





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](#)).