

'Sudden Oak Death Symposium V'
Petaluma CA 19-22 June 2012

EU2, a fourth evolutionary lineage of *Phytophthora* *ramorum*

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And ..

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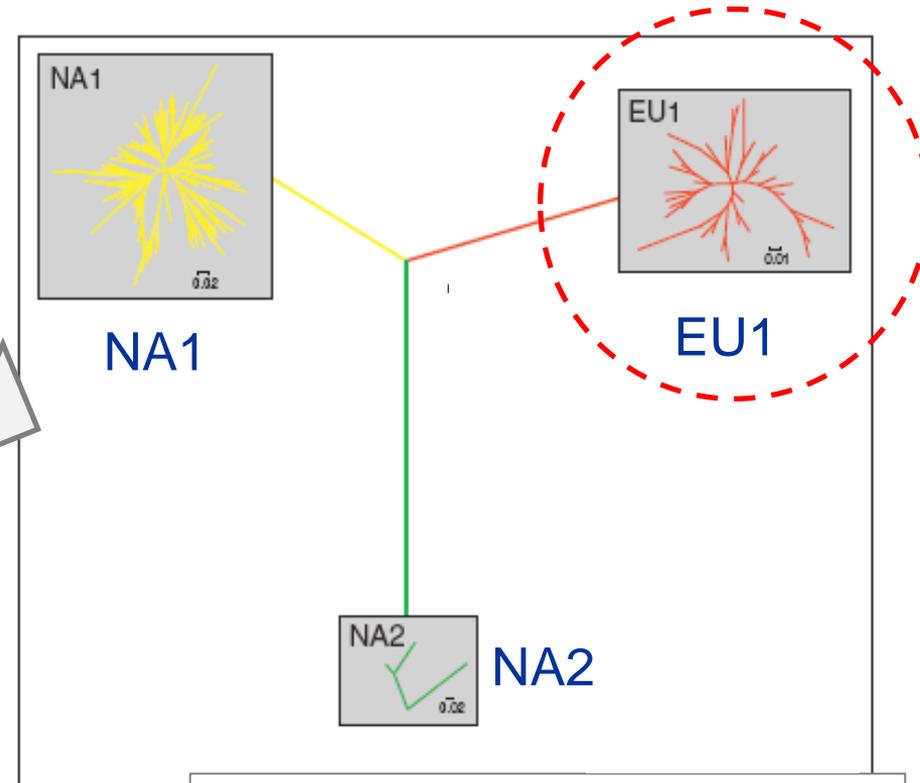
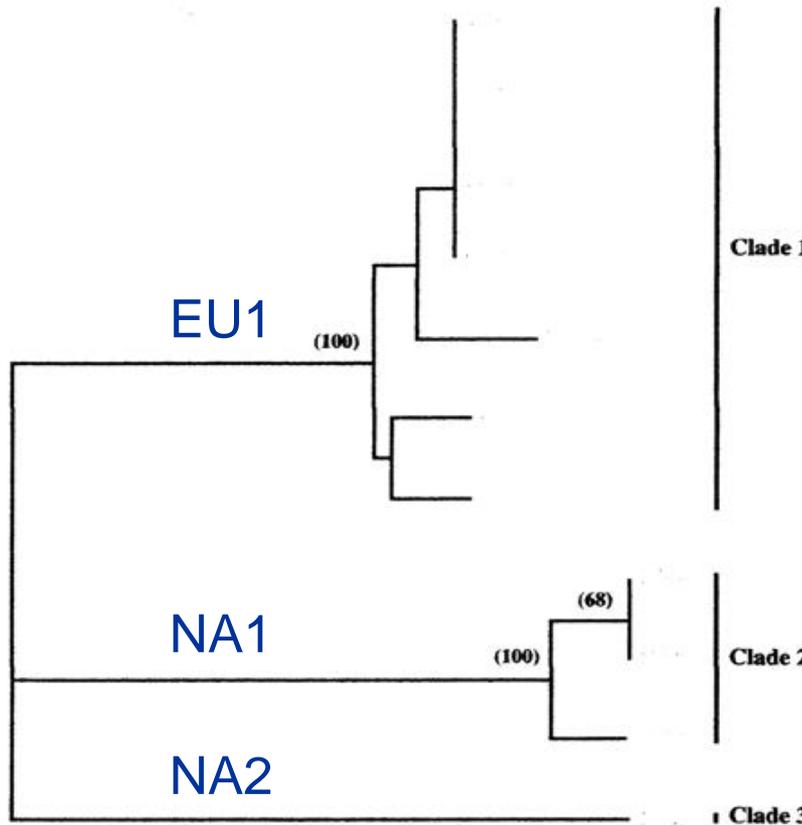
Joan Webber Forest Research

Kurt Heungens ILVO

Judith Turner Fera

Existing P. ramorum lineages

Well known since the pioneering phylogenetic work of Ivors, Garbelotto, Bonants and others that *Phytophthora ramorum* has spread in North America and Europe as three separate lineages



Discrimination of
lineages -
microsatellites

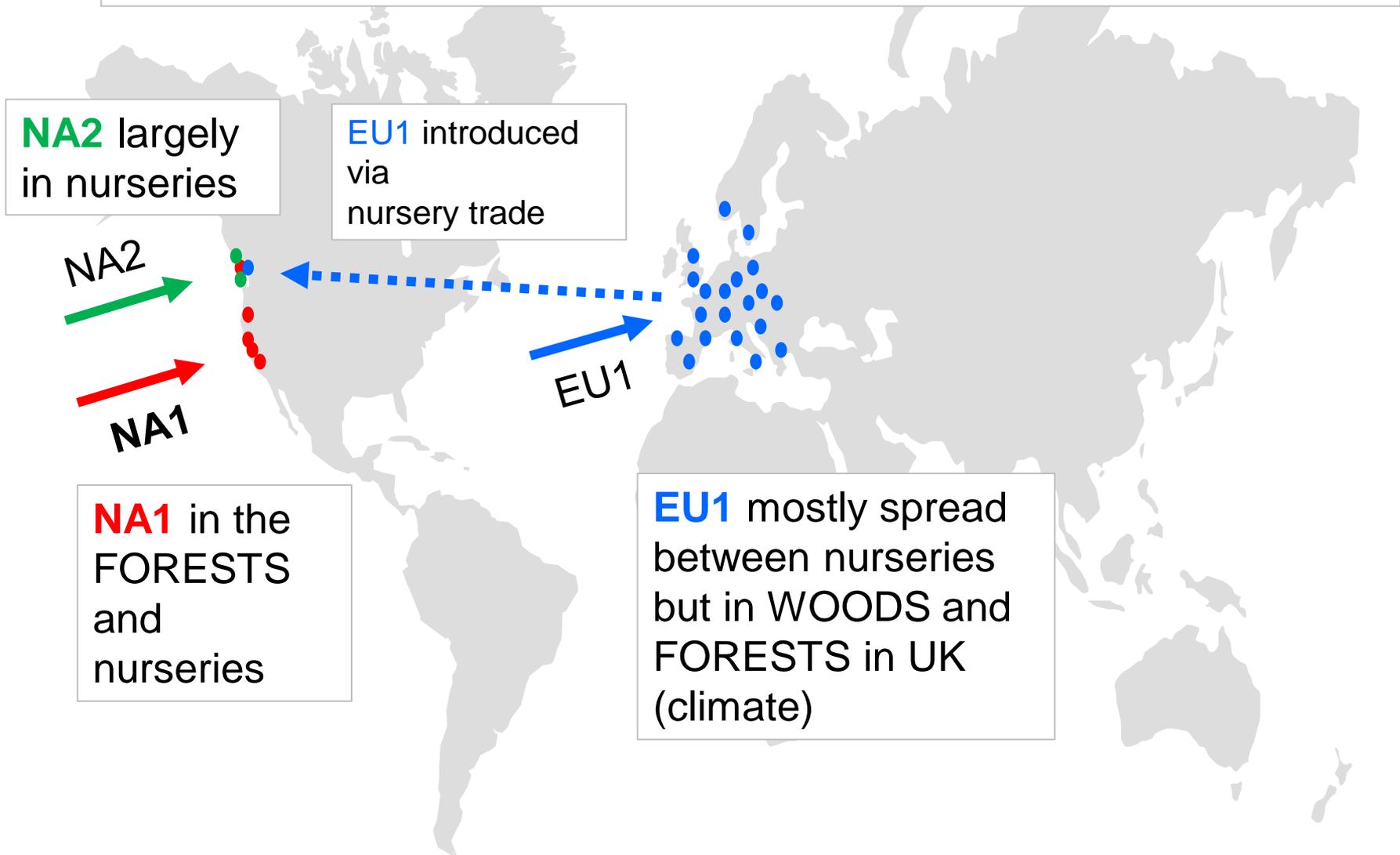
Properties of the lineages

Also know that lineages

Tend initially to be clonal and of a single sexual compatibility type – A1 or A2 – consistent with introduction bottlenecks

Exhibit certain phenotypic/ behavioural differences – colony types, genetic stability, mean growth rates, mean aggressiveness

Introduction and initial spread of lineages ca 1990-2005



In UK ca 2000-2009 EU1 spread from nurseries to wild rhododendrons to woodland trees



ca 2009 EU1 spread to UK Larch plantations -
new epidemic.



>3 million trees
felled to date



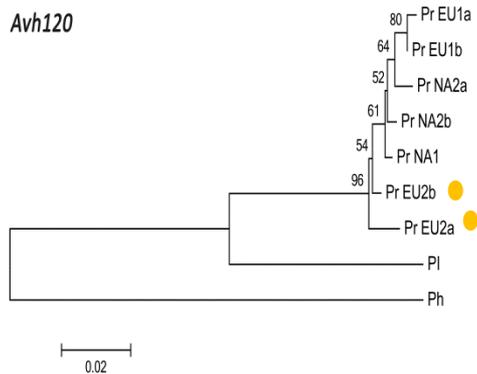
Larch isolates across UK typically EU1 lineage...

But in 2011 isolates from larch in Northern Ireland found to have a microsatellite and a multi gene sequence profile distinct from the three known lineages

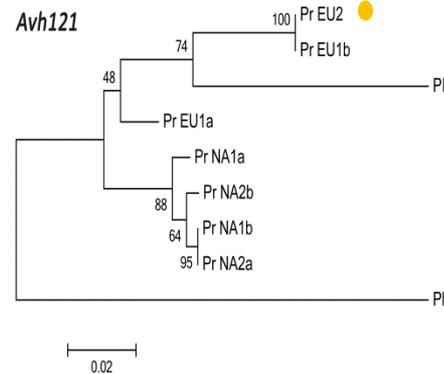
A new evolutionary lineage: EU2

New evolutionary lineage on larch in Northern Ireland: five nuclear gene trees

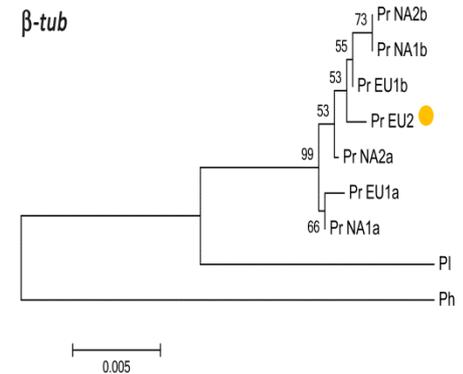
Avh120



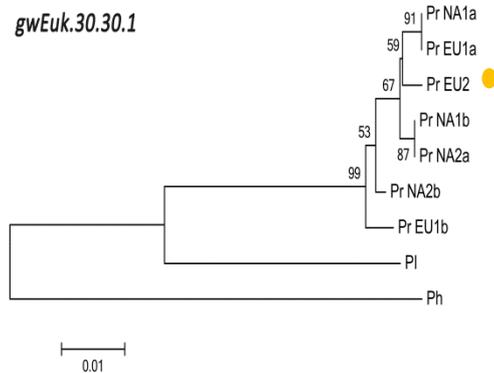
Avh121



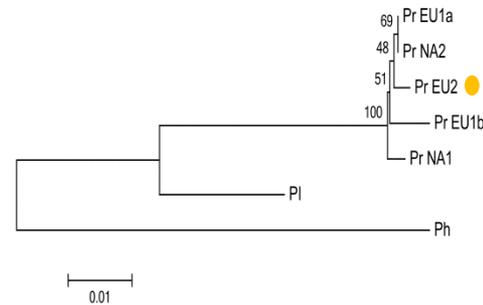
β-tub



gwEuk.30.30.1

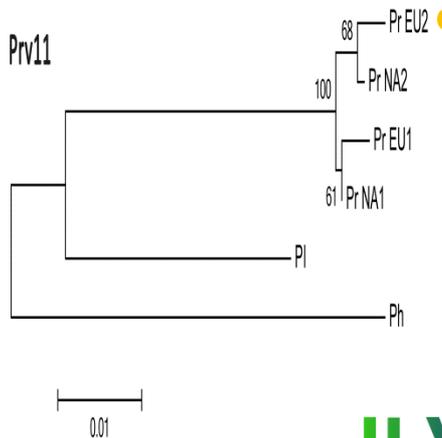
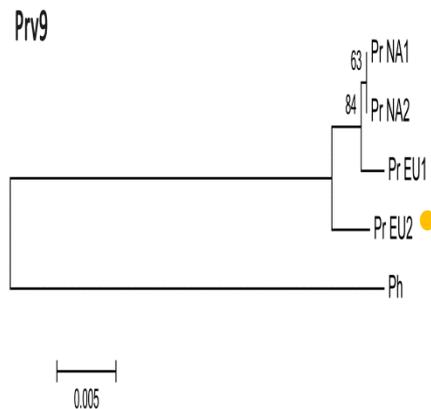
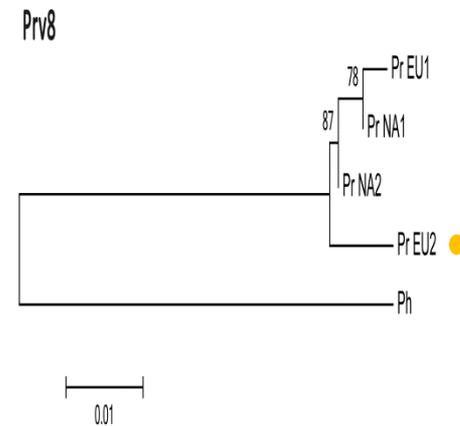
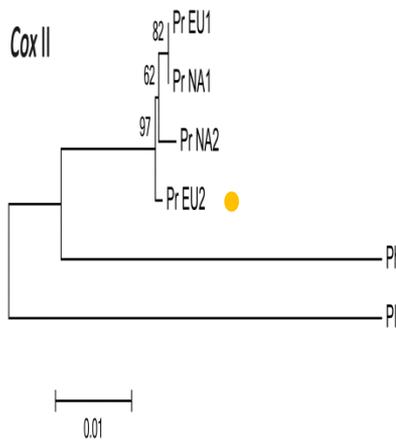
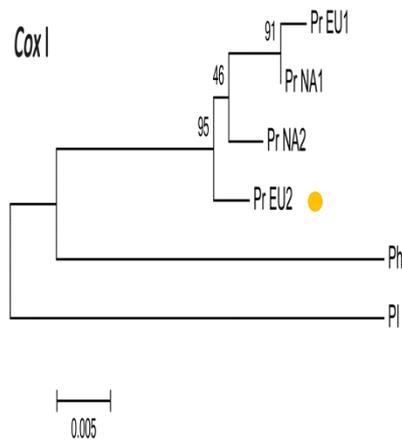


trp1



Outgroups *P. lateralis*
and *P. hibernalis*

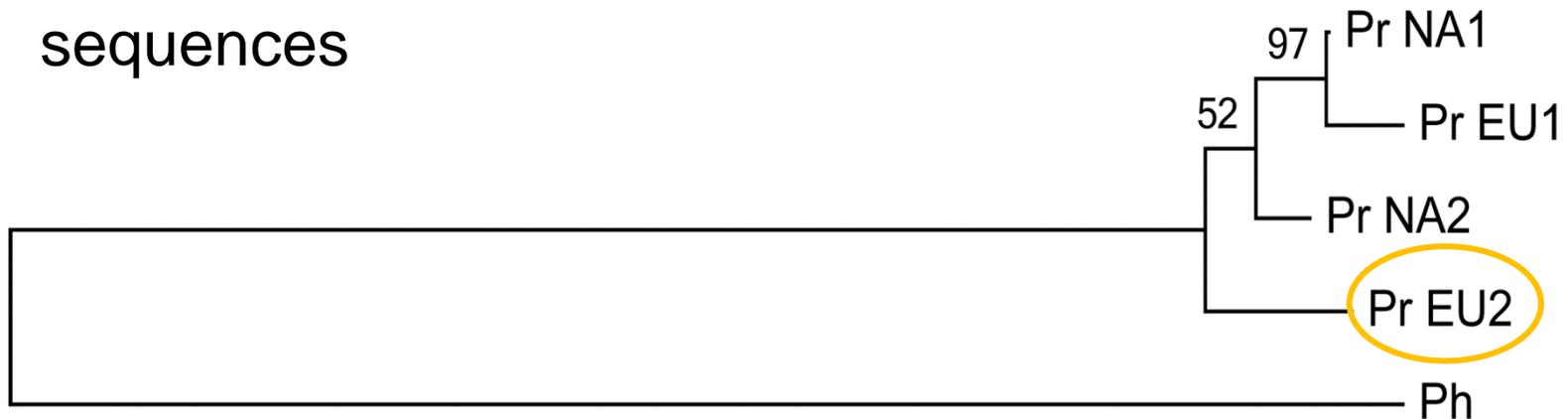
New evolutionary lineage on larch in Northern Ireland: five mitochondrial gene trees



Outgroups *P. lateralis*
and *P. hibernalis*

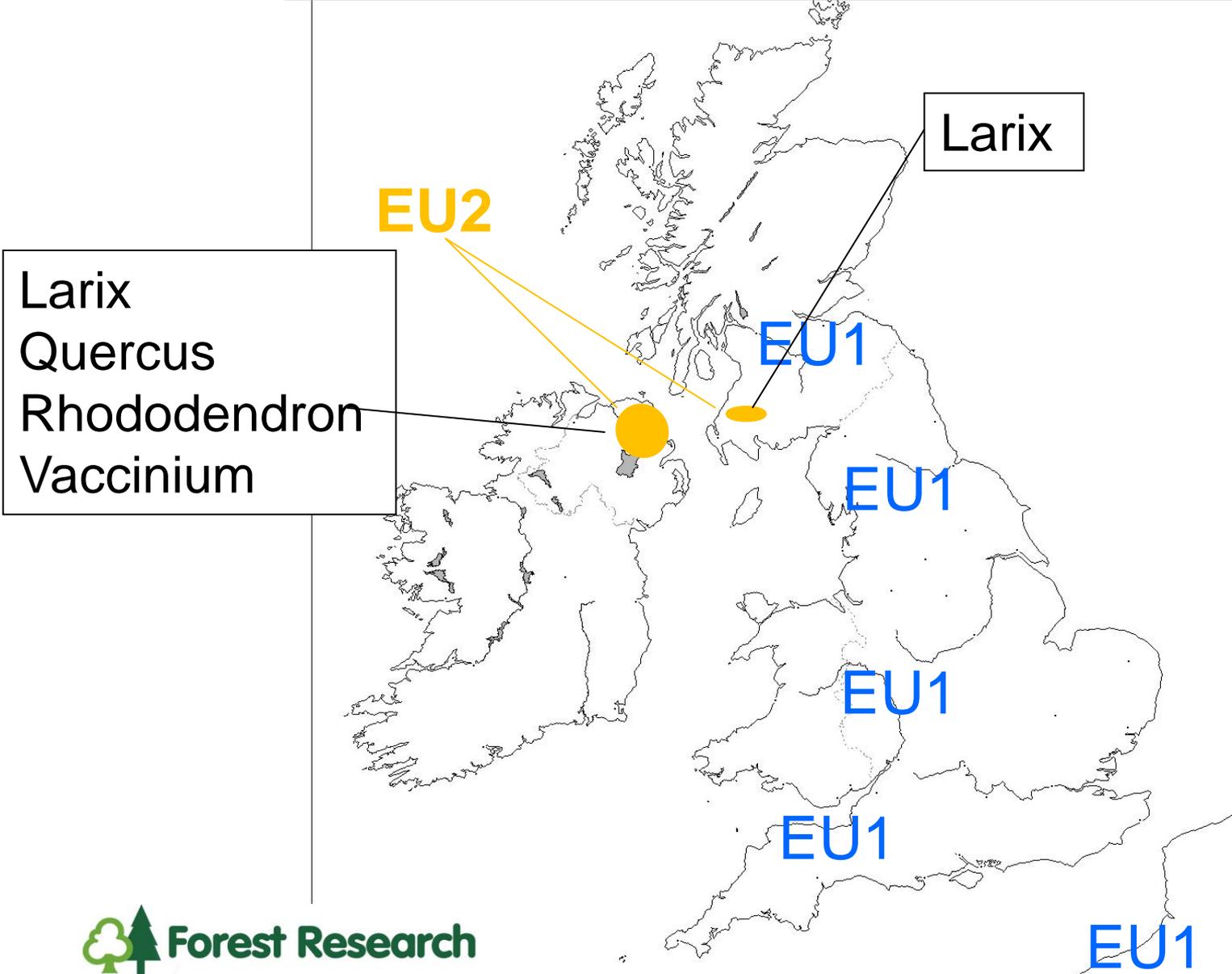
New evolutionary lineage on larch in Northern Ireland

Combined mitochondrial DNA sequences



0.005

Known distribution of EU2 lineage



Larix
Quercus
Rhododendron
Vaccinium

Larix

EU2

EU1

EU1

EU1

EU1

EU1

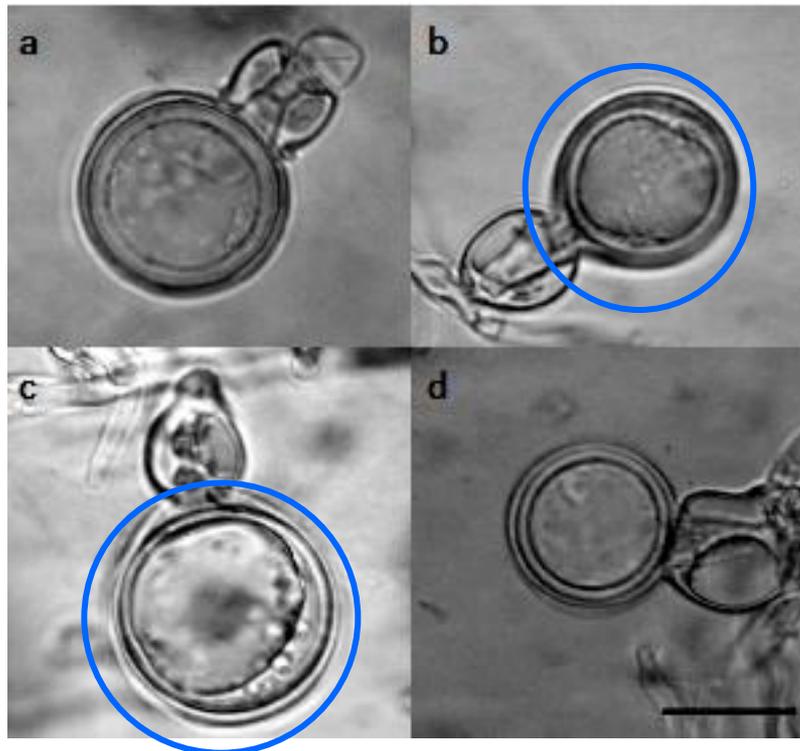
In EU2 to date -

All microsatellite profiles uniform

All gene sequences uniform

All isolates of A1 sexual compatibility type

Oogonia
from EU2 x
NA1 (A2)
pairings



Oosphere
abortion

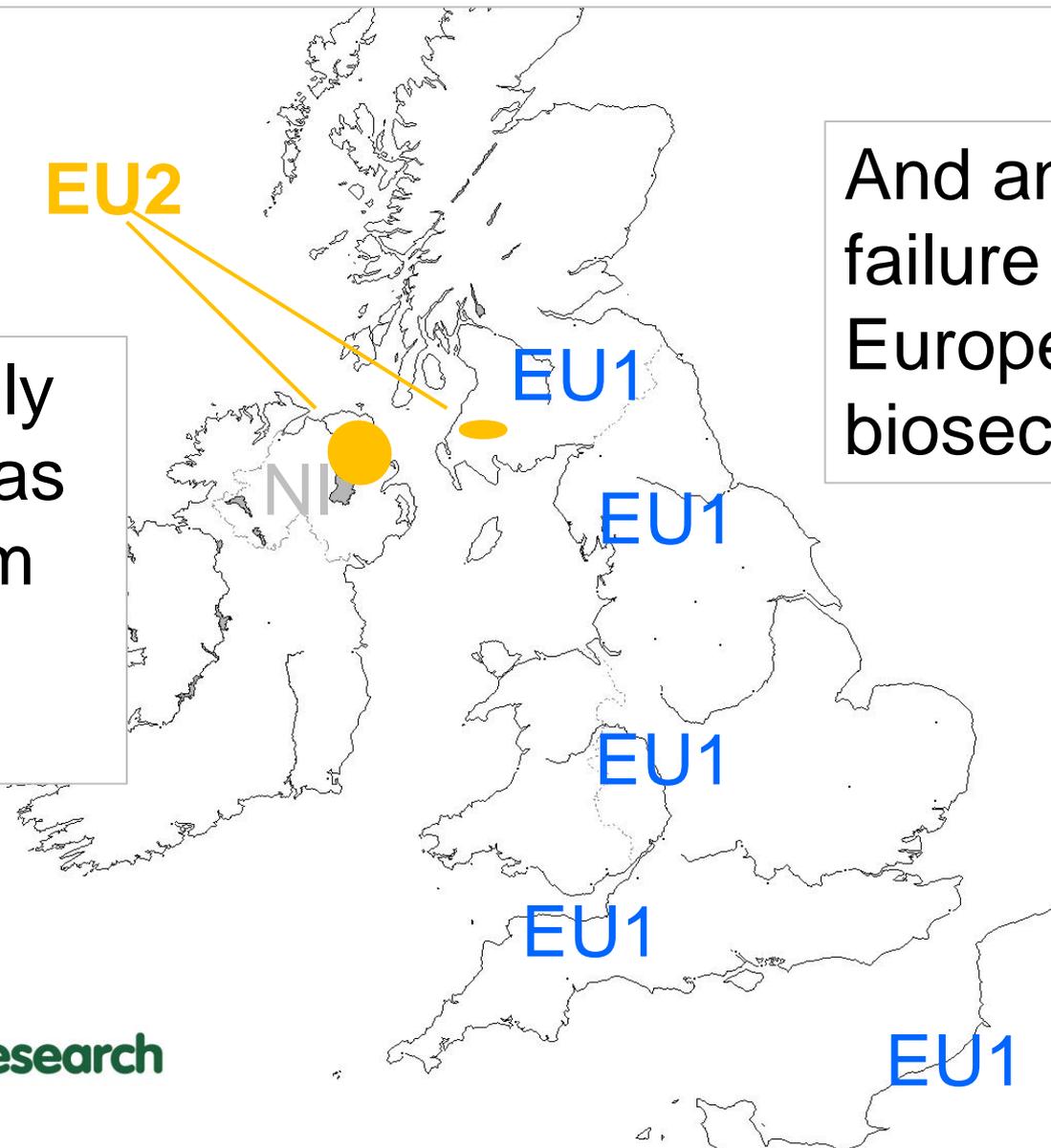
Again consistent
with clonality as
a result of an
introduction
bottle neck

EU2's limited distribution and present SSR clonality suggests a more recent introduction than EU1

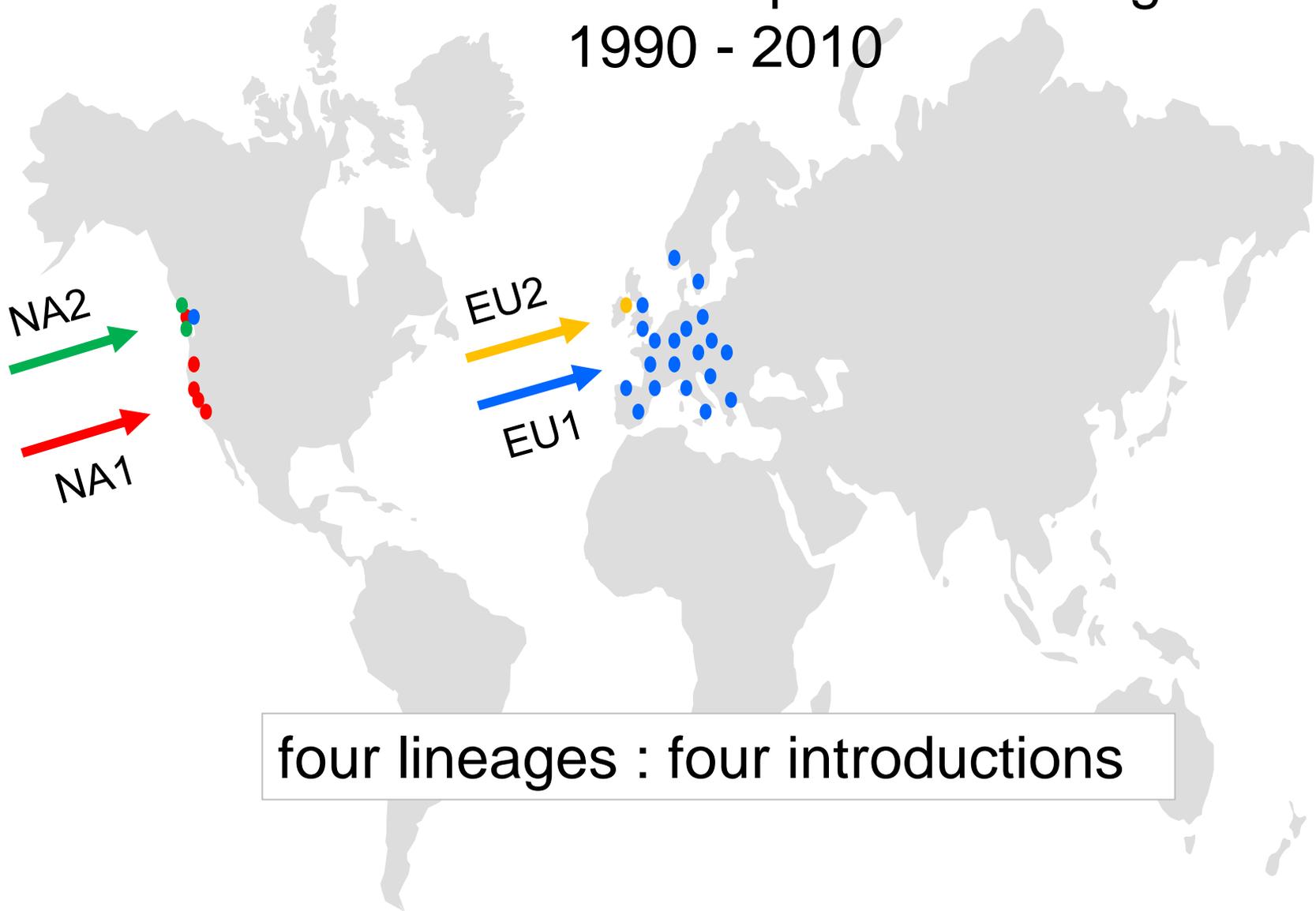
EU2

And another failure of UK / European biosecurity

Seems likely that EU2 has spread from NI to south Scotland

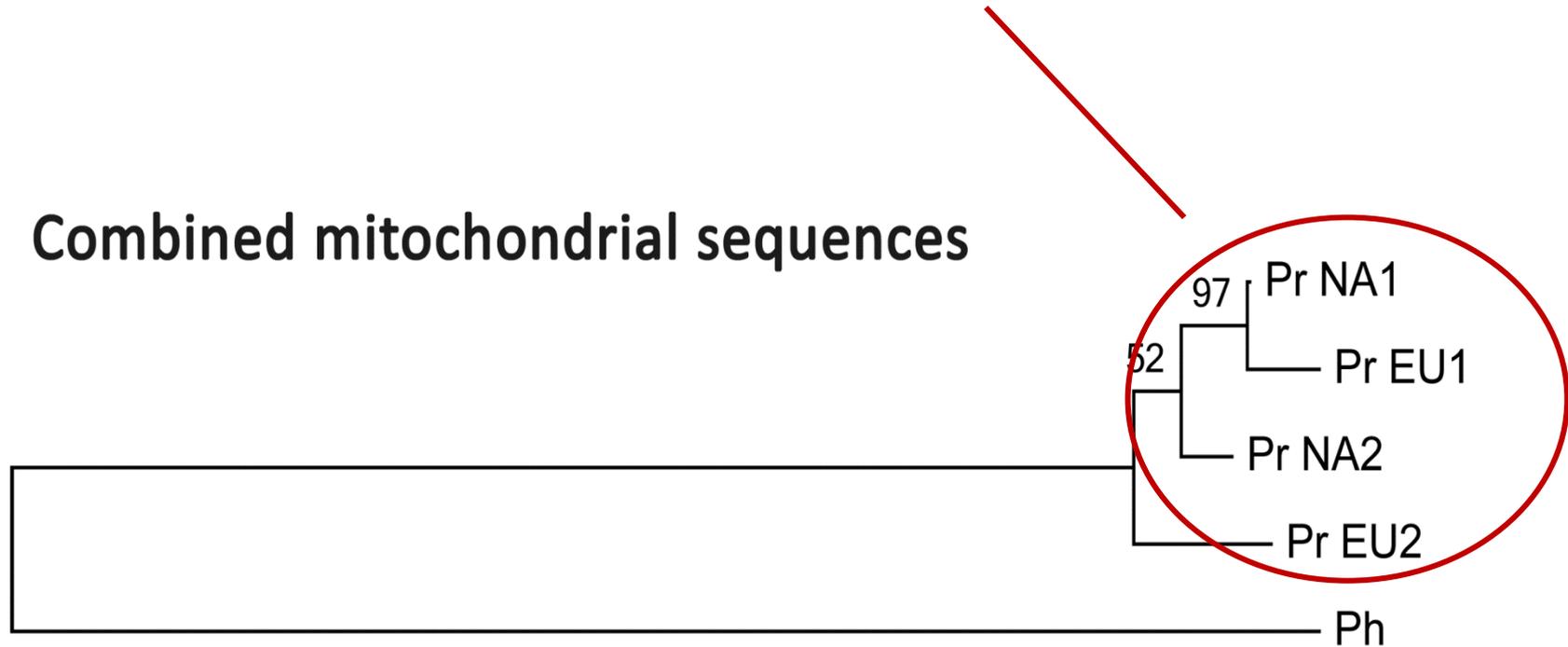


Introduction and initial spread of lineages ca 1990 - 2010



But what do the lineages actually mean?

Combined mitochondrial sequences



0.005

Apart from their phenotypic differences the lineages appear to be partially reproductively isolated because :

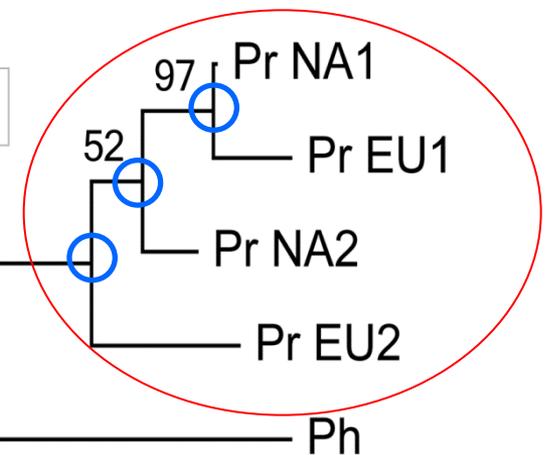
- Inter lineage fecundity is low with high levels of oosphere and oospore abortion (FR)
- Oospore progeny show a high frequency of non-Mendelian segregation and aberrant genome sizes – aneuploidy (ILVO)



Ergo the genomes of the lineages appear incongruent
- as if rearranged ie divergent.

- Coalescence analysis indicates the lineages probably diverged >100K years ago from a sexually reproducing population (Goss et al 2009)

Coalescence analysis of Goss et al 2009 a fine start



- But we still have no firm evidence of what evolutionary processes led to the divergence of the lineages – whether host or geographic, selection or drift

Because we still do not even know where *P. ramorum* has come from

When we study *P. ramorum* here in the North America or in Europe – its pathology, epidemiology, genetics

- we are probably studying an **artifact of introduction**
- an unnatural host range, an unnatural epidemiology, an unnatural population structure, an unnatural breeding system, an unnaturally behaving (clonal) genetic system

We are therefore only studying **half the picture**

To understand *P. ramorum*'s true pathology and ecology - We also need to study it in its centre of origin -

To observe its natural hosts, mechanisms of pathogenicity and resistance, cycles of survival, breeding systems, genetic variation, natural enemies.

And to discover *how* and *why* there are at least four evolutionary lineages

Furthermore, as long as the geographic origin of *P. ramorum* remains unknown –

We will have a veritable black hole in our biosecurity understanding -

- like trying to prevent terrorism in the US without studying Al-Qaeda

This security hole needs to be filled by the funding agencies and by the regulators

This may also mean
more of us getting out
of our comfort zone



We will never properly understand *Phytophthora ramorum* if we don't?

Finally –

We have given the lineages informal phylogenetic labels: NA1, EU1 etc

But what about their formal taxonomic (nomenclatural) status?

Our informal labels are not ideal for the purposes of scientific communication or plant health legislation.

At the 2nd SOD symposium, Monterey 2005 – because the lineages had phenotypic differences and appeared to be reproductively isolated

We suggested that they might be equivalent to formal taxonomic subspecies:

”Adaptive differences between *Phytophthora ramorum* isolates from Europe and North America: Evidence for separate subspecies?” (Brasier *et al.* 2005).

Now the evidence is even stronger.

Should the lineages be accorded subspecies status?

In practice the questions:

What is a lineage? (taxonomy)

and

Why is it a lineage? (evolution)

Are really two different ways of framing the
same question

Time we answered the question?

Thank you