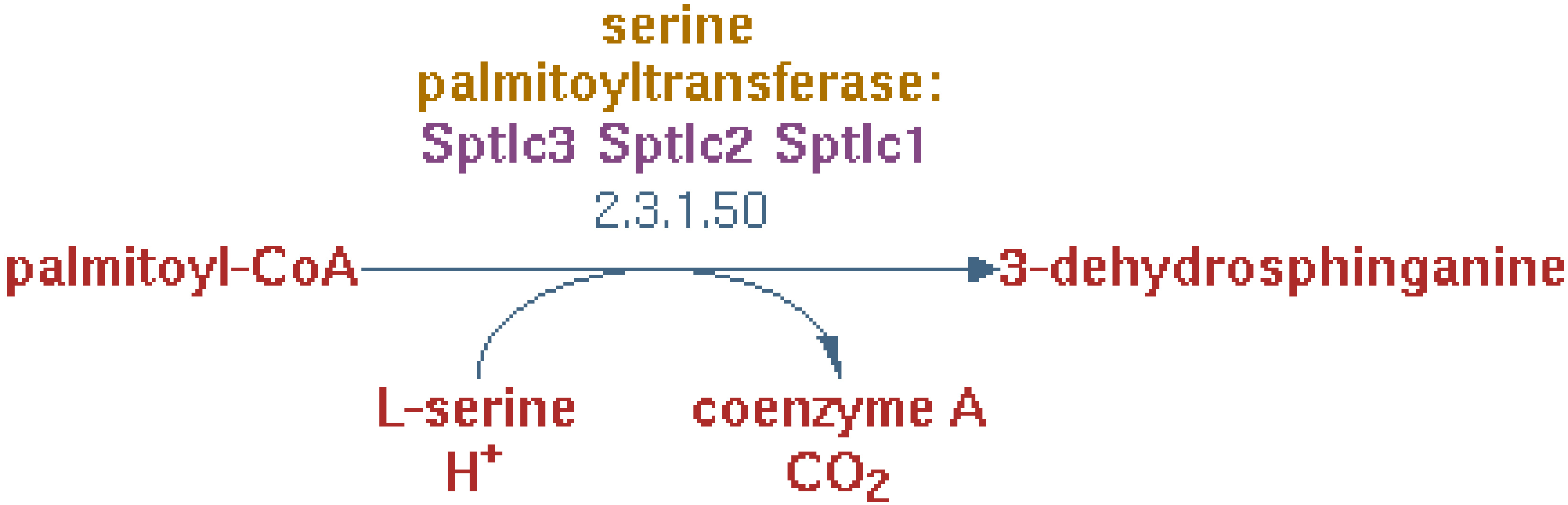
MouseCyc and Reactome are clearly looking at the same biochemical reaction ...



serine palmitoyltransferase:

Sptlc3 Sptlc2 Sptlc1

2.3.1.50

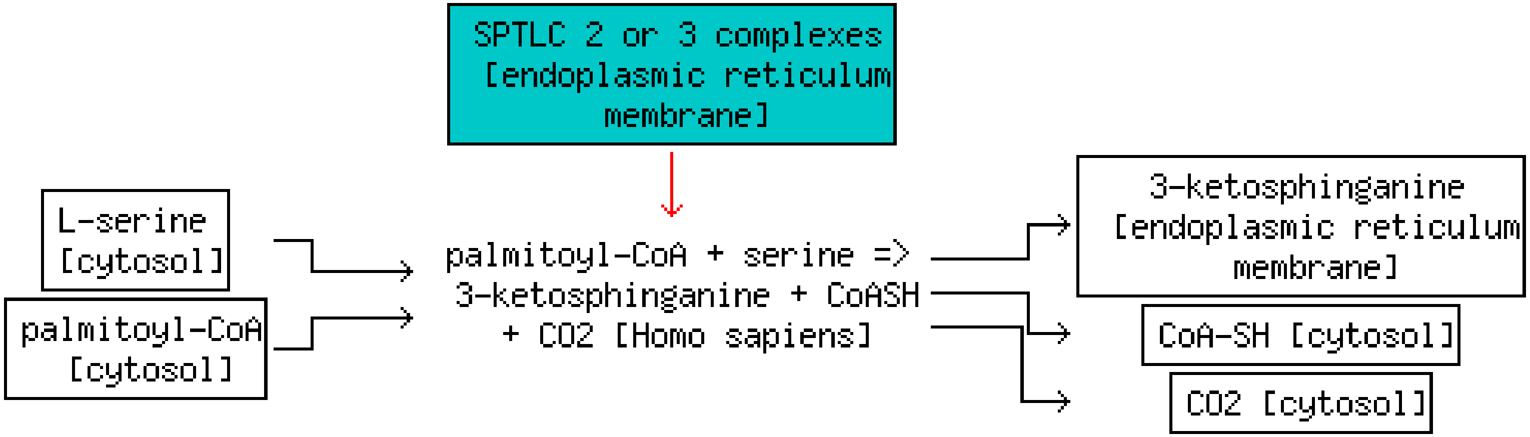
palmitoyl-CoA → 3-dehydrosphinganine

L-serine

H^+

coenzyme A

CO_2



SPTLC 2 or 3 complexes [endoplasmic reticulum membrane]

L-serine [cytosol]

palmitoyl-CoA [cytosol]

palmitoyl-CoA + serine => 3-ketosphinganine + CoASH + CO2 [Homo sapiens]

3-ketosphinganine [endoplasmic reticulum membrane]

CoA-SH [cytosol]

CO2 [cytosol]

... sort of

Summary of the SPT complex in mouse

SPT Complex (PRO:xxxxx)
Subunit 1 (Sptlc1) is part_of SPT (PRO:xxxxx)
Subunit 2 (Sptlc2) is part_of SPT (PRO:xxxxx)

↓

SPT Complex A (PRO:yyyyy)
is_a SPT (PRO:xxxxx)
Subunit 3 (Sptlc3) is part_of SPT A (PRO:yyyyy)

SPT complex _ has_parts polypeptides 1 and 2 and has_function
GO:0004758 serine C-palmitoyltransferase activity
SPT complex A has_parts polypeptides 1 and 2 and 3, has_function
GO:0004758 serine C-palmitoyltransferase activity, and is formed
by binding SPT complex _ and polypeptide 3
but the key publication asserts that the active complex (human) is probably an octamer with unknown, possibly variable, numbers of copies of polypeptides 1, 2, and 3, and deprecates older assertions that 1:2 and 1:3 heterodimers exist and are catalytically active.

Summary of the SPT complex in human

SPTLC1:2 Complex
    Subunit 1 (SPTLC1) is part_of SPTLC1:2 complex
    Subunit 2 (SPTLC2) is part_of SPTLC1:2 complex

SPTLC1:3 Complex
    Subunit 1 (SPTLC1) is part_of SPTLC1:3 complex
    Subunit 3 (SPTLC3) is part_of SPTLC1:3 complex

SPTLC1:2 complex has_parts polypeptides 1 and 2 and has_function
GO:0004758 serine C-palmitoyltransferase activity
SPTLC1:3 complex has_parts polypeptides 1 and 3 and has_function
GO:0004758 serine C-palmitoyltransferase activity

based on those deprecated older publications which assert that 1:2 and 1:3 heterodimers exist and are catalytically active.

What is to be done?

- PRO should be populated now with data for extant human and mouse complexes.
- PRO should strip attributes that its data model can't yet handle, e.g., subunit stoichiometry.
- PRO should allow for different qualitative properties (composition and function) within and between species.
- PRO should allow for alternative forms of a complex within and between species.
- MOD databases should guarantee stable IDs and change tracking so that attributes discarded now can be retrieved later as the PRO data model develops, and so that revisions to MOD data can be propagated to PRO.
- MOD databases should cross-reference their complexes.

Reactome now has available -

4596 human complexes annotated in Reactome (3112 released). Of the 4596

-751 have catalyst or transporter activity (GO molecular function), 125 with explicit literature references

- 60 have GO cell_component annotations, 22 with explicit literature references
- ~639 involve proteins with modified residues
- 2728 mouse complexes matched to human released ones: 98 curated; 2630 computationally inferred

Curated mouse and human complex components, manually aligned

Complex	Genes	Species w/ exptl evidence	human homolog
3-methylcrotonyl-CoA carboxylase	*Mccc1*	*Hs*	methylcrotonyl-CoA carboxylase alpha chain [mitochondrial matrix]
	Mccc2		methylcrotonyl-CoA carboxylase beta chain [mitochondrial matrix]
			methylcrotonyl-CoA carboxylase complex [mitochondrial matrix]
ADP-forming succinate-CoA ligase	*Suclg1*	*Mm,Rn*	Succinyl-CoA synthetase, alpha-chain [mitochondrial matrix]
	Sucla2		Succinyl-CoA synthetase, betaA chain [mitochondrial matrix]
			Succinyl-CoA synthetase heterodimer [ADP-forming] [mitochondrial matrix]
GDP-forming succinate-CoA ligase	*Suclg1*	*Mm,Rn*	Succinyl-CoA synthetase, alpha-chain [mitochondrial matrix]
	Suclg2		Succinyl-CoA synthetase, betaG chain [mitochondrial matrix]
			Succinyl-CoA synthetase heterodimer [GDP-forming] [mitochondrial matrix]
serine palmitoyltransferase	*Sptlc1*	*Mm,Rn*	SPTLC1 [endoplasmic reticulum membrane]
	Sptlc2		SPTLC2 [endoplasmic reticulum membrane]
	Sptlc3		SPTLC3 [endoplasmic reticulum membrane]
			SPTLC1:SPTLC2 [endoplasmic reticulum membrane]
			SPTLC1:SPTLC3 [endoplasmic reticulum membrane]
NADH dehydrogenase (ubiquinone)	*mt-Nd1*	*Bt*	NADH-ubiquinone oxidoreductase chain 1 (EC 1.6.5.3) [mitochondrial inner membr
	mt-Nd2		NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3) [mitochondrial inner membr
	mt-Nd3		NADH-ubiquinone oxidoreductase chain 3 (EC 1.6.5.3) [mitochondrial inner membr
	mt-Nd4		NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3) [mitochondrial inner membr
	mt-Nd4l		NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3) [mitochondrial inner memb
	mt-Nd5		NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3) [mitochondrial inner membr
	mt-Nd6		NADH-ubiquinone oxidoreductase chain 6 (EC 1.6.5.3) [mitochondrial inner membr

extend to other species via RefGenomes?