



Ancestral reconstruction 1. Maximum likelihood phylogeny and geographical origins derived from 61,451 SNPs in the non-repetitive core genome of the Para C Lineage plus Birkenhead. Filled circles at the tips are color-coded according to the source continent (see Continent key). Pie-charts on internal nodes show the geographical inference estimates of the likelihoods of continental sources according to standard MCMC in BayesTraits (Ancestral reconstruction 2). The position of acquisition of SPI-7 by Paratyphi C is indicated at an arbitrary position on the basal branch for that serovar. The numbers on branches indicate the median dating estimates by BEAST from independent subsamples (Table S4). Note that the basal branches are discontinuous, and include breaks. Scale bar: substitution frequency.