

21st Century Guidebook to Fungi

Major morphogenetic events and transcriptional transitions during fruit body development in *Coprinopsis cinerea*

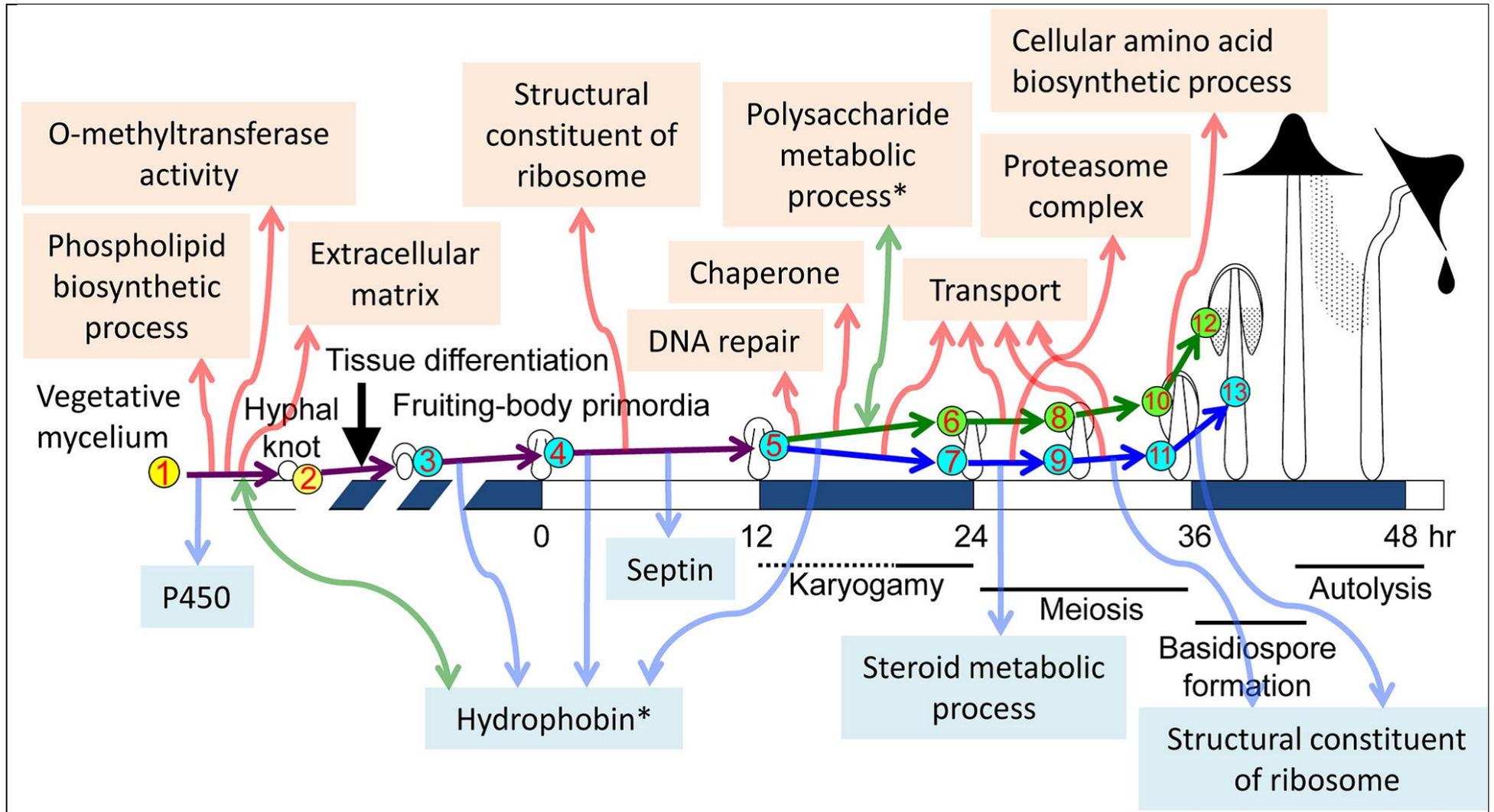


Fig. 28. Summary of major transcriptional events during morphogenetic transitions during fruit body development in *Coprinopsis cinerea*. The cartoon diagrams of fruiting across the centre run from vegetative mycelium at left to autolysing mature fruit body at right and are placed on an average time scale with time zero being set by the illumination cycle that triggers primordium maturation. The nine developmental stages selected to investigate the transcriptome are shown with numbers in circles (cap and stipe tissue samples were taken separately from 24 h onwards). Developmental and cellular events in each stage and tissue are shown in Table 12.1. The study identified **differentially expressed gene sets** using GO enrichment analysis [<http://geneontology.org/page/go-enrichment-analysis>]; that is, sets of gene sequences of related function that are up-regulated or down-regulated in pairwise comparisons between two succeeding developmental stages, and between vegetative mycelium and each individual developmental stage. The program does this by statistically determining which sequence(s) are over-represented (or under-represented) in each member of the pair relative to the other. Notable transcriptional programme events are depicted in the text labels. Events detected by up-regulated differentially expressed genes are indicated in the upper part with upward red arrows; down-regulated differentially expressed gene sets are shown in the lower part with downward blue arrows. Sets which featured a mix of both up-regulated and downregulated gene sequences of related function are indicated with asterisks and bidirectional green arrows. Taken from Muraguchi *et al.* (2015) under Creative Commons licence <https://creativecommons.org/licenses/by/4.0/>.

Table 12.1. Major morphogenetic events and transcriptional transitions during fruit body development in *Coprinopsis cinerea*

Tissue designation	Cellular events	Differential expression in each transition between developmental stages			
		Transition	Regulation	Transcripts	Top 3 enriched sequence annotations (functions)
1	vegetative mycelium	1-2	UP	408	Phospholipid biosynthesis; O-methyltransferase activity; extracellular region↑
			DOWN	134	Cytochrome P450; hydrophobin↑; adenyly nucleotide binding
2	mycelium & hyphal knots	2-3	UP	2	-
			DOWN	3	-
3	small primordia	3-4	UP	85	adenyly nucleotide binding↑
			DOWN	38	adenyly nucleotide binding↑; hydrophobin
4	primordia begin maturation 0-h	4-5	UP	148	Structural constituent of ribosome; zinc ion binding; FAD binding
			DOWN	590	Hydrophobin; fungal phospholipid biosynthesis; septin complex
5	whole primordium at 12-h	5-6	UP	949	DNA repair; chaperonin Cpn60/TCP-1; glucose catabolism↑
			DOWN	1,660	Hydrophobin; cytochrome P450; polysaccharide metabolism
		5-7	UP	3,301*	Transport; FAD binding; ATP coupled proton transport

				DOWN	3,569*	Structural constituent of ribosome; RNA processing; RNA recognition motif, RNP-1
6	cap, 24-h after light trigger	Karyogamy in basidia	6-8	UP	2471	Transport; FAD binding; cytochrome P450
				DOWN	2,034	RNA recognition motif, RNP-1; RNA processing; structural constituent of ribosome
7	stipe, 24-h after light trigger	Stipe nuclei divide before elongation	7-9	UP	457	Proteasome complex; AMP-dependent synthetase and ligase; EF-hand calcium-binding proteins
				DOWN	326	Steroid metabolism; lipase activity; lipid biosynthesis
8	cap, 30-h after light trigger	Karyogamy + 6-h	8-10	UP	3,465*	Transmembrane; FAD binding; cytochrome P450
				DOWN	3,197*	Structural constituent of ribosome; WD40 repeat histone binding proteins; vesicle-mediated transport
9	stipe, 30-h after light trigger	Stipe enlarges	9-10	UP	2,088	Transport; vitamin B6 binding; cytochrome P450
				DOWN	2,356	Structural constituent of ribosome; WD40 repeat histone binding proteins; ribosome biogenesis
10	cap, 36-h after light trigger	Karyogamy + 12-h	10-12	UP	1,743	Nitrogen compound biosynthesis; cellular amino acid biosynthesis; alcohol dehydrogenase GroES-like fold (catalytic domain of alcohol dehydrogenases) proteins
12	cap, 39-h after light trigger	Karyogamy + 15-h spores form		DOWN	1,701	ATP binding; N-terminal FAD linked oxidase; galactose oxidase, beta propeller (ligand-binding)
11	stipe, 36-h after light trigger	Stipe starts to elongate	11-13	UP	136	Cytochrome P450↓; C2H2-type zinc finger proteins (transcription factors); metal ion-binding
13	stipe, 39-h after light trigger	Stipe elongates Cap expands		DOWN	192	Cytochrome P450↑; FAD binding; structural constituent of ribosome
<p>‡, indicates that similar functions are found in both up-regulated and down-regulated differentially expressed genes. *, indicates that only the first 3,000 genes were analysed. Data from Muraguchi <i>et al.</i> (2015).</p>						

From the Second Edition of the *21st Century Guidebook to Fungi* © David Moore, Geoffrey D. Robson and Anthony P.J. Trinci 2019.