

Sequence-based typing of *Legionella pneumophila* serogroup 1 isolates in Belgium from 2011 to 2016

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Introduction

Legionella pneumophila is the etiological agent of legionnaires' disease (severe pneumonia) and Pontiac fever. This microorganism can be found in natural aquatic environment as well as in artificial water systems. Infection occurs mainly through inhalation of contaminated aerosols.

To discriminate between *L. pneumophila* strains, **Sequence Based Typing (SBT)** has been widely used as one of the established epidemiological typing methods. In this study, we have investigated by SBT clinical isolates of *L. pneumophila* collected between 2011 and 2016 in the Belgian National Reference Centre (NRC).

Methods

L. pneumophila serogroup 1 (Sg.1) isolates recovered from respiratory samples of Belgian patients between January 2011 and December 2016 (n=107) were genotyped using the internationally standardised SBT protocol of the European Working Group for Legionella Infections (EWGLI).

Clinical cases 2011-2016

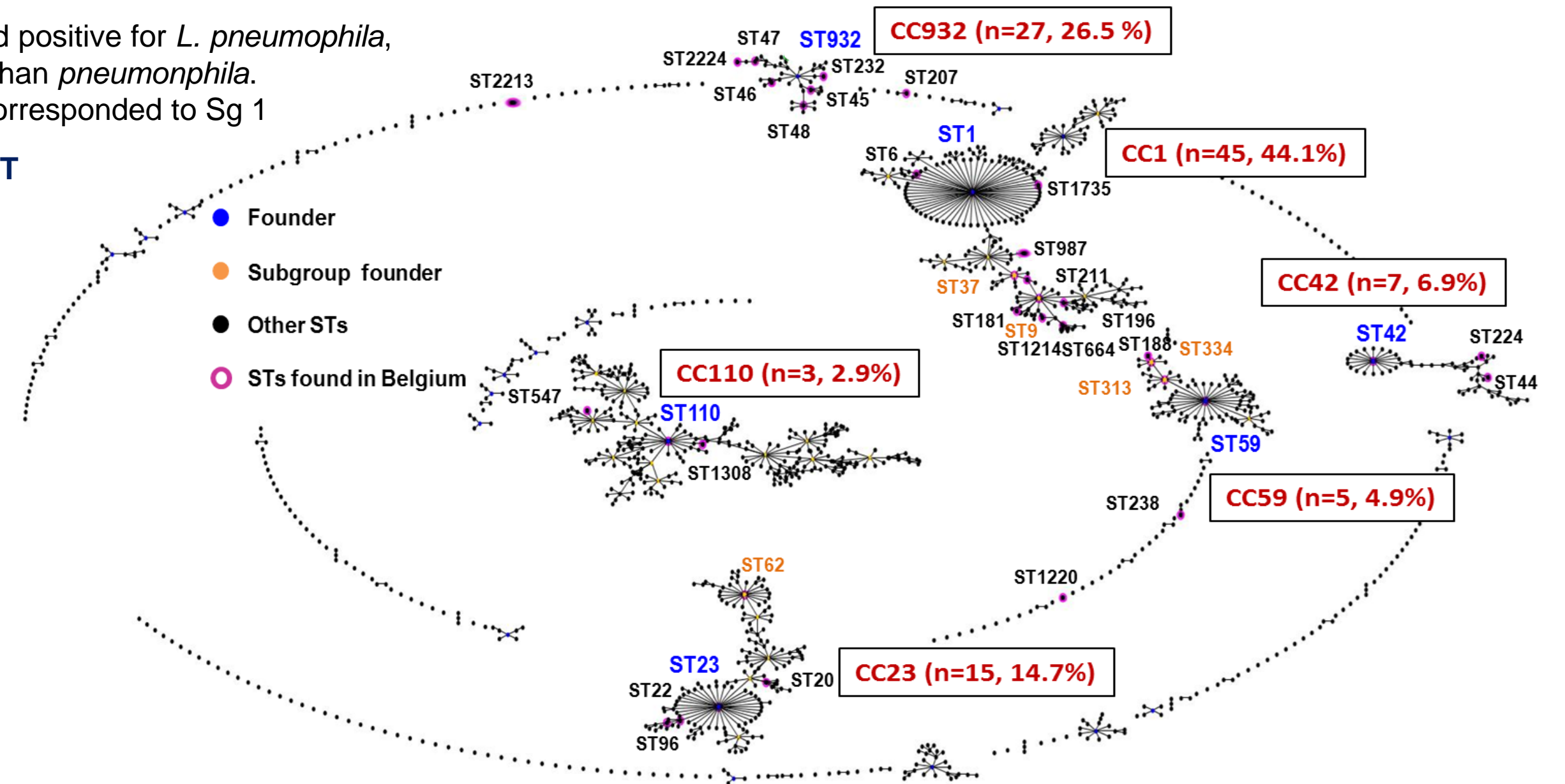
137 cases of suspected pneumoniae were diagnosed positive for *L. pneumophila*, only 5 cases were positive for *Legionella* spp. other than *pneumophila*. 95.5 % of all strains characterised by SBT (n=112) corresponded to Sg 1

Distribution of *L. pneumophila* Sg.1 isolates by ST

Sequence type	N	%
ST1	26	24.3
ST47	21	19.6
ST9	5	4.7
ST42	5	4.7
ST23	4	3.7
ST20	4	3.7
ST6	3	2.8
ST22	3	2.8
ST664	2	1.9
ST62	2	1.9
ST196	2	1.9
ST46	2	1.9
ST211	2	1.9
Single case ST's	26	24.3
total	107	100.00

Total number of STs: 39 (4 STs were new)
Simpson's index of diversity: 0.901

Results



Population snapshot of *L. pneumophila* Sg.1 STs from the EWGLI database (eBURST v3)

STs were included in the same group if they share at least five out of seven SBT loci

Conclusions

- ST1 (24.3 %) and ST47 (19.6 %) were the most frequent STs in Belgium: ST1 is world wide distributed while ST47 is more frequent in Europe.
- Clonal complexes CC1 (44.1 %) and CC932 (26.5 %) were the main lineages in Belgium.

- The comparison of STs between clinical and environmental samples available confirmed the infection source for 5 cases and excluded one case. However, 4 cases linked to the less discriminatory ST1 were inconclusive.
- These results are an update of the Belgian database and in agreement with the epidemiology in northwest Europe.