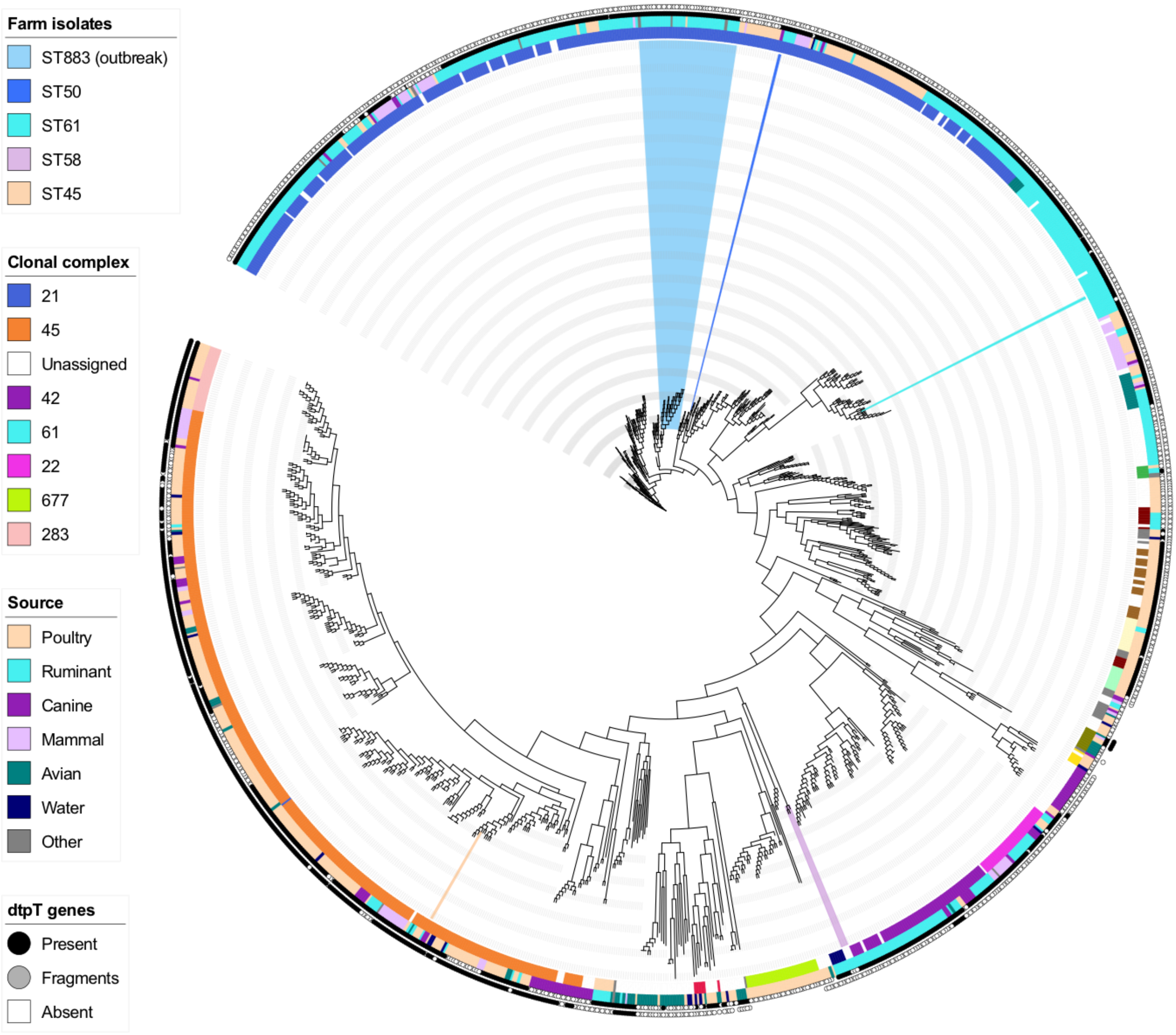

Fig. Presence of genes that encode di-/tripeptide transporter (*dtpT*) within the global genealogy of *C. jejuni*. Core-genome phylogeny of 1205 *C. jejuni* isolates was constructed by aligning 958 core genes using Roary (version 3.8.0) with MAFFT and inferring approximately maximum-likelihood tree using FastTree (version 2.1.9) with the GTR+CAT model [1,2]. The placement of the root is not biologically meaningful, and recombinations are not masked. Farm isolates of this study are highlighted with colored ranges in the tree. Metadata are presented with colored strips and dots in the order starting from the innermost circle: 1. clonal complex, 2. source, 3. *dtpT_1* gene, and 4. *dtpT_2* gene. The tree was visualized using iTOL (version 4.4.2) [3].

Table. Number of *C. jejuni* genomes harboring *dtpT* genes by host among genomes from the INNUENDO database [4].

Source	**Total no. of genomes**	***dtpT_1* (%)**	***dtpT_2* (%)**	**Both genes (%)**
Poultry	497	314 (63.2)	233 (74.2)	155 (31.2)
Ruminant	423	371 (87.7)	10 (2.3)	9 (2.1)
Canine	85	34 (40.0)	35 (41.2)	18 (21.2)
Mammal	76	59 (77.6)	33 (43.4)	31 (40.8)
Avian	52	24 (46.2)	19 (36.5)	17 (32.7)

References

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