

Table S4. Genes related to reductive stress during growth of *Mycobacterium tuberculosis* in fatty acids

(A) Number of genes related to reductive stress with significant expression during growth in different carbon sources.

Relation to reductive stress	Number of genes with significant decreased expression (%)		Number of genes with significant increased expression (%)	
	FE	FS	FE	FS
Known generators of reductive equivalents	1 (0.9)	5 (3.13)	1 (0.86)	3 (2.9)
Known generators of reductive sinks [reductive sinks lipid metabolism-related]	4 (3.6) [4]	1 (0.63) [1]	8 (6.9) [6]	6 (5.77) [4]
Other reductive stress-related genes	1 (0.9)	5 (3.13)	5 (4.3)	4 (3.8)
Heme-related genes	2 (1.8)	1 (0.63)	7 (6.03)	5 (4.8)
Total reductive stress-related genes	8 (7.2)	12 (7.5)	21 (18.1)	18 (17.3)
TOTAL genes compared	111 (100)	160 (100)	116 (100)	104 (100)

Genes with significant increased or decreased expression during growth in fatty acids (FE, FS) (see Supplementary Table S2 E & F) were checked against 371 genes related with reductive stress (www.tuberculist.epfl.ch).

The list of genes related with reductive stress included those within the functional category of “lipid metabolism” as well as genes participating in the Heme-group synthesis and stabilization.

Growth phase: FE, Dubos LC-FA exponential; FS, Dubos LC-FA stationary.

(B) Genes related to the Heme-prosthetic group with significant increase expression during growth in long-chain fatty acids.

Gene tag	Gene name	Growth phase	Functional category	Function	Relationships to the Heme-group	Fisher exact test
Rv0508		FE	unknown	putative thioredoxin	Fe-S cluster stabilization	8.02 E-07
Rv0509	<i>hemA</i>	FE	intermediary metabolism and respiration	Heme biosynthesis		6.16 E-12
Rv0510	<i>hemC</i>	FS	intermediary metabolism and respiration	Heme biosynthesis		3.43 E-06
Rv0512	<i>hemB</i>	FE	intermediary metabolism and respiration	Heme biosynthesis		0.021
Rv1324		FS	intermediary metabolism and respiration	Thioredoxin	Fe-S cluster stabilization	4.27 E-4
Rv1462	<i>sufD</i>	FE	unknown	UNK, putative FeS cluster formation	Fe-S cluster assembly	0.034
Rv1465		FS	intermediary metabolism and respiration	Probable Nitrogen fixation / Suf system	Fe-S cluster assembly	0.002
Rv1466		FS	unknown	UNK, domain of unknown function		0.37 E-4
Rv1932	<i>tpx</i>	FE	virulence, detoxification, adaptation	Thiol peroxidase	Fe-S cluster stabilization	0.012
Rv2007c*	<i>fdxA</i>	FS	intermediary metabolism and respiration	Ferredoxin	Fe-S cluster stabilization	1.09 E-12
Rv2391	<i>nirA</i>	FE	intermediary metabolism and respiration	Ferredoxin-dependent nitrite reductase	Fe-S cluster stabilization	2.64 E-06
Rv3673c		FE	intermediary metabolism and respiration	Possible thioredoxin	Fe-S cluster stabilization	0.028

Asterisks in gene tags indicate those genes members of the DosR regulon.
Growth phase: FE, Dubos LC-FA exponential; FS, Dubos LC-FA stationary.