Genetic diversity in *Solanum dulcamara* populations along Scottish rivers

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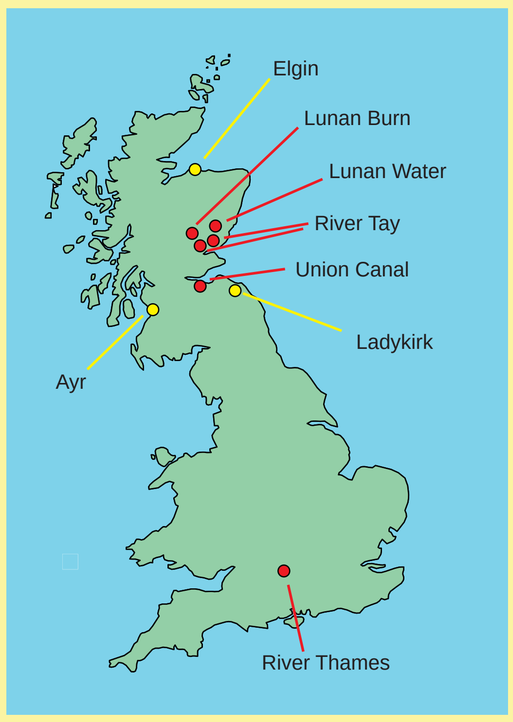
Introduction

Solanum dulcamara (bittersweet), a common weed often found growing alongside streams, has wide distribution in the U.K. Because it acts as a host for *Ralstonia solanacearum*, the causal bacterium of brown rot, its presence along streams and rivers that may be used to irrigate fields is a cause of great concern to the potato industry. In England, *R. solanacearum* is wide spread in streams and watercourses. In marked contrast, the bacterium has never been found in Scottish potatoes and was thought to be absent from its rivers. However, the detection of *R. solanacearum* in a small river, Lunan Burn, in one of Scotland's main potato growing regions caused much concern. As a control measure, bittersweet along this stream was largely eradicated. Such a programme of eradication, if practised more widely, could lead to a dramatic reduction in genetic diversity of this native U.K. plant. It was thought timely, therefore, to assess the level and distribution of genetic diversity of the species *S. dulcamara* in Britain.

Materials and Methods

A study was set up to determine the distribution of bittersweet along all rivers where it could present a threat to the Scottish potato industry; i.e., where infected river water might be used to irrigate potato fields. Bittersweet was found along only six of the 48 rivers surveyed: samples were collected from all of these and from other sites where the plant was found near to rivers (see map). Additionally, samples were collected, more than 600 km to the south, along the Thames in Oxfordshire, where infected population of bittersweet are known to occur. The Thames samples were collected along a short 15km stretch of the river. Diversity analysis was performed using AFLPs (6 primer combinations) and SSRs. For the analysis of AFLP markers, amplified fragments were scored for presence (1) or absence (0) and the resulting binary matrix subjected to Principal Coordinate Analysis (PCO). The first two were plotted. In the case of the SSRs, primer pairs developed for potato were used: a total of 50 primers pairs were tested. Allele sizes were stored as binary data and cluster analysis was carried out using the Dice co-efficient and UPGMA options on the combined data for all 10 markers.



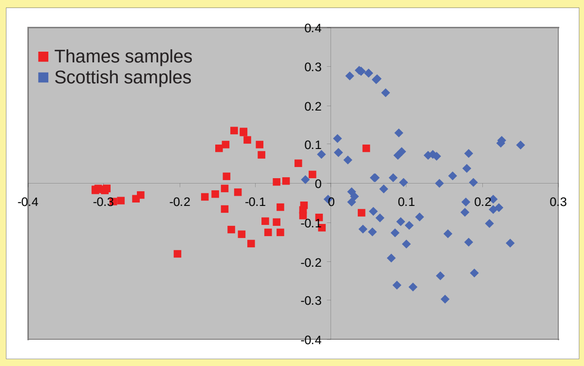
Sites of sample collection: red spots indicate where *S. dulcamara* was collected along a river, yellow spots where the collection was made away from a river.

Marker	Repeat motif	Number alleles observed
StI006	(AT)n (GT)n	1
StI013	(ACC)n	2
StI024	(CAA)n	4
StI050	(ATA)n	1
StI053	(AT)imp	1
StI064	(AT)n (GT)n	1
STM1005	(GTA)6	2
STM1024	(TTG)6	1
STM1106	(ATT)13	1
STM2028	(TAC)5 (TA)3 (CAT)3	3

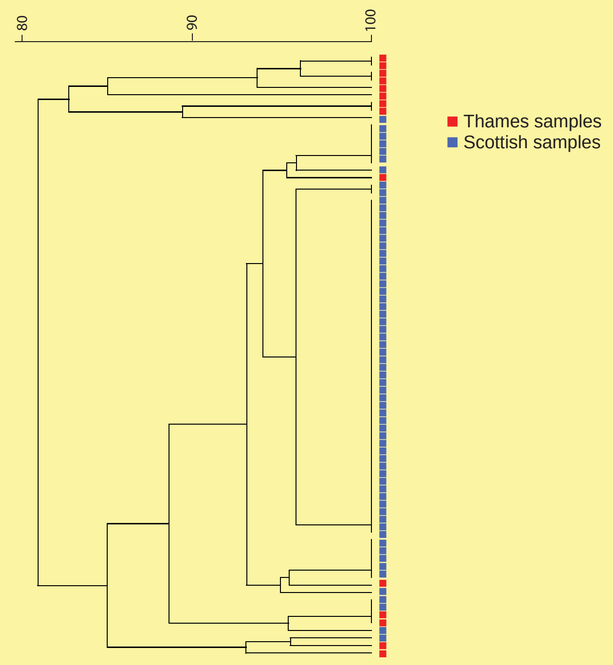
Potato SSR markers that gave amplification products in *S. dulcamara.*

Results

There were 148 clear, scorable AFLP fragments across all samples; 131 (88.5%) were polymorphic. In the Scottish and Thames samples, respectively, there were 134 and 131 fragments of which 88 (65.7%) and 94 (71.8%) were polymorphic. There were 14 bands present in the Thames samples not found in the Scottish samples and, conversely, 17 bands present in the Scottish samples not found in the Thames samples. In most cases, however, these were rare alleles occurring in only one or two samples. PCO analysis evidenced some separation of the Scottish and Thames samples. The percentage variability accounted for by the first coordinate, however, was quite low (12.6%).



Of the 50 potato SSR primer pairs tested only 10 amplified fragments in *S. dulcamara*, and only four were polymorphic and therefore informative. Results are summarised in the form of a dendrogram.



The majority of the Scottish isolates yield identical microsatellite profiles with only a few displaying polymorphic loci. However, isolates collected from the Thames were extremely heterogeneous both between themselves and compared to the Scottish isolates: many contained alleles not found in any of the Scottish samples.

Conclusions

1) There is limited genetic variability among the Scottish samples: the level of variability is similar to that seen in the Thames samples although the former were collected over a much larger geographic area (much of the east coast of Scotland compared to a 15km stretch of a single river).

2) The Thames and Scottish populations, although separated by more than 600 km, are genetically quite similar; they show 97% identity (Nei's unbiased genetic identity) on the basis of AFLP profiles.

3) There is some indication that samples that have returned to the Lunan Burn (the Scottish river where eradication was carried out) are somewhat more diverse than those found on other Scottish rivers.

Acknowledgements
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