

Table 1. Comparison of MLST and SNP-based approaches used in study to assess genetic similarity between genomes. Adapted from Uelze L, Grützke J, Borowiak M, Hammerl JA, Juraschek K, Deneke C, et al. Typing methods based on whole genome sequencing data. *One Health Outlook* . 2020;2:3. Published 2020 Feb 18. doi:10.1186/s42522-020-0010-1 (Uelze et al., 2020) [60]

Comparison of WGS-Based Typing Methods Used in Study			
Method	Approach	Reference	Genomic Comparison Result
cgMLST	Alignment to scheme of core loci found to be present in $\geq 98\%$ of the representative <i>Salmonella</i> genomes used to build the EnteroBase [31] allele scheme (n=3,002)	Repository of allele calls for a set of core loci	Allele distance matrix; UPGMA phylogenetic tree
wgMLST (chromosome-associated loci)	Alignment to a scheme of all chromosome-associated loci (including core) (n=22,457)	Repository of allele calls for a set of chromosome-associated loci	Allele distance matrix; UPGMA phylogenetic tree
wgMLST (all loci)	Alignment to scheme of all chromosomal and plasmid loci, as well as 7-gene MLST loci (n= 25,365)	Repository of allele calls for a set of chromosome-associated loci and accessory loci, and 7-gene MLST scheme [31]	Allele distance matrix; UPGMA phylogenetic tree
hqSNP	Mapping to reference genome; phage regions and plasmid contigs were masked	Closely related reference genome; [SNPs with less reliability were filtered out to produce a list of high-quality SNPs (hqSNPs)]	SNP alignment and SNP distance matrix; maximum-likelihood phylogenetic tree