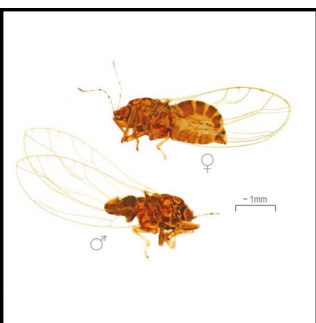




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To understand the biology and epidemiology of '*Candidatus Liberibacter solanacearum*' and its psyllid vectors

The plant-pathogenic bacterium '*Candidatus Liberibacter solanacearum*' (Lso) is vectored by psyllids and infects plants primarily in the families Solanaceae and Apiaceae. In potato (Solanaceae), the bacterium affects the growing crop reducing yield and in tubers causes a brown internal discolouration (Zebra chip), which intensifies when cooked leaving a zebra-like pattern rendering tubers unmarketable. In carrot (Apiaceae) the bacterium causes yellowing and reddening of the foliage and growth of extra shoots and secondary roots. This leads to yield losses and unmarketable produce.



Lso is confined to the host plant phloem, multiplies within the psyllid and can pass through the egg. Most psyllid species that are responsible for spreading Lso in potato and carrot are relatively host specific and species differ depending on country. Additionally, different Lso genetic haplotypes are associated with different geographical regions. Knowledge of the biology and epidemiology of both Lso and its vectors is at the foundation of any management strategy.

Due to the difficulties in identifying psyllid species using classical taxonomy (microscopic observations) and the lack of specialist psyllid taxonomists, DNA-based identification methods are being developed. The consortium has built a genetic database of the important psyllid vectors of Lso and common wild species. This has been coordinated using a suction trap network across Europe and via field sampling. This database is being used to develop rapid PCR-based tests to quickly identify species of concern. These techniques can be used as a standard across different laboratories for surveillance of outbreaks of the major vectors including *Bactericera cockerelli* (see image), *B. nigricornis*, *B. trigonica* and *Trioza apicalis*. These will be particularly valuable in areas at risk of accidental psyllid introduction and that lack personnel with the expertise to identify psyllids via observation of their anatomy.



Field surveys are being carried out to monitor Lso distribution and determine psyllid diversity. The consortium has found the following new Lso plant hosts: the Apiaceae crop hosts chervil, fennel, parsley and parsnip; the weed hosts cow parsley (*Anthriscus sylvestris*, Apiaceae), stinging nettle (*Urtica dioica*, Urticaceae) and *Galium* spp.. Further screenings of psyllid species have uncovered species previously unknown to harbour Lso including *Trioza anthrisci* and *T. urticae*. The latter harbouring a novel Lso haplotype (haplotype U). Intensive field studies have also shown that more novel Lso haplotypes exist in wild populations of psyllids but these are not expected to have any impact on potato or other crops.

A multilocus sequence typing (MLST) protocol has been developed to more closely analyse the Lso genome. This has shown that Lso in *T. anthrisci* and most *A. sylvestris* plants in Finland are different strains to those found in *T. apicalis* and the cultivated carrot and potato. A new haplotype of Lso named haplotype U, most closely related to A and D, has been found associated with *T. urticae* and stinging nettle (*Urtica dioica*, Urticaceae). These results suggest that different haplotypes of Lso remain separate even within the same region, if they are transmitted by different psyllid species that feed on different host plants. Genetic analysis has suggested that haplotype D is more closely related to the America-associated haplotype A than to C. To understand how Lso interacts with its plant host, Lso genes are being studied to assess which genes may play a role in pathogenicity, infection or interaction with the insect host.

Project ID: The biology and epidemiology of ‘*Candidatus Liberibacter solanacearum*’ and potato phytoplasmas and their contribution to risk management in potato and other crops ([PHYLIB II](#)).