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Correction

Correction: Genetic and Metabolomic Dissection of the Ergothioneine and Selenoneine Biosynthetic Pathway in the Fission Yeast, *S. pombe*, and Construction of an Overproduction System

The *PLOS ONE* Staff

There are formatting errors in Tables 1, 3, and 4 of the published article. The correct tables can be viewed here.

Table 1. Normalized peak areas of the four compounds composing the EGT biosynthetic pathway obtained by metabolomic analysis of WT and newly constructed strains. Values were measured from metabolome samples of three different *S. pombe* strains in three different cultivation conditions, as indicated. Mass values (m/z) and LC retention times (min) of each peak are included for reference.

Strain	Cultivation condition	Histidine, 156.077 m/z @12.4 min	Trimethyl histidine (hercynine), 198.124 m/z @10.3 min	Hercynylcysteine sulfoxide, 333.123 m/z @12.2 min	Ergothioneine, 230.096 m/z @12.6 min
WT 972	EMM2	14.4	1.7	0	0.1
WT 972	EMM2-N (24 h)	2.2	3.2	2.2	13.7
WT 972	EMM2-LG (24 h)	55.4	65.9	3.5	6.7
Δ*egt1*	EMM2	10.7	0.3	0	0
Δ*egt1*	EMM2-N (24 h)	2.8	0.1	0	0
Δ*egt1*	EMM2-LG (24 h)	54.1	0	0	0
Δ*egt2*	EMM2	11.4	0.9	3.9	0
Δ*egt2*	EMM2-N (24 h)	1.9	1.8	58.2	3.1
Δ*egt2*	EMM2-LG (24 h)	61.1	64.7	44.1	1.6

doi:10.1371/journal.pone.0097774.t001

Citation: The *PLOS ONE* Staff (2014) Correction: Genetic and Metabolomic Dissection of the Ergothioneine and Selenoneine Biosynthetic Pathway in the Fission Yeast, *S. pombe*, and Construction of an Overproduction System. PLoS ONE 9(7): e105177. doi:10.1371/journal.pone.0105177

Published July 31, 2014

Table 3. Absolute intracellular EGT concentrations (μM) in *S. pombe* cells. Intracellular concentrations were derived from measured normalized peak areas using a calibration curve generated by injections of pure EGT in 10-fold dilution steps. The detailed calculation method is described in Figure S6.

Cell condition	Culture medium	Intracellular EGT (μM)
WT vegetative	EMM2	0.3
WT nitrogen starvation	EMM2-N (24 h)	157.4
WT glucose starvation	EMM2-LG (24 h)	41.6
P81nmt1-egt1$^+$	EMM2	32.4
P41nmt1-egt1$^+$	EMM2	181.2
P3nmt1-egt1$^+$	EMM2	1606.3

doi:10.1371/journal.pone.0097774.t003

Table 4. *S. pombe* strains used in this manuscript. Strains from the Bioneer haploid deletion mutant collection [24] were backcrossed with WT 972 to remove auxotrophic markers.

Strain name	Genotype	Source
972	*h*$^-$ (WT)	Leupold (1950) [52]
975	*h*$^+$ (WT)	Leupold (1950) [52]
KS1366	*h*$^-$ Δ*sty1::ura4*$^+$ *ura4-D18*	Shiozaki and Russell (1995) [53]
TP1701	*h*$^-$ Δ*nfs1::kanMX4*	Bioneer collection [24]
TP1704	*h*$^-$ Δ*SPBC660.12c::kanMX4*	Bioneer collection [24]
TP1705	*h*$^-$ Δ*SPAC11D3.10::kanMX4*	Bioneer collection [24]
TP1706	*h*$^+$ Δ*SPCC777.03c::kanMX4*	Bioneer collection [24]
TP1707	*h*$^-$ Δ*SPAC11D3.10::hphMX6*	Marker switch of TP1705 to hphMX6
TP1732	*h*$^-$ Δ*SPBC660.12c::natMX6*	Marker switch of TP1704 to natMX6
TP1733	*h*$^+$ Δ*SPBC660.12c::natMX6*	TP1732 crossed with WT 975
TP1736	*h*$^-$ Δ*SPBC660.12c::natMX6* Δ*nfs1::kanMX4*	TP1701 crossed with TP1733
TP1737	*h*$^-$ Δ*SPBC660.12c::natMX6* Δ*SPCC777.03c::kanMX4*	TP1706 crossed with TP1732
TP1739	*h*$^+$ Δ*SPBC660.12c::natMX6* Δ*SPAC11D3.10::hphMX6*	TP1707 crossed with TP1733
TP1740	*h*$^-$ Δ*SPCC777.03c::kanMX4* Δ*SPAC11D3.10::hphMX6*	TP1706 crossed with TP1707
TP1743	*h*$^-$ Δ*SPBC660.12c::natMX6* Δ*SPAC11D3.10::hphMX6* Δ*SPCC777.03c::kanMX4*	TP1739 crossed with TP1740
TP1770	*h*$^-$ Δ*egt1::kanMX6*	Constructed as part of this study
TP1771	*h*$^-$ Δ*egt2::kanMX6*	Constructed as part of this study
TP1857	*h*$^-$ *egt1::P81nmt1-egt1*$^+$	Constructed as part of this study
TP1855	*h*$^-$ *egt1::P41nmt1-egt1*$^+$	Constructed as part of this study
TP1803	*h*$^-$ *egt1::P3nmt1-egt1*$^+$	Constructed as part of this study
TP1813	*h*$^-$ Δ*egt2::hphMX6*	Marker switch of TP1771 to hphMX6
TP1814	*h*$^+$ Δ*egt2::hphMX6*	TP1813 crossed with WT 975
TP1879	*h*$^-$ *egt1::P3nmt1-egt1*$^+$ Δ*egt2::hphMX6*	TP1803 crossed with TP1814

doi:10.1371/journal.pone.0097774.t004

Reference

1. Pluskal T, Ueno M, Yanagida M (2014) Genetic and Metabolomic Dissection of the Ergothioneine and Selenoneine Biosynthetic Pathway in the Fission Yeast, *S. pombe*, and Construction of an Overproduction System. PLoS ONE 9(5): e97774. doi:10.1371/journal.pone.0097774