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Adaptation to the Host Environment by Plant-Pathogenic Fungi
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Supplemental Table 1: selected transcriptomics studies of plant-pathogenic fungi

Species	Host	Methods	Comparison	Main emerging hypotheses	Reference
Colletotrichum higginsianum	Arabidopsis	RNA-seq	Pre-penetration appressoria (22 hpi[1]), early biotrophic phase (40 hpi), transition to necrotrophy (60 hpi); appressoria formed *in vitro* (22 hpi on polystyrene).	Appressoria sense the host and induce expression of genes required for invasion and biotrophic growth; necrotrophy requires nutrient transporters and secretion of hydrolases.	(15)
Colletotrichum higginsianum	Arabidopsis	EST sequencing, RT-qPCR, FACS	Penetrating appressoria and nascent biotrophic hyphae (22 hpi), biotrophic hyphae (45 hpi), necrotrophic hyphae (72 hpi); additional conditions for RT-qPCR.	Appressoria sense the host and induce expression of effector genes required for biotrophic growth; necrotrophy requires secretion of toxic proteins such as NLPs[2].	(11)
Colletotrichum orbiculare	*Nicotiana benthamiana*	Microarrays	Ungerminated conidia, infected epidermal peels (1 and 3 dpi[3]), infected leaves (7 dpi); growth on complete medium.	Many SSPs[4] and secondary metabolites are required for initial stages of host colonization; necrotrophic growth requires secreted PCWDEs[5] and proteases; quinate is used as carbon source.	(5)
Colletotrichum gloeosporioides	Tomato	RNA-seq	Conidia germinating on unripe tomato fruit cuticle (19hpi), quiescent stage in unripe fruits (4 dpi), necrotrophic stage in ripe fruit (2 dpi).	Appressoria sense the host and induce expression of genes required for biotrophic growth; chromatin remodelling, fatty acid degradation and tissue alkalization occur in the quiescent stage; necrotrophic growth requires glycolysis, secretion of PCWDEs and an NLP.	(1)
Colletotrichum graminicola	Maize	RNA-seq	Appressorial maturation (20 hpi), biotrophic growth (36 hpi) and necrotrophic growth (70 hpi) on/in detached leaf sheaths; wild-type was compared with a mutant strain impaired in the establishment of biotrophy.	Appressoria sense the host and induce expression of genes required for biotrophic growth; biotrophic growth requires Pth11-like sensors, secretion of SSPs and hydrolases and nutrient uptake; necrotrophic growth requires secretion of proteases, PCWDEs and an NLP.	(20)
Fusarium graminearum	Wheat, barley	Microarrays	Growth in wheat heads (1, 2, 3, 4, 6 dpi); growth on complete medium and during carbon or nitrogen starvation; infection of barley.	Growth *in planta* requires detoxification of host compounds and secretion of hydrolases and specific SMs[6]; growth in wheat heads requires allantoin/allantoate uptake and secretion of specific SMs.	(13)
Fusarium graminearum	Wheat	Microarrays , laser microdissection	Colonization of coleoptiles (protective sheath covering the emerging shoot) (16, 40 and 64 hpi); growth in rich medium.	Early stages of coleoptile colonization require scavenging of ROS and fatty acid oxidation; later stages require production of ROS by the fungus, secretion of a specific SM and extensive secretion of PCWDEs; Pth11-like sensors are required for *in planta* growth.	(21)
Fusarium graminearum	Maize	Microarrays, laser microdissection	Pith tissues of infected maize stalk (0, 12, 18, 36, 48, 72, 108, 132 and 144 hpi); growth in rich medium.	Detoxification of host compounds and secretion of specific SMs are required for maize stalk colonization; different sets of PCWDEs are required for early (around 38 hpi) and late (after 108 hpi) stages of colonization; phosphorus-free membrane lipids are synthesized to adapt to a phosphate-limited extracellular environment during	(22)

				early stages of colonization.	
Fusarium graminearum	Barley, maize, wheat	Microarrays	Early infection of barley spikes, wheat spikes and maize kernels (1, 2 and 4 dpi).	Colonization of each host requires distinct Pth11-like sensors, nutrient transporters and SMs.	(8)
Fusarium graminearum	Wheat	RNA-seq	Living versus cold-killed flowering wheat heads (3 and 5 dpi); *in vitro* growth under mycotoxin-inducing conditions (5 mM L-ornithine as N-source).	PCWDEs and nutrient import are required for growth in live as well as dead plant tissue; the living plant actively suppresses fungal growth and promotes toxin production; growth in living host requires arginine metabolism, detoxification of host compounds and secretion of specific SMs and SSPs.	(3)
Fusarium oxysporum f. sp. medicaginis	*Medicago truncatula*	RNA-seq	Infected roots of susceptible and resistant seedlings at early (2 dpi) or late (7 dpi) stages of infection; growth on rich medium.	Root colonization requires secretion of PCWDEs and SSPs, nutrient import and detoxification of host compounds.	(19)
Magnaporthe oryzae	Rice, barley	Microarrays	Invasive growth (3 dpi); growth in complete medium, under nutrient limitation, temperature up-shift or oxidative stress.	*M. oryzae* experiences nutrient-limitation at 3 dpi, but no oxidative stress, and is degrading plant cell walls at that time.	(14)
Magnaporthe oryzae	(Hydrophobic glass slide)	HT-SuperSAGE	Appressorium development (conidia germinated on a hydrophobic glass slide for 4, 6, 8, 14 and 16 h); growth on rich medium and minimal medium; *mpk1* mutant 4h after germination on a glass slide.	Appressorium development requires autophagy, cell cycle regulation, beta oxidation of fatty acids and melanin biosynthesis; appressoria are primed for plant cell wall degradation, sugar import, quinate utilization and secretion of secondary metabolites.	(18)
Magnaporthe oryzae	Rice	RNA-seq	Compatible versus incompatible isolates penetrating leaf epidermal cells (1 dpi); *in vitro* germinated conidia.	For establishing itself in leaf epidermal cells the fungus requires secretion of cutinases, chitinases, oxidoreductases, glycosyl hydrolases, LysM proteins and HsbA (hydrophobic surface binding) proteins.	(9)
Zymoseptoria tritici	Wheat, *Brachypodium distachyon*	RNA-seq	Early stages (4 dpi) of colonization of wheat and *Brachypodium distachyon* (incompatible host); yeast-like cells from solid rich medium.	For (initial) growth in both hosts, the fungus requires detoxification of host compounds and secretion of proteins. Colonization of wheat requires secretion of specific secondary metabolites.	(10)
Zymoseptoria tritici	Wheat	RNA-seq	Germination on leaf surface (1 dpi), early post-stomatal penetration and intercellular growth (4 dpi), onset of rapid intercellular growth and appearance of disease symptoms (9 dpi), necrotrophic growth and onset of sporulation (14 dpi), mature pycnidia (21 dpi); yeast-like cells from rich and minimal liquid medium.	At early stages (1,4 dpi) beta-oxidation of fatty acids provides energy for growth, and secretion of many proteins including effectors, cutinases and chloroperoxidases is required; the transition at 9 dpi requires secretion of proteases and secondary metabolites; necrotrophic growth and sporulation (14 and 21 dpi) require secretion of PCWDEs and nutrient import.	(16)
Leptosphaeria maculans	Oilseed rape	RNA-seq	Infected cotyledons (7 dpi), symptomless stem tissue (14 and 24 dpi), necrotic stem tissue (24 dpi); growth in liquid minimal medium.	Colonization of cotyledons requires secretion of a different set of effectors from colonization of stem tissue; stem colonization requires secretion of PCWDEs, oxidoreductases and chitin-binding proteins.	(6)

Leptosphaeria maculans	Oilseed rape	RNA-seq	Infected cotyledons at 0, 2, 4 and 6 dpi and necrotrophic stage (8 dpi); *in vitro* growth.	Early colonization requires secretion of pectin-degrading enzymes, chitinases, effectors and LysM domain proteins; more advanced stages require secretion of more abundant and diverse PCWDEs, secondary metabolites, and an NLP.	(7)
Dothistroma septosporum	Monterey pine	RNA-seq	Epiphytic/biotrophic growth on needles (3 wpi[7]), initial necrosis (8 wpi) and mature sporulating lesions (12 wpi); mycelium grown in liquid medium.	Growth in needles requires alcohol and aldehyde dehydrogenases; initial biotrophic growth requires fungal cell wall-modifying enzymes; necrotrophic growth requires secretion of PCWDEs, secondary metabolites, effectors and oxidoreductases, and nutrient import.	(4)
Botrytis cinerea	(Apple wax-coated surfaces)	Microarray	Dormant conidia, conidia at pre-germination (1 h), germinated conidia (2.5 h), appressoria (4h), early mycelium (15 h); wild-type strain and a non-pathogenic MAP kinase mutant (*bmp1*)	Growth on the plant surface and subsequent invasion requires secretion of lytic enzymes including PCWDEs, a chitin deacetylase and a cutinase.	(12)
Penicillium expansum	Apple	RNA-seq	Leading edge of colonized apple tissue (5 dpi); mycelium from cultures grown at pH 4 or 7.	Growth in apple requires the mycotoxin patulin, various amidases as a possible source of NH_4^+ production, PCWDEs, oxidoreductases and catalase.	(2)
Ustilago maydis	Maize	Microarrays	Seedling leaves at 1 and 3 dpi, adult leaves and tassels (male reproductive inflorescences) at 3 and 9 dpi.	Growth in different organs of maize requires expression of unique genes in each organ and secretion of unique sets of proteins.	(17)

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[1] hpi: hours post inoculation
[2] NLP: NEP1-like protein
[3] dpi: days post inoculation
[4] SSP: small secreted protein
[5] PCWDE: plant cell wall-degrading enzyme
[6] SM: secondary metabolite
[7] wpi: weeks post inoculation