

Supplemental Data

A

PaNo.	gene	juv PQ	ma PQ	sen PQ	aging	grisea
Pa_2_510	<i>PaPks1</i>	0.49	0.08	0.35	3.11	
Pa_5_11880		0.04	0.05	0.00	1.10	0.11
Pa_7_11610		0.29	0.06	0.07	1.72	0.30
Pa_5_1990		0.10	0.06	0.06	1.13	0.24

0.2 0 5

B

PaNo.	gene	juv PQ	ma PQ	sen PQ	aging	grisea
Pa_1_15010	<i>PaAl-1</i>	6.15	1.33	4.30	0.88	1.33
Pa_1_15240	<i>PaAl-2</i>	5.88	3.00	0.70	2.07	1.89
Pa_2_610	<i>PaAl-3</i>	2.04	1.05	0.60	1.31	0.23

C

PaNo.	homolog	e-value	juv PQ	ma PQ	sen PQ	aging	grisea
Pa_5_11970	<i>ScFre1/ScFre2</i>	9.0E-32, 8.0E-30	0.05	0.13	0.22	0.39	0.00
Pa_7_5660	<i>ScFre1/ScFre2</i>	9.0E-29, 2.0E-28	0.42	1.52	0.40	0.85	0.68
Pa_5_10230	<i>ScFre1/ScFre2</i>	1.0E-23, 3.0E-27	1.21				
Pa_1_19630	<i>ScFre1/ScFre2</i>	5.0E-22, 2.0E-23	1.54	0.50	0.85	2.06	0.44
Pa_1_16410	<i>ScFre1/ScFre2</i>	2.0E-21, 1.0E-17	0.11	2.80	1.25	0.04	0.21
Pa_1_19550	<i>ScFre1/ScFre2</i>	2.0E-16, 6.0E-12	1.95	0.81	1.46	0.48	2.57
Pa_6_4210	<i>ScFtr1</i>	2.00E-55	1.42	2.06	0.55	0.38	0.31
Pa_6_4220	<i>ScFet3</i>	1.00E-130	0.30	0.44	0.26	1.11	0.13
Pa_2_530	<i>ScFet3</i>	3.00E-78	0.42	0.22	0.09	7.40	0.08
Pa_6_2550	<i>ScFet3</i>	3.00E-56	0.12	0.10	0.28	1.01	1.01
Pa_5_1200	<i>ScFet3</i>	7.00E-47	4.40	1.98	15.64	0.43	0.55

D

PaNo.	homolog	e-value	juv PQ	ma PQ	sen PQ	aging	grisea
Pa_6_1720	<i>AfSreA</i>	2E-40	1.30	18.08	2.52	0.18	0.47
Pa_4_4430	<i>AfSidA</i>	1E-119	3.26	2.99	4.12	0.64	2.49
Pa_5_4760	<i>AfSidF</i>	1E-107	3.12	2.57	5.09	0.78	1.09
Pa_3_11200	<i>AfSidD</i>	0.0	3.41	2.04	2.32	1.44	1.52
Pa_4_4640	<i>AfSidD</i>	0.0	1.05	0.45	0.34	0.90	0.48
Pa_5_1070	<i>AfSidD</i>	5E-92	0.87	0.52	1.62	0.99	0.85
Pa_4_4440	<i>AfSidC</i>	0.0	1.66	2.11	1.84	1.25	3.06
Pa_4_4640	<i>AfSidC</i>	1E-121	1.05	0.45	0.34	0.90	0.48
Pa_2_7870	<i>AfSidC</i>	1E-119	0.14	0.01	0.11	0.92	0.02
Pa_7_120	<i>AfMirB</i>	6E-88	4.14	4.95	4.04	0.44	2.34
Pa_5_3540	<i>AfMirB</i>	1E-117	2.26	1.70	1.02	0.90	0.73
Pa_5_4490	<i>AfSit1</i>	0.0	1.92	3.54	0.65	1.69	0.78
Pa_7_6950	<i>AfMirC</i>	1E-151	1.96	4.74	2.48	0.20	1.60
Pa_3_1250	<i>AfEstB</i>	2E-38	1.06	0.99	0.86	0.95	10.93
Pa_2_8330	<i>AfEstB</i>	1E-37	1.18	4.96	0.29	0.91	0.39
Pa_4_1300	<i>AfEstB</i>	8E-30	0.39	0.12	0.24	2.58	1.22

Supplemental Figure 1: Transcriptome data of transcripts associated with (A) melanin synthesis, (B) carotenoid synthesis, (C) reductive iron assimilation and (D) siderophore mediated iron uptake. Relative expression was calculated by dividing tpm of juvenile PQ-stressed samples by tpm of juvenile control (juv PQ), middle-aged PQ-stressed samples by middle-aged control (ma PQ), senescent PQ-stressed samples by senescent control (sen PQ), senescent control by juvenile control (aging) and of grisea by wild-type control (grisea).

Supplemental Table 1: GO enrichment analysis of transcriptome data PQ-stressed senescent wild-type cultures of *P. anserina*.

up-regulated						
	GO ID	p-value	C	S	Description	
CC	GO:0044429	1.73E-10	118	581	mitochondrial part	
	GO:0005740	1.22E-07	83	408	mitochondrial envelope	
	GO:0005743	1.31E-06	57	261	mitochondrial inner membrane	
	GO:0019866	3.61E-06	57	269	organelle inner membrane	
	GO:0005739	4.14E-06	176	1121	mitochondrion	
	GO:0005759	7.53E-06	47	212	mitochondrial matrix	
	GO:0044455	9.33E-06	38	159	mitochondrial membrane part	
	GO:0031966	1.26E-05	73	386	mitochondrial membrane	
	GO:0031975	1.52E-04	101	617	envelope	
	GO:0031967	1.93E-04	96	584	organelle envelope	
	GO:0005758	1.48E-03	12	40	mitochondrial intermembrane space	
	GO:0000313	1.52E-03	11	35	organellar ribosome	
	GO:0005761	1.52E-03	11	35	mitochondrial ribosome	
	GO:0045275	1.81E-03	5	9	respiratory chain complex III	
	GO:0005750	1.81E-03	5	9	mitochondrial respiratory chain complex III	
	GO:0005744	2.07E-03	6	13	mitochondrial inner membrane presequence translocase complex	
	GO:0044420	2.29E-03	4	6	extracellular matrix part	
	GO:0005581	2.29E-03	4	6	collagen	
	GO:0031970	2.38E-03	14	53	organelle envelope lumen	
	GO:0000314	3.27E-03	6	14	organellar small ribosomal subunit	
	GO:0005763	3.27E-03	6	14	mitochondrial small ribosomal subunit	
	GO:0005578	3.27E-03	5	10	proteinaceous extracellular matrix	
	GO:0016021	3.76E-03	241	1796	integral to membrane	
	GO:0030015	4.84E-03	4	7	CCR4-NOT core complex	
	GO:0031304	7.11E-03	6	16	intrinsic to mitochondrial inner membrane	
	GO:0031305	8.42E-03	5	12	integral to mitochondrial inner membrane	
	BP	GO:0007005	2.65E-07	56	243	mitochondrion organization
		GO:0070585	2.29E-05	19	59	protein localization to mitochondrion
		GO:0072655	2.29E-05	19	59	establishment of protein localization to mitochondrion
		GO:0006839	2.67E-05	29	113	mitochondrial transport
		GO:0006626	5.03E-05	18	57	protein targeting to mitochondrion
GO:0030026		2.65E-04	7	13	cellular manganese ion homeostasis	
GO:0055071		2.65E-04	7	13	manganese ion homeostasis	
GO:0006783		4.72E-04	9	22	heme biosynthetic process	
GO:0006779		4.83E-04	11	31	porphyrin-containing compound biosynthetic process	
GO:0006778		6.59E-04	11	32	porphyrin-containing compound metabolic process	
GO:0042168		6.96E-04	9	23	heme metabolic process	
GO:0006627		8.43E-04	4	5	protein processing involved in protein targeting to mitochondrion	
GO:0055114		8.53E-04	66	388	oxidation-reduction process	
GO:0033014		1.53E-03	11	35	tetrapyrrole biosynthetic process	
GO:0045333		1.72E-03	40	215	cellular respiration	
GO:0033013		1.98E-03	11	36	tetrapyrrole metabolic process	
GO:0055085		2.20E-03	111	740	transmembrane transport	
GO:0030150		2.90E-03	7	18	protein import into mitochondrial matrix	
GO:0000002		2.95E-03	12	43	mitochondrial genome maintenance	
GO:0000963		3.29E-03	5	10	mitochondrial RNA processing	
GO:0032543		4.30E-03	15	62	mitochondrial translation	
GO:0046148		4.30E-03	15	62	pigment biosynthetic process	
GO:0010508		4.47E-03	8	24	positive regulation of autophagy	
GO:0007006		4.47E-03	9	29	mitochondrial membrane organization	
GO:0006673		4.86E-03	4	7	inositolphosphoceramide metabolic process	
GO:0006675		4.86E-03	4	7	mannosyl-inositol phosphorylceramide metabolic process	
GO:0017038		5.50E-03	24	120	protein import	
GO:0006091		5.58E-03	56	344	generation of precursor metabolites and energy	
GO:0042180		6.75E-03	113	781	cellular ketone metabolic process	
GO:0015980		7.19E-03	44	261	energy derivation by oxidation of organic compounds	
GO:0046364	7.75E-03	12	48	monosaccharide biosynthetic process		
GO:0009060	8.04E-03	23	117	aerobic respiration		
GO:0000050	8.83E-03	4	8	urea cycle		
GO:0006094	8.85E-03	11	43	gluconeogenesis		
GO:0051188	9.36E-03	29	159	cofactor biosynthetic process		
GO:0010506	9.83E-03	8	27	regulation of autophagy		
MF	GO:0016679	2.47E-04	14	42	oxidoreductase activity, acting on diphenols and related substances...	

GO:0015450	3.88E-04	9	21	P-P-bond-hydrolysis-driven protein transmembrane transporter activity
GO:0045551	4.09E-04	6	10	cinnamyl-alcohol dehydrogenase activity
GO:0008320	8.64E-04	9	23	protein transmembrane transporter activity
GO:0022884	8.64E-04	9	23	macromolecule transmembrane transporter activity
GO:0003824	1.38E-03	705	5566	catalytic activity
GO:0004605	1.74E-03	3	3	phosphatidate cytidyltransferase activity
GO:0016783	2.07E-03	5	9	sulfurtransferase activity
GO:0008121	2.42E-03	6	13	ubiquinol-cytochrome-c reductase activity
GO:0016681	2.42E-03	6	13	oxidoreductase activity, acting on diphenols and related substances as...
GO:0016746	2.54E-03	60	350	transferase activity, transferring acyl groups
GO:0016747	5.00E-03	51	297	transferase activity, transferring acyl groups other than amino-acyl groups
GO:0016491	5.51E-03	263	1920	oxidoreductase activity
GO:0016782	5.72E-03	6	15	transferase activity, transferring sulfur-containing groups
GO:0043115	6.33E-03	3	4	precorrin-2 dehydrogenase activity
GO:0004325	6.33E-03	3	4	ferrochelatase activity
GO:0016410	6.81E-03	25	125	N-acyltransferase activity
GO:0008080	9.22E-03	23	115	N-acetyltransferase activity
GO:0004479	9.56E-03	5	12	methionyl-tRNA formyltransferase activity

down-regulated

	GO ID	p-value	C	S	Description
BP	GO:0006260	5.57E-04	69	275	DNA replication
	GO:0006083	1.61E-03	8	15	acetate metabolic process
	GO:0030989	3.87E-03	4	5	dynein-driven meiotic oscillatory nuclear movement
	GO:0051691	4.40E-03	8	17	cellular oligosaccharide metabolic process
	GO:0019236	4.67E-03	29	104	response to pheromone
	GO:0043406	5.19E-03	3	3	positive regulation of MAP kinase activity
	GO:0000169	5.19E-03	3	3	activation of MAPK activity involved in osmosensory signaling pathway
	GO:0000187	5.19E-03	3	3	activation of MAPK activity
	GO:0000189	5.19E-03	3	3	MAPK import into nucleus
	GO:0000208	5.19E-03	3	3	MAPK import into nucleus involved in osmosensory signaling pathway
	GO:0032005	5.20E-03	12	32	signal transduction involved in conjugation with cellular fusion
	GO:0007124	5.47E-03	25	87	pseudohyphal growth
	GO:0010033	5.86E-03	45	181	response to organic substance
	GO:0032787	6.57E-03	56	236	monocarboxylic acid metabolic process
	GO:0019748	6.77E-03	15	45	secondary metabolic process
	GO:0036267	9.50E-03	22	77	invasive filamentous growth
	GO:0001403	9.50E-03	22	77	invasive growth in response to glucose limitation
MF	GO:0004497	1.65E-06	85	298	monoxygenase activity
	GO:0004339	1.40E-04	9	14	glucan 1,4-alpha-glucosidase activity
	GO:0016712	2.03E-04	19	47	oxidoreductase activity, acting on paired donors, with incorporation...
	GO:0016709	5.32E-04	35	115	oxidoreductase activity, acting on paired donors, with incorporation...
	GO:0008470	8.79E-04	5	6	isovaleryl-CoA dehydrogenase activity
	GO:0005337	9.04E-04	7	11	nucleoside transmembrane transporter activity
	GO:0050839	9.04E-04	7	11	cell adhesion molecule binding
	GO:0070330	9.06E-04	15	37	aromatase activity
	GO:0004312	9.60E-04	21	60	fatty acid synthase activity
	GO:0004085	9.74E-04	4	4	butyryl-CoA dehydrogenase activity
	GO:0052890	9.74E-04	4	4	oxidoreductase activity, acting on the CH-CH group of donors, with a flavin...
	GO:0018664	1.13E-03	12	27	benzoate 4-monooxygenase activity
	GO:0004316	1.36E-03	13	31	3-oxoacyl-[acyl-carrier-protein] reductase (NADPH) activity
	GO:0016872	1.84E-03	7	12	intramolecular lyase activity
	GO:0016491	2.30E-03	381	1920	oxidoreductase activity
	GO:0016229	4.03E-03	16	46	steroid dehydrogenase activity
	GO:0004474	4.18E-03	4	5	malate synthase activity
	GO:0005488	4.87E-03	1066	5839	binding
	GO:0016627	4.90E-03	44	171	oxidoreductase activity, acting on the CH-CH group of donors
	GO:0016705	5.33E-03	99	442	oxidoreductase activity, acting on paired donors, with incorporation...
	GO:0004708	5.52E-03	3	3	MAP kinase kinase activity
	GO:0047616	5.52E-03	3	3	acyl-CoA dehydrogenase (NADP+) activity
	GO:0015926	5.68E-03	20	64	glucosidase activity
	GO:0016405	5.74E-03	7	14	CoA-ligase activity
	GO:0033764	6.53E-03	15	44	steroid dehydrogenase activity, acting on the CH-OH group of donors...
	GO:0003995	8.05E-03	16	49	acyl-CoA dehydrogenase activity

All transcripts with differential expression (Factor < 3; pV < 0.01) in senescent PQ-stressed samples were analyzed. Entries high-lighted in red refer to terms discussed in the text. GO terms with pV < 1E-3 are shown. The GO terms referred to in the text are high-lighted in red. CC: Cellular Component; BP: Biological Process; C: Count (number of genes of respective GO term in the group (up- or down-regulated)); S: Size (total number of *P. anserina* genes with the respective GO term).

Supplemental table 2: Summary of primer sequences used for qRT-PCR.

PaNo.	gene	Primer	sequence
<i>Pa_1_16400</i>	<i>PaCtr1</i>	<i>Pa_1_16400-1</i>	CTCACAATGTCACACTCC
		<i>Pa_1_16400-2</i>	TTAGCGATCAGTGCTACC
<i>Pa_2_4660</i>	<i>PaSod2</i>	<i>PaSod2-1</i>	TGGCTGCTGTTGAGAAGACC
		<i>PaSod2-2</i>	TCGGCCGTCTCCAGTTGAT
<i>Pa_2_9780</i>	<i>PaPorin</i>	<i>Porin-RT-for</i>	TCTCCTCCGGCAGCCTTG
		<i>Porin-RT-rev</i>	GAGGGTGTGCGCAAGTTC
<i>Pa_3_1710</i>	<i>PaAox</i>	<i>PaAox1-1</i>	CGCTGACAGAAGCTCAAT
		<i>PaAox1-2</i>	ATTCGTGGCGAGATCAAG
<i>Pa_3_10440</i>	<i>PaCtr3</i>	<i>PaCtr3-1</i>	GCGGATGTACTACAATGG
		<i>PaCtr3-2</i>	CCGTCGTCGTAATACTTC
<i>Pa_4_650</i>	<i>PaRpl19</i>	<i>PaRpl19-1</i>	AGATCTCCAACGCCAACTCC
		<i>PaRpl19-2</i>	TCGTGGTAGAGGTGCTTGTC
<i>Pa_4_4770</i>	<i>PaCtr2</i>	<i>Pa_4_4770-1</i>	CTGACGAGCACATACATGG
		<i>Pa_4_4770-2</i>	CGACGTTCATCGTCATCAC