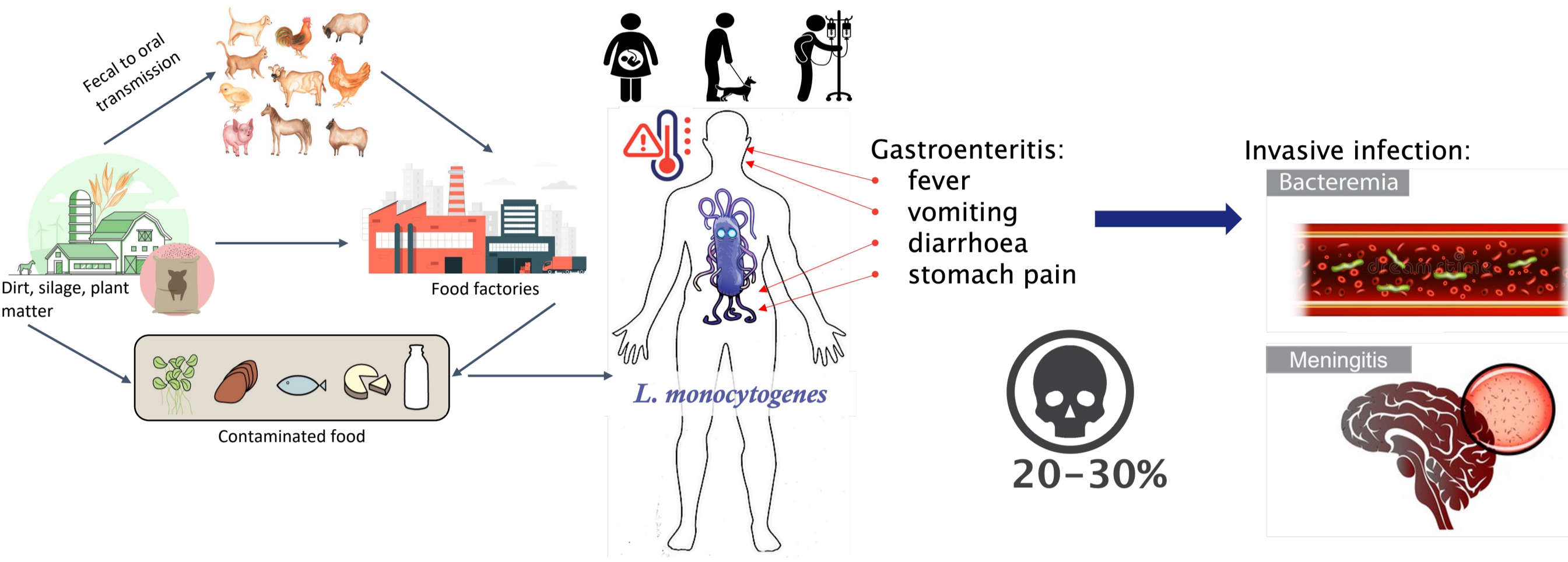


INTRODUCTION

Listeriosis is an uncommon disease caused by the bacteria *Listeria monocytogenes* with a high fatality rate. It is caused by consumption of contaminated products and affects vulnerable groups.



METHODS

Computational descriptive analysis of the UK's Health Security Agency (UKHSA) national *Listeria* whole genome sequence (WGS) surveillance database.

UKHSA's database generated from i) routine surveillance of hospitalised patients with Listeriosis performed between 2015-2020 and ii) food and food production environment samples, from sampling studies and outbreak investigations of potential contaminated food, where *L. monocytogenes* was recovered. The database includes samples from England, Wales, Scotland and Northern Ireland.

Population structure of *L. monocytogenes*, was assessed through MS phylogeny (Fig 1), which confirmed CC1 as the most abundant clonal complex associated with human infection.

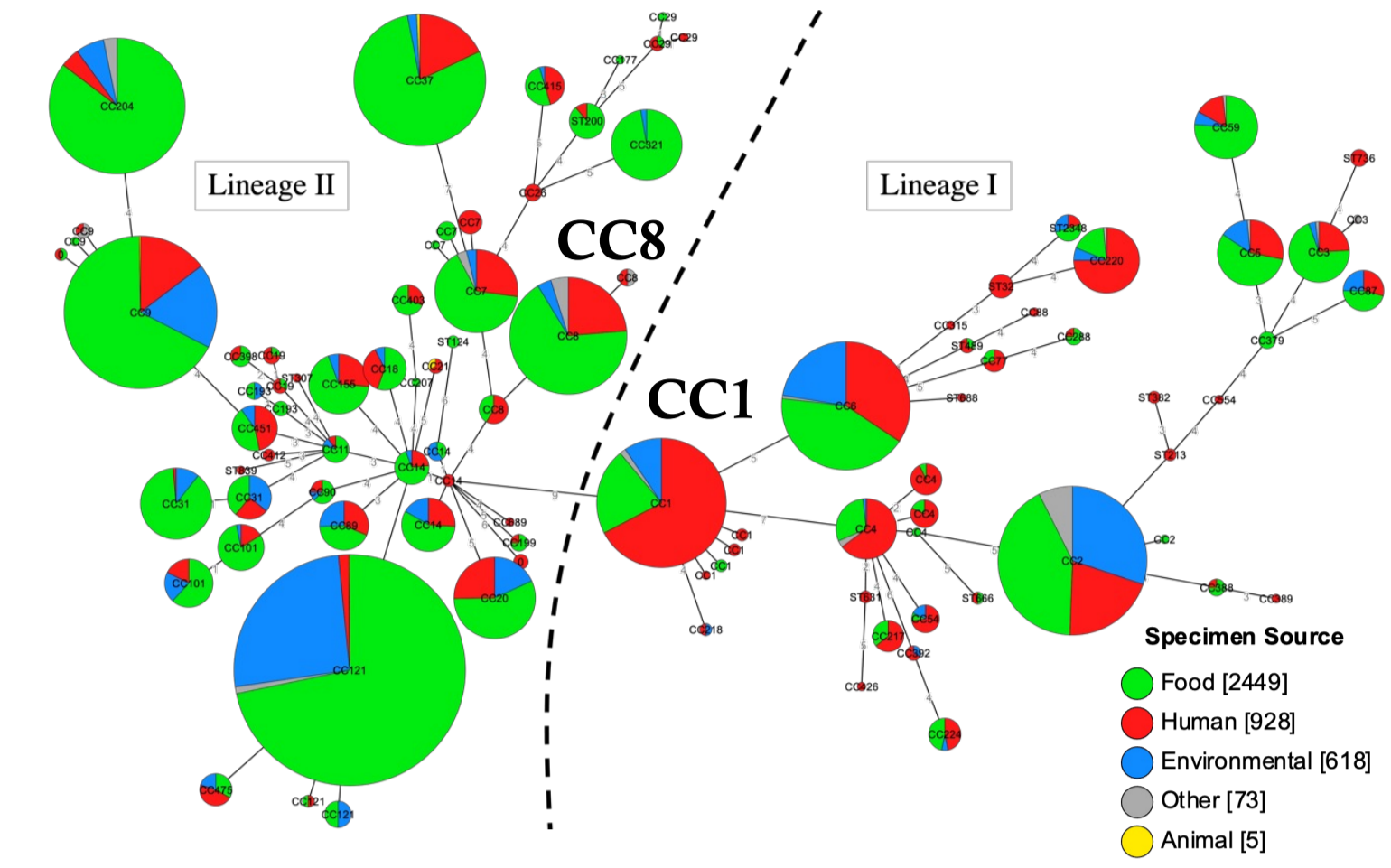
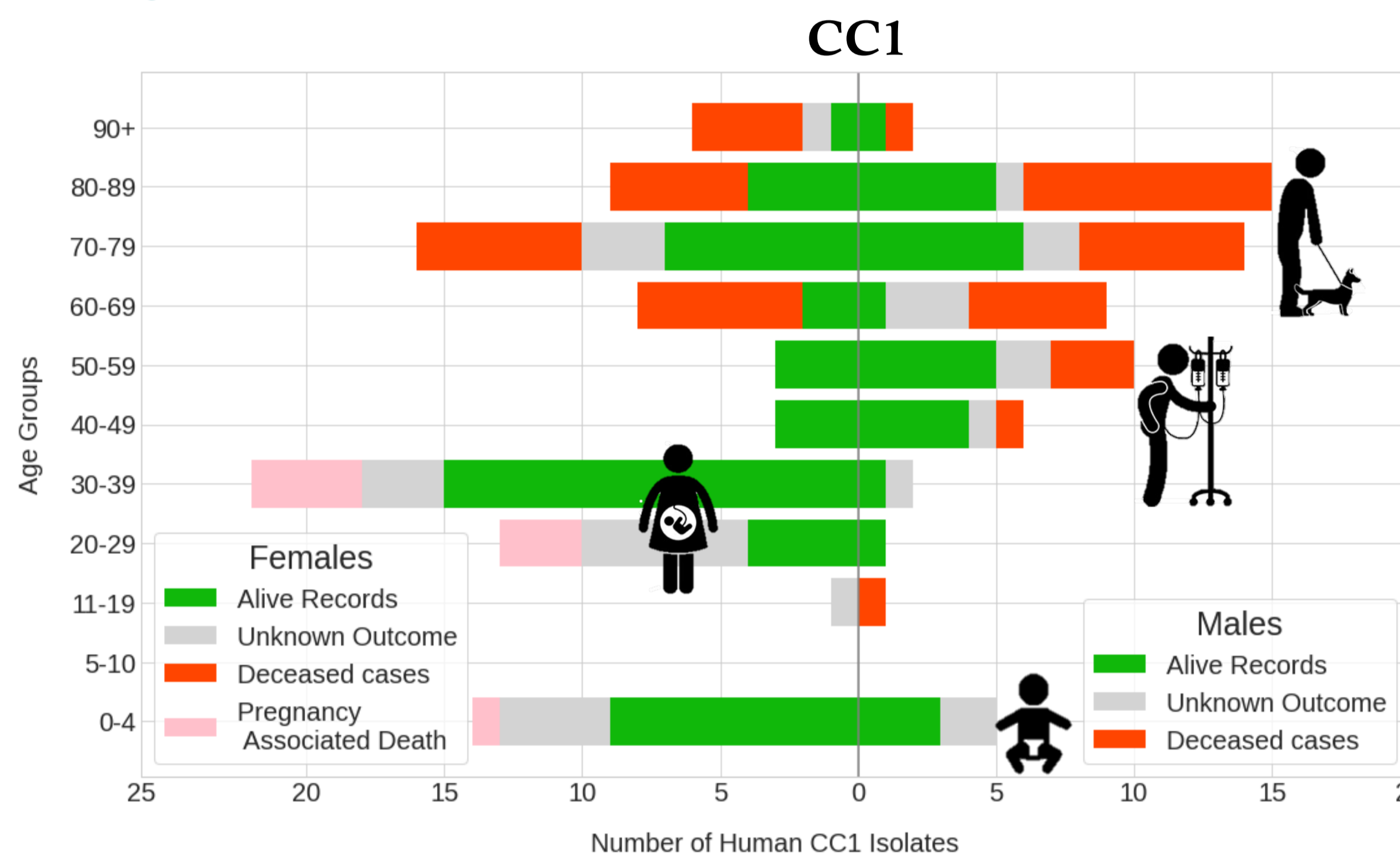
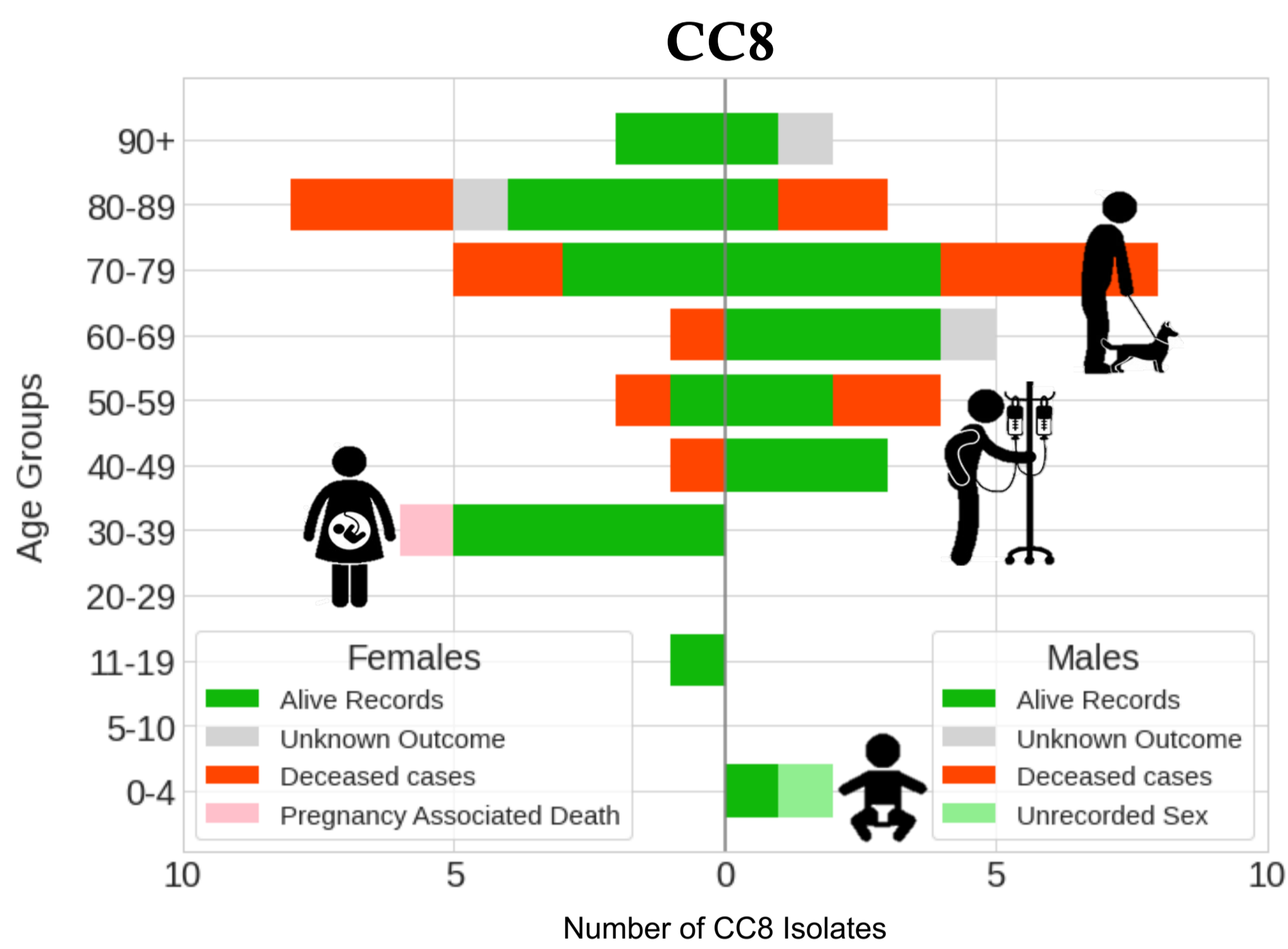


Figure 1: Minimum Span (MS) Population Structure Phylogeny Tree. Population structure of *L. monocytogenes* in the UK from 2015-2020.

RESULTS – CC1 EPIDEMIOLOGY

1 WHO



- CC8 = Lineage II **VS** CC1 = Lineage I
- CC8 = 53 human cases **VS** CC1 = 160 human cases.
- CC8 = 50% female cases **VS** CC1 = 59% female cases.
- Pregnancy impact: CC8 = 12% population **VS** CC1 = 27.5% population.
- Highest incidence: CC8 = 70-79yrs old Males **VS** CC1 = 30-39yrs old Females.
- Highest case death: CC8 = 70-79yrs old Males **VS** CC1 = 80-89yrs Females.

Figure 2: Age and sex distribution of C8 and CC1 clinical outcome of human infection. Isolates from hospitalized cases between 2015-2020. Clinical outcome is assessed through fatality records. Maternal and Neonatal isolates were entered as a single case.

2 HOW

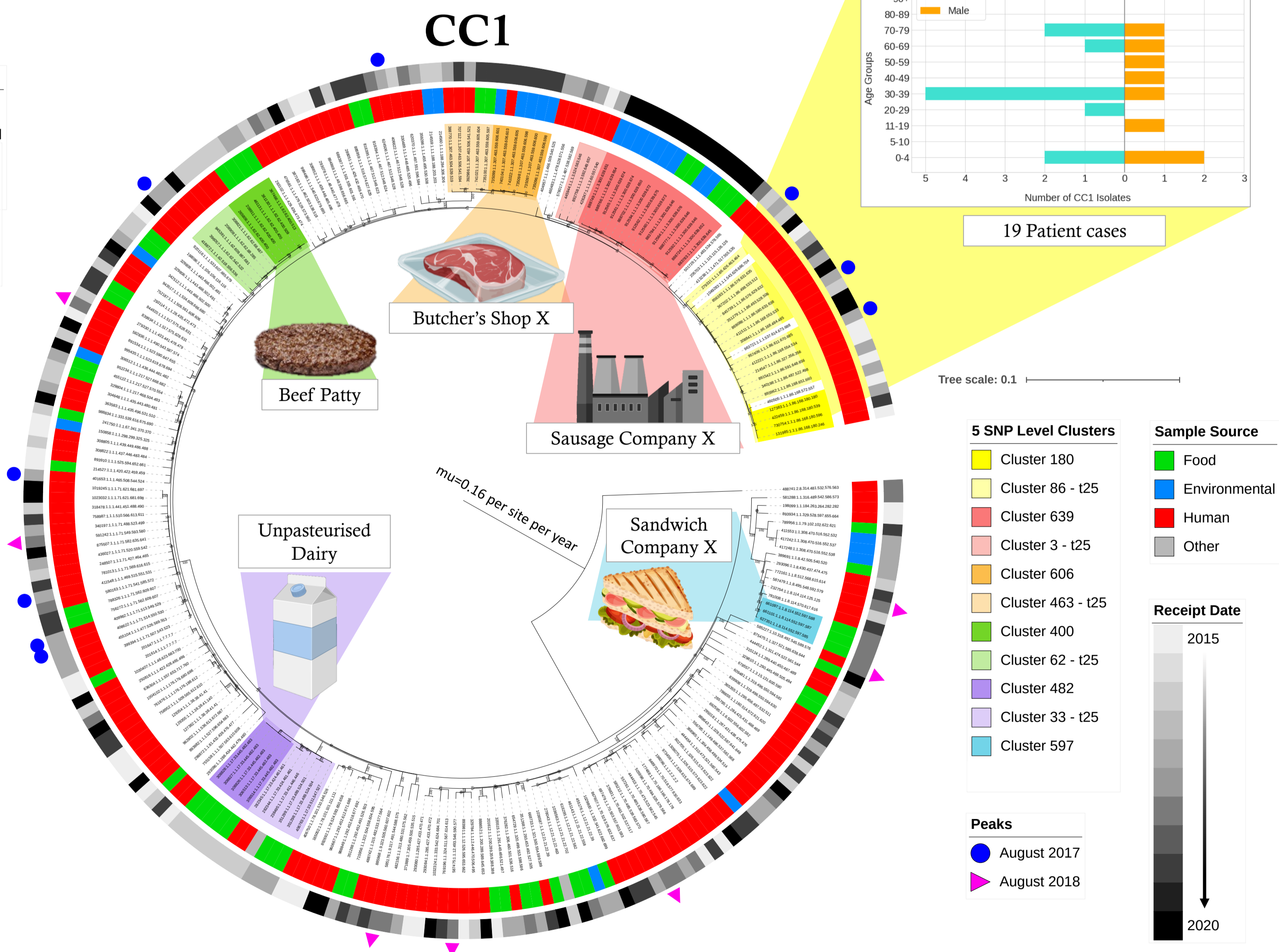
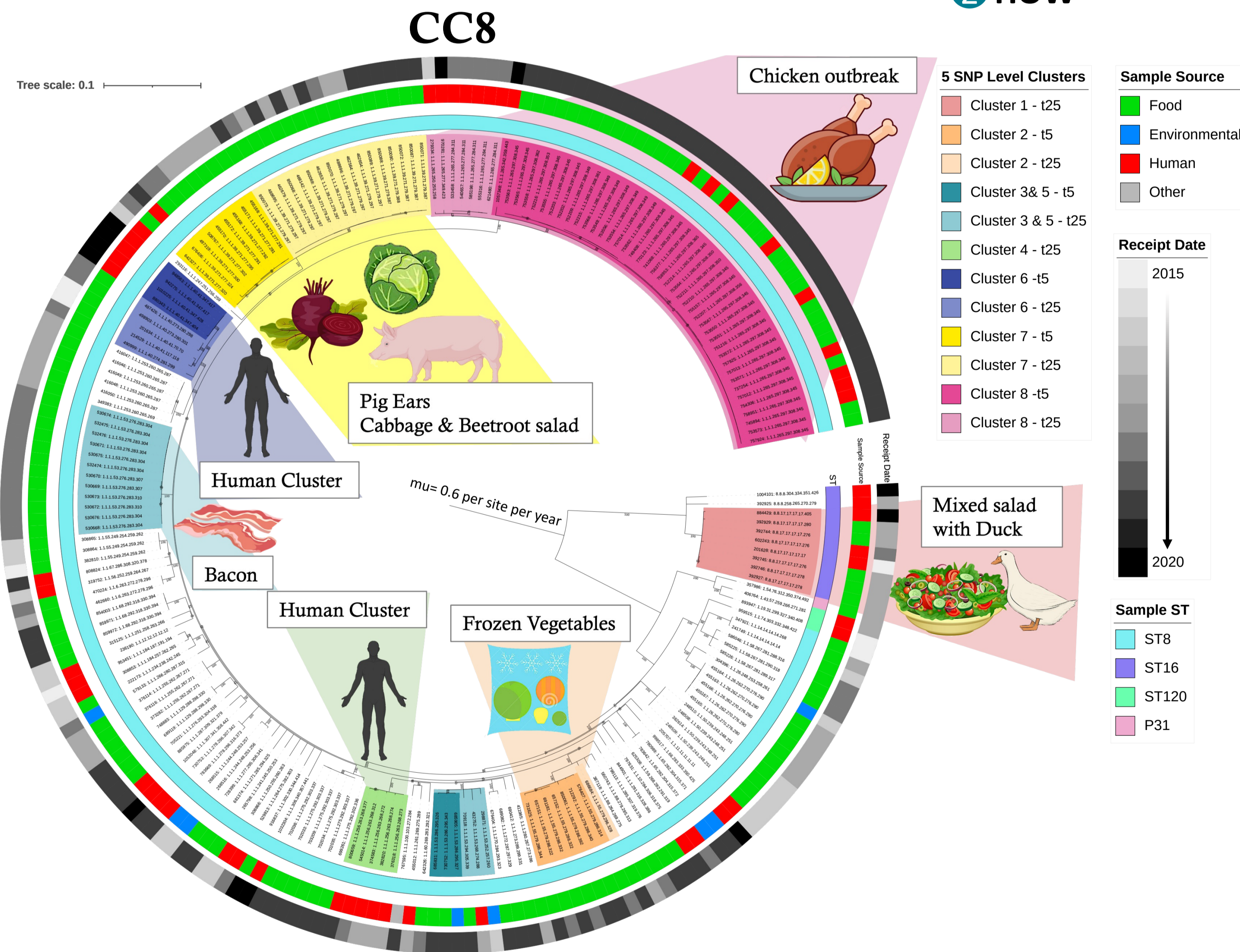


Figure 2: CC8 and CC1 phylogeny with 5 and 25 SNP distance clusters. Maximum likelihood trees for CC8 and CC1 isolates. Trees are rooted on the most distant isolate. The highlighted clades on the tree represent clusters within a 25 SNP difference and their suspected vehicle or setting. The darker colour clusters highlight the clusters at a t5 level.

- CC8 – 209 isolates: human cases (n=53), food (n=145) environment (n=10) and undetermined sources (n=1) **VS** CC1 – 237 isolates: human cases (n=160), food (n=51) environment (n=24) and undetermined sources (n=2)
- Genomic diversity: CC8 Average soft-core distance matrix = 86 (598-0). **VS** CC1 Average soft-core distance matrix = 153 (1135-0)
- CC8 Human isolates are clustered **VS** CC1 Human isolates not clustered

DISCUSSION

- Clones are unevenly distributed, in relation to sample source. Clones belonging to lineage I are statistically associated with human samples (eg. CC1), whereas lineage II is more commonly sampled from food and environmental sources (eg. CC8).
- We report a notable sex bias in CC1 incidence, with females ages 30-39 showing the highest infection rate. These cases are strongly linked to pregnancy listeriosis. In contrast, CC8 infections are higher in males over 70 years old.

- CC8 clusters 3 and 5 have the same 5 SNP difference, however, are distant in the phylogeny. This could be due to mobile elements however further investigation is needed.
- CC1 case distribution illustrates typically unspecific human infection patterns, in contrast to CC8, where human cases cluster.
- Phylogeny analysis and cluster identification suggests that expanding SNP distance to a t25 level could lead to the identification of larger clusters of interest to help with outbreak investigations.

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