Date estimation 3. Comparison of MRCA dating estimates by BEAST using ancient plus modern, and only modern strains.

| Parameters | | | Median MRCA (CI95%) | | | Mutation rate | | Model (Marginal Likelihood[1]) | | | | | |
| | | | | | | | | Strict | | | UCLD | | |
Ragna	Strains[2]	Subsample	Para C Lineage (w/o Lomita)	Paratyphi C (including Ragna)	Modern Paratyphi C (crown)	Median	CI 95%	Constant	Skyride	BDP-SS	Constant	Skyride	BDP-SS
1200	Para C Lineage (w/o Lomita)	1	3687 (1744-7286)	1202 (885-1864)	480 (264-881)	1.38E-7	5.80E-8 - 2.32E-7	-6845066	-6845084	-6845158	**-6845001**	-6845038	-6845047
		2	3861 (2005-6744)	1288 (928-1979)	576 (305-978)	1.24E-7	6.05E-8 - 1.98E-7	-6832249	-6832264	-6832331	**-6832246**	-6832279	-6832293
	Paratyphi C (incl. Ragna)	1	-	1212 (1030-1440)	482 (380-611)	1.11E-7	8.40E-8 - 1.38E-7	**-6742493**	-6742523	-6742512	-6742654	-6742675	-6742665
		2	-	1544 (1233-1949)	685 (513-924)	7.79E-8	5.35E-8 - 1.00E-7	**-6744367**	-6744389	-6744389	-6744563	-6744571	-6744562
1073	Para C Lineage (w/o Lomita)	1	4066 (1758-8687)	1370 (1040-2307)	517 (250-1054)	1.29E-7	4.35E-8 - 2.22E-7	-6845060	-6845097	-6845151	**-6845003**	-6845046	-6845055
		2	4258 (2100-7601)	1437 (1056-2264)	624 (331-1085)	1.15E-7	5.36E-8 - 1.86E-7	-6832246	-6832277	-6832296	**-6832228**	-6832269	-6832337
	Paratyphi C (incl. Ragna)	1	-	1274 (1092-1506)	481 (382-614)	1.10E-7	8.23E-8 - 1.37E-7	**-6742498**	-6742520	-6742495	-6742670	-6742682	-6742670
		2	-	1611 (1298-2047)	688 (512-941)	7.80E-8	5.47E-8 - 1.03E-7	**-6744370**	-6744387	-6744381	-6744554	-6744577	-6744564
no Ragna	Modern Paratyphi C (w/o Ragna)	1	-	-	484 (384-617)	1.09E-7	8.16E-8 - 1.36E-7	/	/	/	/	/	/
		2	-	-	681 (507-922)	7.86E-8	5.39E-8 - 1.02E-7	/	/	/	/	/	/

NOTE: Bold face indicates the likeliest model for that subsample
[1]Strict -- strict clock model. UCLD -- uncorrelated relaxed clock model with an underlying lognormal distribution. Constant -- Constant population size model. Skyride -- Bayesian skyride model. BDP-SS -- General birth-death process model.
[2]Only genomes whose collection year was known were analysed.