Trends amongst genotypes of *Listeria monocytogenes* from clinical cases of listeriosis, food and the environment

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INTRODUCTION

- Listeriosis is a systemic infection caused by the Gram-positive bacterium *Listeria monocytogenes*.
- Listeriosis symptoms vary from the common gastrointestinal symptoms (fever, diarrhoea, vomiting and stomach pain), to severe invasive infection presenting as bacteraemia, meningitis, or central nervous system (CNS) infections.
- Listeriosis typically affects patients over 60 years of age, the immunocompromised and is commonly seen in pregnancy and neonatal cases [1].
- These conditions contribute to have a high case fatality rate of 20-30% [2][3].
- *Listeria monocytogenes* can be found throughout the food chain and transmission is most common from consumption of contaminated foods.

METHODS

- Computational descriptive analysis of the UK's Health Security Agency (UKHSA) national *Listeria* whole genome sequence surveillance (WGS) 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.
- All Listeria isolates have been characterised by WGS. Thus, cumulating to a dataset of approximately 5000 genomes.
- To reduce isolate redundancy, diminish background noise and reduce bias driven from large outbreaks and selective sampling, the data set was normalised.
- Outbreak investigations have shown isolates originating from the same source to remain tightly clustered within <5SNP pairwise distance [4]. Therefore, the data were normalised by grouping isolates with the same 5 SNP level address and the same receipt quarterly period, as a single entry. This resulted in a large reduction of the data set as illustrated in Table 1.

Source Type	Original	Normalised
Food	3015	949
Human	1000	846
Environmental	749	307
Total	4764	2102

Table 1. *L. monocytogenes* original and normalised dataset.

RESULTS

Analysing hospitalised human listeriosis cases from 2015-2020 in England, Scotland, Wales, Northern Ireland.

Figure 1 illustrates:

- Excess in female hospitalised cases, in childbearing ages.
- Higher levels of listeriosis in children under the age of 4 compared to older children.
- Higher prevelance in patients over the age of 60.

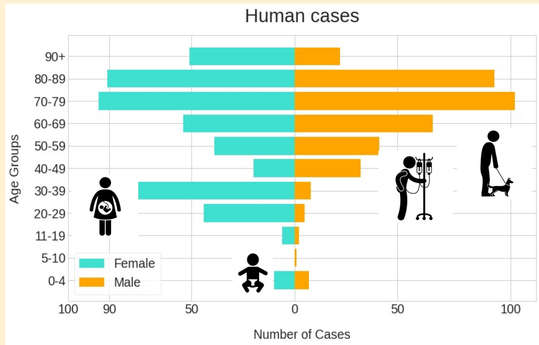
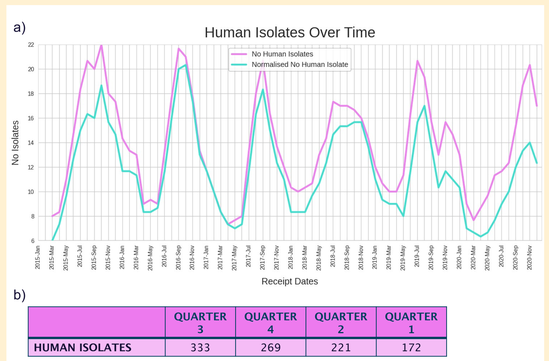


Figure 1. Human case distribution across age and sex.

Data from human hospitalised cases from England, Scotland, Wales, Northern Ireland. 2015- 2020.



b)

	QUARTER 3	QUARTER 4	QUARTER 2	QUARTER 1
HUMAN ISOLATES	333	269	221	172

Figure 2. Human case distribution.

a) Time series of hospitalised human listeriosis cases from January 2015 till December 2020. b) Months divided into four quarters to quantify reoccurring trends.

Time series analysis to visualise human case distribution in the UK over time.

Figure 2 illustrates:

- Reoccurring trends in hospitalised human listeriosis cases.
- Normalisation reduces bias from outbreaks, however the reoccurring trends remain.
- Most cases appear in Quarter 3, July, August, September.

To examine population structure of listeriosis, clonal complex distribution was investigated and visualized through a bar chart.

Figure 3 illustrates:

- Clinical isolates span across more diverse clonal complexes.
- Isolates appear equally distributed between Lineage I (50.1%) and Lineage II (49.9%)
- CCs linked to human VS food & food production environments

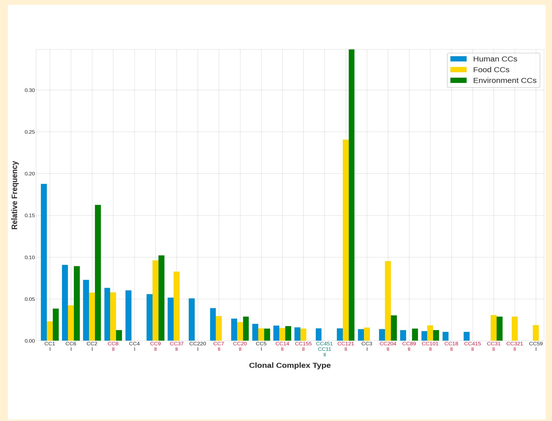


Figure 3. Population structure, clonal complex distribution.

DISCUSSION

- The first aim of this work was to create a descriptive analysis of the UKHSA genomic surveillance database on listeria.
- Distribution, time series analyses and statistics illustrate the same infection patterns, lineage correlations and clonal complex distribution as reported in literature.
- This data set reports a smaller disparity between Lineage I and Lineage II isolates, than most reports in literature. Although this is likely due to the large sampling of food and food related environments.
- There is sufficient evidence that clones are unevenly distributed, in relation to sample source. More specifically, clones belonging to lineage I are statistically associated with human samples, with the most common clonal complex being CC1. In contrast, lineage II isolates are more commonly sequenced from food and food production environments, with CC121 the leading clonal complex.
- Seasonal bias occurred in the clinical isolates with the most common months of infection being July, August and September. Further investigation is required to identify the causality driving these patterns.

CONCLUSIONS

- UKHSA database contains a considerable investigated resource.
- Age and Clonal complex distribution is consistent with literature reports from other countries.
- Next steps: characterise clonal complex using patient metadata and virulence/persistence gene profiles.

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