC	zinc finger	*Magnaporthe oryzae*	barley and rice	partial loss in virulence towards barley and rice	loss in growth rate from pH 5 to 8, loss in conidia production at pH 8 in vitro, decreased production of secreted lytic enzymes.	expression increased under alkaline conditions Conidia formation and germination were affected by pH (HOW??) whereas fungal growth and appressorium formation were not. Growth in vitro and in planta was characterized by alkalinization and ammonia accumulation in the surrounding medium.
(148)	PacC	PdPacC	zinc finger	*Penicillium digitatum*	citrus fruit (post harvest)	attenuated virulence on citrus fruit	reduced growth on neutral or alkaline medium and on medium with pectin as a sole C-source. Lack of induction of polygalacturonase Pdg2 and pectin lyase Pdpn1.	virulence phenotype may be caused by lack of Pdpg2 expression in the PdPacC knock-out elevated under alkaline conditions, in planta (despite pH3-3.5), and in the presence of Na+ or pectin
(5)	PacC	PacC	zinc finger	*Penicillium expansum*	fruit (post harvest)	degree of pathogenicity correlates with PacC expression and patulin production		downregulation of GOX2 (D-gluconic acid - GLA- synthesis) and IDH (patulin synthesis - SM). Decrease in GLA accumulation, and not low pH, seems to be the cause for patulin accumulation.
(102)	PacC	Pac1	zinc finger	*Sclerotinia sclerotiorum*	flowers & vegetables	essential for pathogenicity	required for sclerotial development	

(102)	PacC	Rim101	zinc finger	*Ustilago maydis*	maize	no effect	Deletion mutants were not affected in the in vitro pH-induced dimorphic transition, their growth rate, resistance to hypertonic sorbitol or KCl stress, and pathogenicity. However, they displayed a pleiotropic phenotype with alterations in morphogenesis, impairment in protease secretion, and increased sensitivity to Na+ and Li+ ions, increased sensitivity to lytic enzymes, and augmented polysaccharide secretion).	expression at neutral pH higher than at acidic pH
(38; 79)	part of SAGA complex	SPT3	components of SAGA complex	*Botrytis cinerea*	bean	yes, virulence	growth differentiation and H2O2 resistance	SPT3 was also identified as a virulence factor in F. oxysporum in an insertional muatgenesis screen.
(37)	part of SAGA complex	SPT3	components of SAGA complex	*Fusarium graminearum*	wheat	90% decrease in virulence on wheat	reduced growth, loss of conidia production, no sexual reproduction on infected wheat kernels, altered pigment formation. Increased DON production.	Expression of sporulation related genes FgFlbC and FgRen1 significantly reduced in the deletion mutants. Increased expression of *TRI5* and *TRI6.*
(37)	part of SAGA complex	SPT8	components of SAGA complex	*Fusarium graminearum*	wheat	90% decrease in virulence on wheat	reduced growth, loss of conidia production, no sexual reproduction on infected wheat kernels, altered pigment formation. Increased DON production.	Expression of sporulation related genes FgFlbC and FgRen1 significantly reduced in the deletion mutants. Increased expression of *TRI5* and *TRI6.*
(72)	PF	VdPF	Zn2Cys6	*Vericillium dahliae*	tomato	reduced virulence	reduced formation of conidia, impaired in microsclerotia formation, melanin deficient	
(19)	PF2	AbPf2	GAL4-like Zn2Cys6	*Alternaria brassicicola*	Brassica oleracea	The hyphae of the mutants grew slowly but did not cause disease symptoms on the surface of host plants.	frequency and timing of germination and appressorium formation on host plants were similar between the non-pathogenic Δabpf2 mutants and wild-type A. brassicicola. The mutants were also similar in vitro to wild-type A. brassicicola in terms of vegetative growth, conidium production, and responses to a	AbPF2 dependent upregulation of eight putative effector genes in planta.

							phytoalexin, reactive oxygen species and osmolites.	
(45)	PRF1	PRF1	HMG box	*Ustilago maydis*	maize	loss of pathogenicity	prf1 mutants do not express the a and b mating genes and are sterile.	
(17)	PRO1	AbPRO1	Zn2Cys6	*Alternaria brassicicola*	cabbage	reduced virulence	reduced vegetative growth	
(48; 49)	RBF1	RBF1	C2H2	*Ustilago maydis*	maize	reduced pathogenicity	Required for b-dependant filament formation. Required and sufficient to induce filamentous growth and a G2 cell-cycle arrest. Rbf1 is a master regulator for b-dependent transcriptional changes	expression induced directly by the bE/bW heterodimer.
(80)	RFX	RFX	RFX DBD	*Fusarium graminearum*	wheat	unable to infect	genome integrity	
(119)	RFX1	MoRFX1	RFX DBD	*Magnaporthe oryzae*	rice and barley	required for pathogenicity	Required for cell division and development. KO shows reduced growth, reduced conidiation, decreased appressorium turgor, increased sensitivity to UV, DNA damaging agents. Mixed effect of cell wall preturbing agents. Increased chitin content of cell wall, reduced cell division speed. Down regulation of MoCDA1 and MoCDA2 (chitin deacetylases, resposible for cell wall phenotype)	
(63)	SFL1	SFL1		*Magnaporthe oryzae*	rice and barley	reduced virulence on rice and barley seedlings and defective in invasive growth in penetration assays with rice leaf sheaths.	increased sensitivity to elevated temperatures. In deletion mutants grown at 30 degrees C the production of aerial hyphae and melanization were reduced but their growth rate was not altered.	phosphorylated by Pmk1 in vitro. Interacts with Pmk1 in vivo
(54)	SKN7	FgSKN7		*Fusarium graminearum*	wheat	ΔFgskn7ΔFgatf1 shows further reduced virulence compared to ΔFgatf1	reduced conidiation, reduced DON production	

(112)	SKN7	SKN7		*Cochliobolus heterostrophus*	maize	virulence not affected in single mutant, but reduced in ChAP1 skn7 double mutants	reduced expression of oxidative stress responsive genes; this effect is enhanced in ChAP1 skn7 double mutants	Both proteins are predicted to work together in a complex and regulate oxidative stress. Antioxidant gene expression is impaired in both mutants and almost completely absent in the double mutant.
(13)	SKN7	SKN7		*Alternaria alternata*		Induced significantly fewer necrotic lesions on the susceptible citrus cultivar.	altered conidia morphology, increased sensitivity to H2O2, increased resistance to fungicides	physically interacts with the Tup1-Cyc8 complex and recruits Tup1p to its targets. Tup1 deletion mutants are reduced in virulence in Ustilago and Magnaporthe
(131; 142)	SKN7	BcSkn7		*Botryris cinerea*		reduced virulece when mycelium used as inoculum	reduced vegetative growth, reduced conidia numbers, enhanced sensitivity to oxidative, osmotic and cell wall stress	about BcAP1 & BcSKN7: both have major influence on OSR genes. Function of BAP1 restricted to oxidatevi stress, role of BcSKN7 is broader.
(24)	SNT2	SNT2	PHD Zn finger and a GATA-type Zn finger	*Fusarium oxysporum f.sp. melonis*	melon	yes	autophagosome abundance. reduction in conidia production and biomass accumulation, slower vegetative growth and frequent hyphal septation.	Suppressive subtraction hybridization analysis of the D122 mutant versus wild-type isolate detected four genes (idi4, pdc, msf1, eEF1G) that were found previously in association with the target of rapamycin (TOR) kinase pathway. Expression of the autophagy-related idi4 and pdc genes was found to be up-regulated in the Δsnt2 FOM mutant.
(139)	SOM1	MoSOM1		*Magnaporthe oryzae*	rice and barley	non-pathogenic	important in vegetative growth and colony pigmentation. Deletion completely blocks production of asexual and sexual spores. KO is easy wettable. Required for appressorium formation from mycelium.	MoSOM1 can complement flo8 defects in haploid invasive growth of S. cerevisiae and diploid pseudohyphal development. MoSom1 strongly interacts with MoStu1 (Mstu1), an APSES transcription factor protein, and with MoCdtf1, while also interacting more weakly with the catalytic subunit of protein kinase A (CpkA) in yeast two hybrid assays. Five splice variants of MoSom1 were found.
(16)	SRE1	SRE1	GATA	*Cochliobolus heterostrophus*	maize	yes	siderophore biosynthesis repressor. Iron and oxidatise stress sensitivity	
(67)	SreA	SreA	HLH Leu Zip	*Penicillium digitatum*	citrus fruit (post harvest)	defectve in virulence towards citrus fruit	sterol regulatory element-binding protein. increased susceptibility to prochloraz	prochloraz induced expression of cyp51A and cyp51B abolished in KO

(140)	SRF-type	MCM1	MADS box	*Fusarium graminearum*	wheat	yes	Deletion of FgMCM1 resulted in the loss of perithecium production and phialide formation. The Fgmcm1 mutant was significantly reduced in virulence, deoxynivalenol biosynthesis, conidiation and vegetative growth.	Interacts with Mat1-1-1 and Fst12
(92)	SRF-type	Fmt1	MADS box	*Fusarium verticilioides*	maize	no effect	decreased vegetative growth and FB1 production when compared to the wild-type. Fmt1 showed reduced expression of 14 polyketide synthase (PKS) genes present in the organism. Significantly, the deletion of MADS1 in the MAT1-2 genotype led to strains that failed to produce perithecia and ascospores when crossed with the MAT1-1 wild-type strain.	
(152)	SRF-type	MCM1	MADS box	*Magnaporthe oryzae*	rice and barley	Reduced virulence	Deletion of MoMCM1 resulted in the loss of male fertility and microconidium production. The Momcm1 mutant was defective in appressorium penetration and formed narrower invasive hyphae, which may be responsible for its reduced virulence.	Interacts with Mst12 and MatA1
(138)	SRF-type	VdMCM1	MADS box	*Vericillium dahliae*	tomato	reduced virulence	impaired conidiation, SM production & microsclerotia formation	
(17)	STE12	AbSTE12	C2H2	*Alternaria brassicicola*	cabbage	loss of pathogenicity	Inable to produce mature conidia, slight reduction of vegetative growth rates	addition of long polypeptides to spores during inoculations resulted ina complete restoration of pathogenicity through a yet to be defined mechanism.
(106)	STE12	STE12	C2H2	*Botrytis cinerea*	bean & soft fruit	delayed infection as a result of low penetration efficiency		

(127)	STE12	CST1	C2H2	*Colletotrichum lagenarium*	cucumber	non-pathogeneic on intact leafs but can infect wounded. Cannot produce infectious hyphae from appressoria	low amount of lipid droplets in appressoria,but normal amount in conidia	
(136)	STE12	ClSte12	C2H2	*Colletotrichum lindemuthianum*	bean	yes, according to Tollot 2009 New Phyt. Glomus interadices STE12 transcomplements KO (200-400 #21)	reduced pectinase activity and adhesion to polystyrene, major cell wall protein(Clsp1) missing	two different splice variants with different expression patterns, full length can transcomplement, partial ranscript has a dominant negative effect.
(40)	STE12	FgSTE12	C2H2	*Fusarium graminearum*	wheat	impaired in virulence	impaired in secretion of cellulase and protease, although it did not show recognizable phenotype changes in hyphal growth, conidiation or deoxynivalenol (DON) biosynthesis.	FgGpmk1 controls the nuclear localization of FgSte12. Yeast two-hybrid and affinity capture assays indicated that FgSte12 interacts with the FgSte11-Ste7-Gpmk1 complex.
(3)	STE12	FoSt12	C2H2	*Fusarium oxysporum*	tomato	substantial reduction in virulence when inoculated in common bean seedlings	Disruption of fost12 resulted in no visible alterations of colony morphology or in vitro growth characteristics.	upregulated during plant infection
(58; 93)	STE12	MST12/ MoHOX8	C2H2	*Magnaporthe oryzae*	rice and barley	nonpathogenic on rice and barley leaves. When inoculated through wound sites, mst12 mutants failed to cause spreading lesions and appeared to be defective in infectious growth.	No obvious defect in vegetative growth, conidiation, or conidia germination was observed in mst12 mutants. mst12 mutants produced typical dome-shaped and melanized appressoria. However, the appressoria formed by mst12 mutants failed to penetrate onion epidermal cells.	
(132)	STE12	PdSTE12	C2H2	*Penicillium digitatum*	citrus (post harvest)	significantly reduced virulence in mature and immature fruit	defective in asexual reproduction (prducing only few conidia)	details down stream genes
(41)	STE12	StSTE12	C2H2	*Setosphaeria turcica*		yes, regulates appressorium development and penetration	HT toxin production unaltered, STE12 involved in vegetative growth & conidiation.	

(73)	STUA	FgSTUA	APSES bHLH	*Fusarium graminearum*	wheat	greatly reduced in pathogenicity on wheat heads	greatly reduced inproduction of secondary metabolites. Spore production was significantly impaired in ΔFgStuA, which did not develop perithecia and sexual ascospores, and lacked conidiophores and phialides, leading to delayed production of aberrant macroconidia.	
(125)	STUA	STUA	APSES bHLH	*Glomerella cingulata*	apple	required for generation of appressorial turgor pressure and full pathogenicity.	Mobilization of glycogen and triacylglycerol during formation of appressoria by the GcSTUA deletion mutant appeared normal and melanization of the maturing appressoria was also indistinguishable from that of the wild type.GcSTUA also was required for the formation of aerial hyphae, efficient conidiation, and the formation of perithecia.	
(116)	STUA	LmSTUA	APSES bHLH	*Leptospaeria maculans*	canola	abolished	retarded growth and conidia production & perithicia foration. Decrease in effector gene expression	most fungi contain around five APSES genes
(88)	STUA	MSTU1	APSES bHLH	*Magnaporthe oryzae*	rice and barley	deficient in appressorium-mediated invasion of rice leaves.	reduced conidiation and mycelial growth. Mstu1 formed a number of appressoria comparable to the wild type, although appressorium formation was delayed. Appressorial turgor was low in mstu1. The transfer of conidial glycogen and lipid droplets was remarkably delayed in mstu1, and a consequent delay in degradation of these conidial reserves was observed.	

(53)	STUA	SnStuA	APSES bHLH	*Stagnospora nodorum*	wheat	essentially non-pathogenic	growth retarded on glucose, failure to sporulate. Plays a key role in carbon metabolism, glycolysis, the TCA cycle, amino acid synthesis and regulates expression of the effector SnTox3, but not ToxA.	
(4)	STUA	UST1	APSES bHLH	*Ustilago maydis*	*maize*	yes	Deletion strains were darker, grew more slowly and presented a dry-looking colony surface. Furthermore, cultures of ust1 null mutants produced abundant thick-walled, highly pigmented cells resembling teliospores which are normally produced only in planta. Ust1 is required for mating and gall formation in planta.	ssp1, a gene highly induced in teliospores produced in the host, is also abundantly expressed in cultures of ust1 null mutants containing pigmented cells. the pheromone encoding mfa1 gene is strongly downregulated in the Δust1 strain compared with the wild type
(98)	SW16	SW16	APSES	*Magnaporthe oryzae*	rice and barley	Required for pathogenicity	reduced hyphal growth, abnormal formation of conidia and appressoria, and impaired appressorium function. The reduction in appressorial turgor pressure also contributed to an attenuation of pathogenicity. The ΔMoswi6 mutant also displayed a defect in cell wall integrity, was hypersensitive to oxidative stress, and showed a significant reduction in transcription and activity of extracellular enzymes, including peroxidases and laccases.	MoSwi6 interacted with MoMps1 both in vivo and in vitro.
(68)	SWI6	FgSWI6	APSES	*Fusarium graminearum*	wheat, barley and other small grain cereals	attenuated virulence on wheat	sensitivity to Carbendazim, reduced mycelial growth, impaired production and development of conidia, perithicia, ascus and ascospores. Impaired cellulose utilization, lithium tolerance and DON production.	Putative target of Fg Virus1 Plant Pathol J. 2016 Aug;32(4):281-9. doi: 10.5423/PPJ.OA.12.2015.0267. Epub 2016 Aug 1. The Transcription Cofactor Swi6 of the Fusarium graminearum Is Involved in Fusarium Graminearum Virus 1 Infection-Induced Phenotypic Alterations. Son M1, Lee Y2, Kim KH3.
(7)	TDG2	TDG2		*Magnaporthe oryzae*	rice and barley	required for virulence	requierd for normal adhesion	expression depends on TRA1

(1)	TOXE	TOXE	bZIP & 4 ankyrin repeats	*Cochliobolus carbonum*	maize	yes	required for expression of all the other TOX2 genes	The only known phenotype of *TOXE* mutants is inhibition of mRNA expression of the *TOX2* genes dedicated to HC-toxin biosynthesis, with concomitant loss of specific pathogenicity of *C. carbonum* on maize
(7)	TRA1	TRA1	Zn(2)-Cys(6), GAL4-like DBD, Myb domain	*Magnaporthe oryzae*	rice and barley	yes, CON7 dependent	reduced attachment, germination, appressorium formation and virulence. Adhesion to artificial and plant surfaces was affected	Transcription accumulates during germination and depends on the transcription factor Con7p.
(111; 121)	TRI10	TRI10		*Fusarium graminearum*	wheat	non-pathogenic	production of mycotoxins	affects expresison of a pth11- homolog
(121)	TRI10	TRI10		*Fusarium sporotrichioides*	head blight on wheat	not determined	Disruption of Tri10 in Fusarium sporotrichioides abolished T-2 toxin production and dramatically decreased the transcript accumulation for four trichothecene genes (Tri4, Tri5, Tri6, and Tri101) and an apparent farnesyl pyrophosphate synthetase (Fpps) gene.	A TRI6 homolog was identified in Myrothecium roridum, with the same DNA binding specificity.
(107)	TRI6	TRI6	C2H2	*Fusarium culmorum*	durum wheat	influences severity of crown and foot rot		silencing
(86; 111)	TRI6	TRI6	C2H2	*Fusarium graminearum*	wheat	non-pathogenic	production of mycotoxins	Seong 2009 Mol Mic, Nasmith 2011 PLoS Path
(97)	TRI6	TRI6	C2H2	*Fusarium sporotrichioides*	head blight on wheat	nd	trichothecene biosynthesis	
(15)	TUP1	MoTUP1	transcriptional repressor	*Magnaporthe oryzae*	rice and barley	KO makes appr. Like structures, but is non-pathogenic	mycelial growth, conidiogenesis, cell wall integrety	

(30)	TUP1	Tup1	transcriptional repressor	*Ustilago maydis*	maize	reduced virulence phenotype	plays a key role in orchestrating the yeast to hypha trasition. KO drastically reduced in mating and filamentation capacity.	transcriptional repressor. Tup seems to control expression of the Prf1 transcription factor, via control of the transcriptional activators of Prf1: Rop1 and Hap2. Prf1 is requred for mating because expression of the mating type loci depend on it.
(118)	VF19	AbVf19	C2H2	*Alternaria brassicicola*	cabbage	reduced virulence	reduced growth on pectin	regulates a set of CWDE
(20)	VF8	AbVf8	a putative SET domain	*Alternaria brassicicola*	cabbage	reduced virulence	none reported	
(9)	WCC complex	BcWCL1	GATA	*Botrytis cinerea*	bean & soft fruit	required for full virulence	mediating transcriptional response to white light, inhibiting conidiation in white light, coping with excessive light and oxidative stress	KO still shows rudimentary response to light, indicating the existance of a parrallel light responsive system. Physically interacts with BcWCL2, another GATA TF, forming the WCC complex.
(77)	WOR1	REG1	WOPR	*Botrytis cinerea*	bean & soft fruit	Required for pathogenicity. The bcreg1 mutant is able to penetrate plant tissue but is not able to cause necrotic lesions.	blocked in conidia formation and does not produce detectable levels of the sesquiterpene botrydial and the polyketide botcinic acid.	bcreg1 is a downstream target of two mitogen-activated protein kinases, BcSak1 and Bmp3.
(91)	WOR1	CfWOR1	WOPR	*Cladosporium fulvum*	tomato	non pathogenic	Δcfwor1 mutants produce sclerotium-like structures and rough hyphae, which are covered with a black extracellular matrix. These mutants do not sporulate. Overexpression of CfWOR1 downregulates effector gene expression,results in fewer spores with altered morphology and also reduced virulence.	

(78)	WOR1	FfSGE1	WOPR	*Fusarium fujikuroi*	rice	no effect	FfSge1 is not required for formation of conidia, but is involved in vegetative growth. Transcriptome analysis of the mutant Δffsge1 compared with the wild type, as well as comparative chemical analysis between the wild type, Δffsge1 and OE:FfSGE1, revealed that FfSge1 functions as a global activator of secondary metabolism in F.□fujikuroi.	
(55)	WOR1	FGP1	WOPR	*Fusarium graminearum*	wheat	required for pathogenicity	loss of trichothecene toxin accumulation in infected wheat plants and in vitro. Involved in the developmental processes of conidium formation and sexual reproduction and modulates a morphological change that accompanies mycotoxin production in vitro.	
(79)	WOR1	SGE1	WOPR	*Fusarium oxysporum*	tomato	non pathogenic	reduced conidiation, fails to express effector genes	
(8)	WOR1	FvSGE1	WOPR	*Fusarium verticilioides*	maize	required for pathogenicity	Not required for vegetative growth or conidiation. Affects synthesis of multiple SM, including fumonisins and fusarins. Affects expression of numerous putative effector genes, genes encoding cell surface proteins, gene clusters required for synthesis of fusarins, bikaverin, and an unknown metabolite, as well as the gene encoding the fumonisin cluster transcriptional activator.	
(64)	WOR1	MoGTI	WOPR	*Magnaporthe oryzae*	rice	non-pathogenic. Normal in appressorium formation and turgor pressur, but defective in penetration and growth of normal invasive hyphae.	Affects the majority of the effector genes, conidiation and cell wall integrity.	Expression of MoGTI1 appered to be controlled by the Mps1 but not the PMK1 MAPK. But MoGTI1 seems not to be a direct target of PMK1.

(124)	WOR1	ROS1	WOPR	*Ustilago maydis*	maize	required for completion of the lifecycle on plant: during late stages of infection Ros1 is essential for fungal karyogamy, massive proliferation of diploid fungal cells and spore formation	major regulator of spore formation	expressed during late stages of infection. controls expression of 80 TF genes and counteracts the b-filamentation program (controling filamentation and pathogenic development). Ros1 downregulates 128 effector genes involved in biotrophic phases and upregulates 70 'late' effector genes.
(105)	WOR1	VdSGE1	WOPR	*Vericillium dahliae*	tomato	required for pathogenicity	required for radial growth and production of asexual conidiospores. Required for the expression of six putative effector genes, whereas two of the putative effectors genes were found to be negatively regulated by VdSge1	
(81)	WOR1	ZtWOR1	WOPR	*Zymoseptoria tritici*	wheat	non pathogenic	ZtWor1 is up-regulated during the initiation of colonization and fructification, and regulates candidate effector genes	
(14)	Ycp4	MoYcp4		*Magnaporthe oryzae*	rice and barley	the ability to infect rice and barley was reduced, resulting in decreased pathogenicity.	The growth rate of a ΔMoycp4 mutant was reduced slightly, but conidial production was increased significantly (more than 10-fold), compared with the wild-type strain. Although the rate of appressorium formation was unaffected, the appressorial turgor was abnormal.	expression affected by MoAP1. Significantly up-regulated during conidiation, appressorium formation and infection.
(6; 34)	ZFR1	ZFR1	Zn2Cys6	*Fusarium verticilioides*	maize	reduced growth on maize kernels	ZFR1 deletion mutants exhibited normal growth and development on maize kernels, but fumonisin production was reduced to less than 10% of that of the wild-type strain.	hypothesized taht ZFR1 control SM production by regulating the perception or uptke of carbohydrates (Bluhm 2008).
(134)	ZIF1	FgZIF1	bZIP	*Fusarium graminearum*	flowering wheat heads	reduced in virulence: defective in spreading tothe rachis and other spikelets	reduced in DON production and female specific defects in sexual reproduction	FgZIF1 transcomplements the Mo ΔMozif1 KO.

(134)	ZIF1	MoZIF1	bZIP	*Magnaporthe oryzae*	rice	reduction in virulence and invasive growth	female specific defects in sexual reproduction	FgZIF1 transcomplements the Mo ΔMozif1 KO.
(145)	ZNF1	ZNF1	C2H2	*Magnaporthe oryzae*	rice and barley	nonpathogenic and unable to develop appressoria.	Δznf1 mutants also produce significantly more conidia. Δznf1 mutants are affected in mitosis and impaired in mobilization and degradation of lipid droplets and glycogen reserves during appressorium differentiation.	expression of ZNF1 was highly induced during germination and appressorium development

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