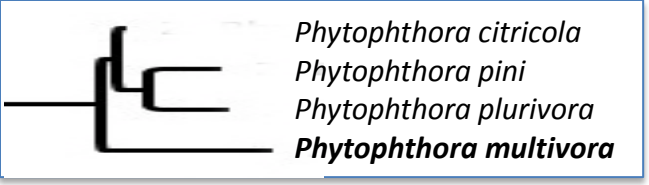
Determining the origin of the emerging pathogen, *Phytophthora multivora*

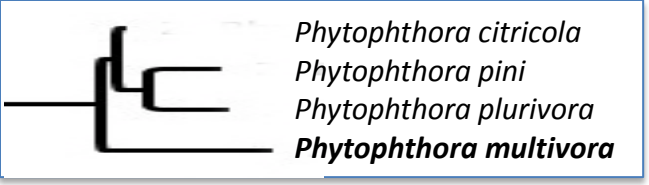
Alex Rea, Giles Hardy, Mike Stukely
and Treena Burgess

CPSM
Centre for *Phytophthora*
Science and Management

Department of
Environment and Conservation

MURDOCH
UNIVERSITY
PERTH, WESTERN AUSTRALIA


Phytophthora citricola
Phytophthora pini
Phytophthora plurivora
Phytophthora multivora


Phytophthora citricola
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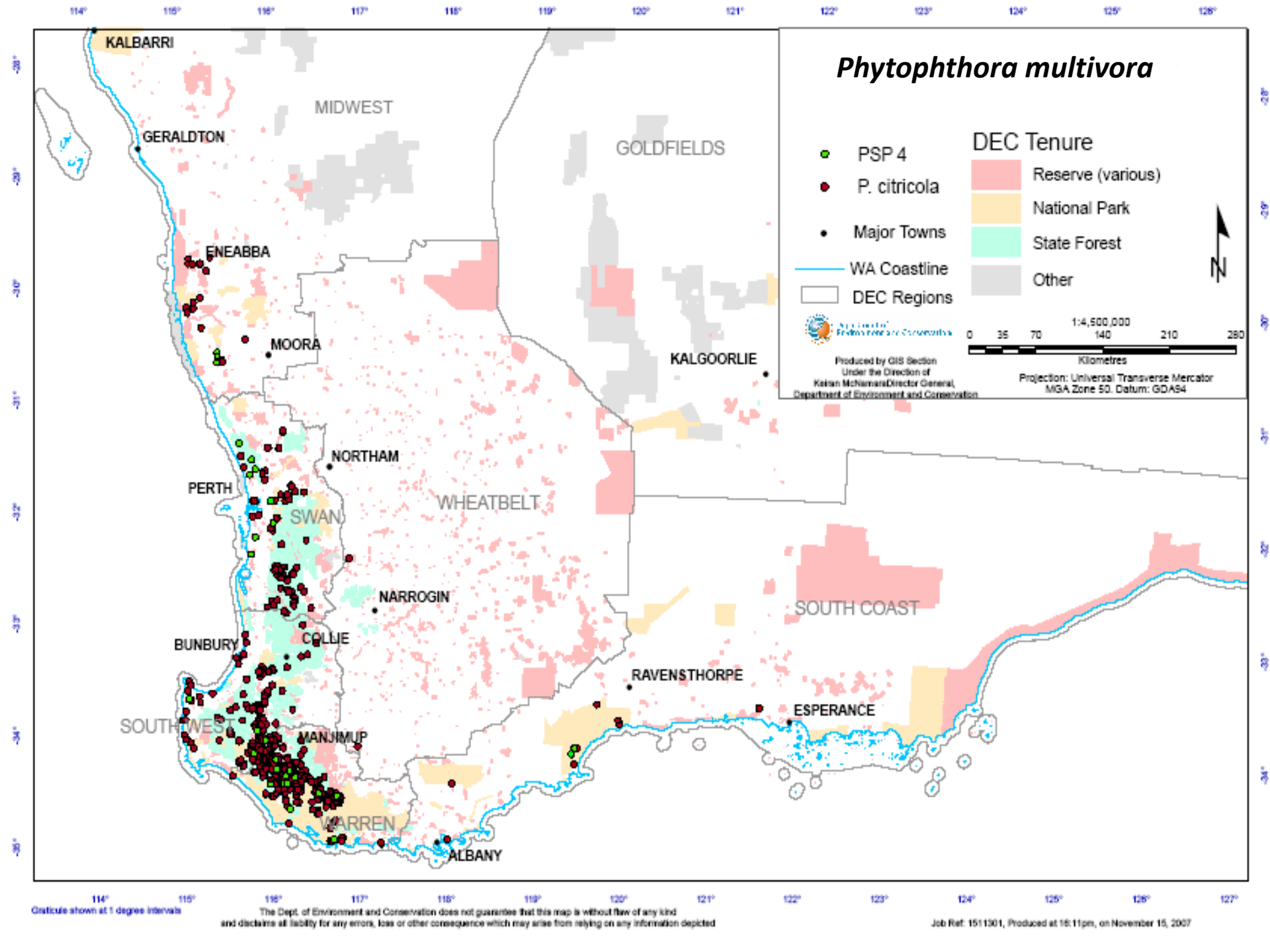
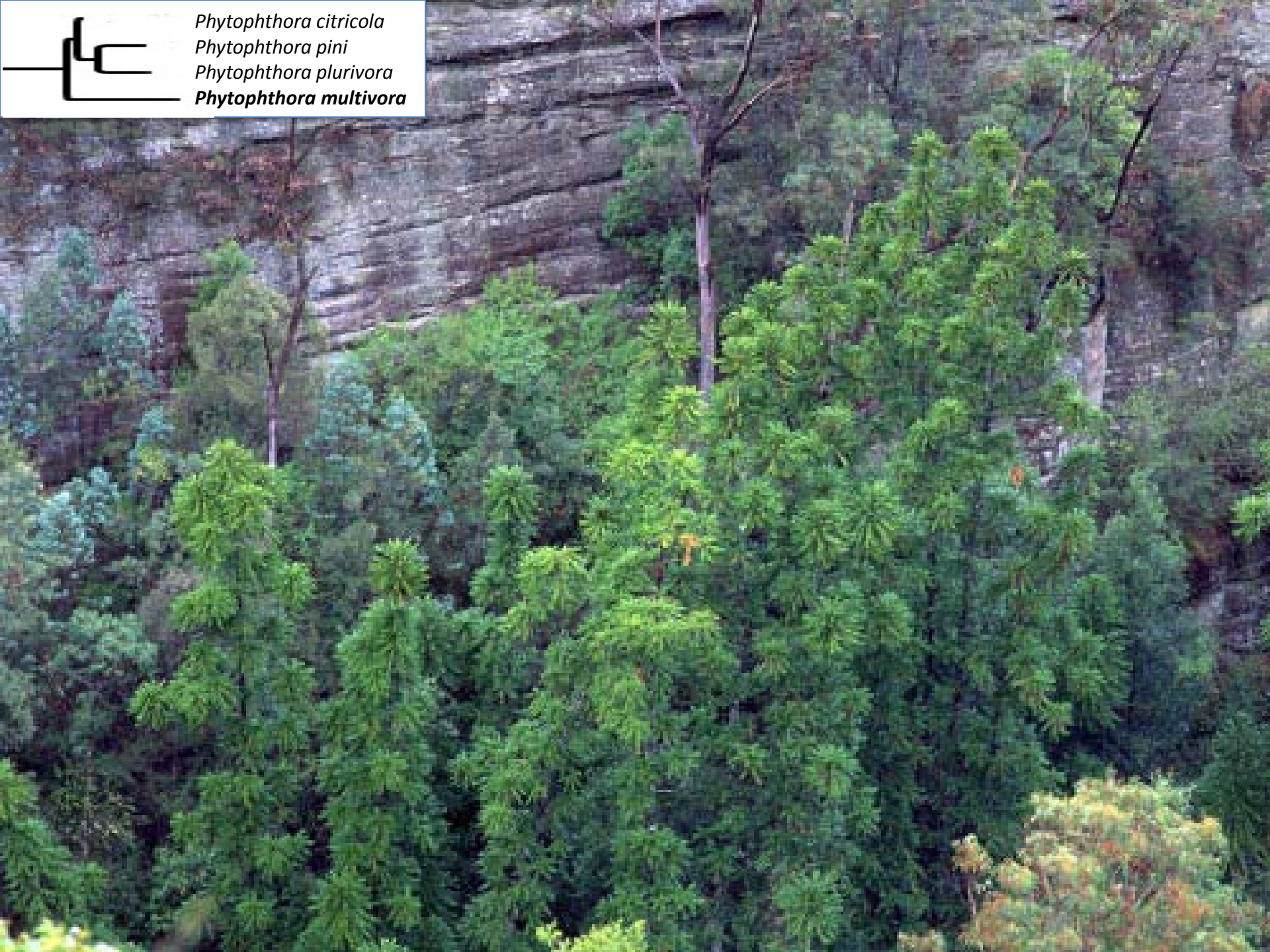

Phytophthora multivora
PSP 4
P. citricola
Major Towns
WA Coastline
DEC Regions
DEC Tenure
Reserve (various)
National Park
State Forest
Other
N
1:4,500,000
0 35 70 140 210 280
Kilometres
Produced by GIS Section
Under the Direction of
Keiran McNamaraDirector General,
Department of Environment and Conservation
Projection: Universal Transverse Mercator
MGA Zone 50. Datum: GDA94
KALBARRI
GERALDTON
ENEABBA
MOORA
NORTHAM
PERTH
SWAN
WHEATBELT
NARROGIN
BUNBURY
COLLIE
SOUTH WEST
MANJIMUP
WARREN
ALBANY
KALGOORLIE
MIDWEST
GOLDFIELDS
SOUTH COAST
RAVENSTHORPE
ESPERANCE
Graticule shown at 1 degree intervals
The Dept. of Environment and Conservation does not guarantee that this map is without flaw of any kind
and disclaims all liability for any errors, loss or other consequence which may arise from relying on any information depicted
Job Ref: 151301, Produced at 16:11pm, on November 15, 2007


Phytophthora citricola
Phytophthora pini
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Phytophthora citricola
Phytophthora pini
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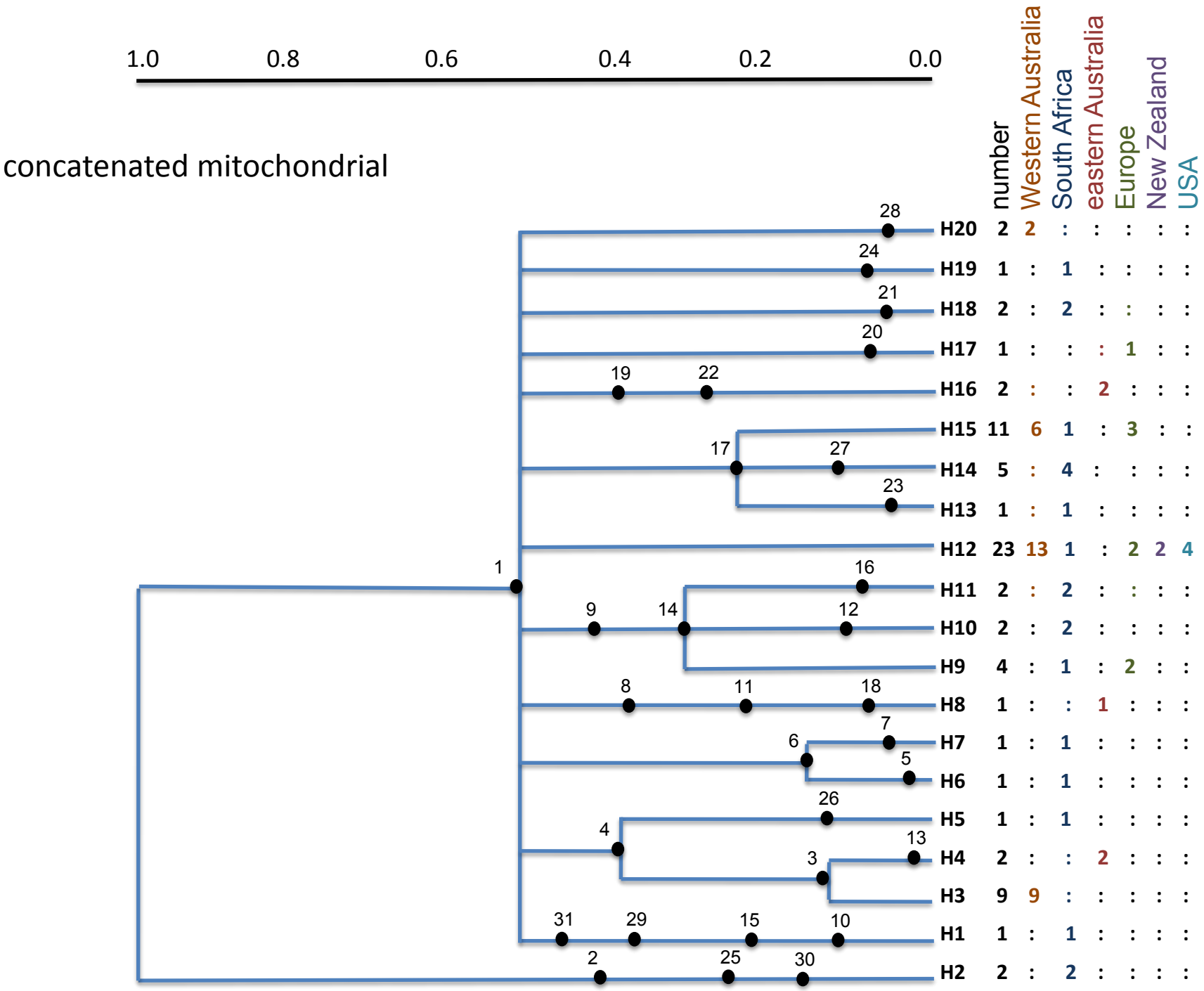
Phytophthora citricola
Phytophthora pini
Phytophthora plurivora
Phytophthora multivora

- When *P. multivora* was described in 2009; there were 7 matching ITS sequences on GenBank from Hungary, Canada, Switzerland, Spain, Korea and Japan
- due to sequence polymorphism and widespread occurrence we postulated and Australian origin for this species
- Since the description *P. multivora* was identified in South Africa, New Zealand, USA and other European countries
- In Australia, *P. multivora* has been isolated once in NSW from Wollemi pine and once in Victoria from a pipeline survey
- In Western Australia approximately 500 sequence verified isolates and it is now being routinely isolated from peri-urban and urban areas
- through collaboration at FABI in South Africa found *P. multivora* to be the most common species in health natural forest ecosystems and readily isolated in forest streams
- we gathered a set of isolates to test the hypothesis that *P. multivora* was endemic to Australia
- sequenced 5 nuclear genes and 3 mitochondrial genes and conducted coalescence analysis

Location	no.	Hosts
Western Australia	30	numerous hosts, isolates selected from wide geographic distribution, commonly isolated
Australia (elsewhere)	5	Wollemi pine (NSW), rarely from natural vegetation (VIC)
South Africa	21	from soil beneath asymptomatic natural vegetation, also from water
New Zealand	2	forest survey (highly impacted region)
Europe	8	nurseries and young plantings
USA	4	forest survey (encountered rarely)


1.0
0.8
0.6
0.4
0.2
0.0
concatenated mitochondrial
number
Western Australia
South Africa
eastern Australia
Europe
New Zealand
USA
H20 2 2 : : : : :
H19 1 : 1 : : : :
H18 2 : 2 : : : :
H17 1 : : : 1 : :
H16 2 : : 2 : : :
H15 11 6 1 : 3 : :
H14 5 : 4 : : : :
H13 1 : 1 : : : :
H12 23 13 1 : 2 2 4
H11 2 : 2 : : : :
H10 2 : 2 : : : :
H9 4 : 1 : 2 : :
H8 1 : : 1 : : :
H7 1 : 1 : : : :
H6 1 : 1 : : : :
H5 1 : 1 : : : :
H4 2 : : 2 : : :
H3 9 9 : : : : :
H1 1 : 1 : : : :
H2 2 : 2 : : : :
28
24
21
20
19
22
17
27
23
1
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9
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3
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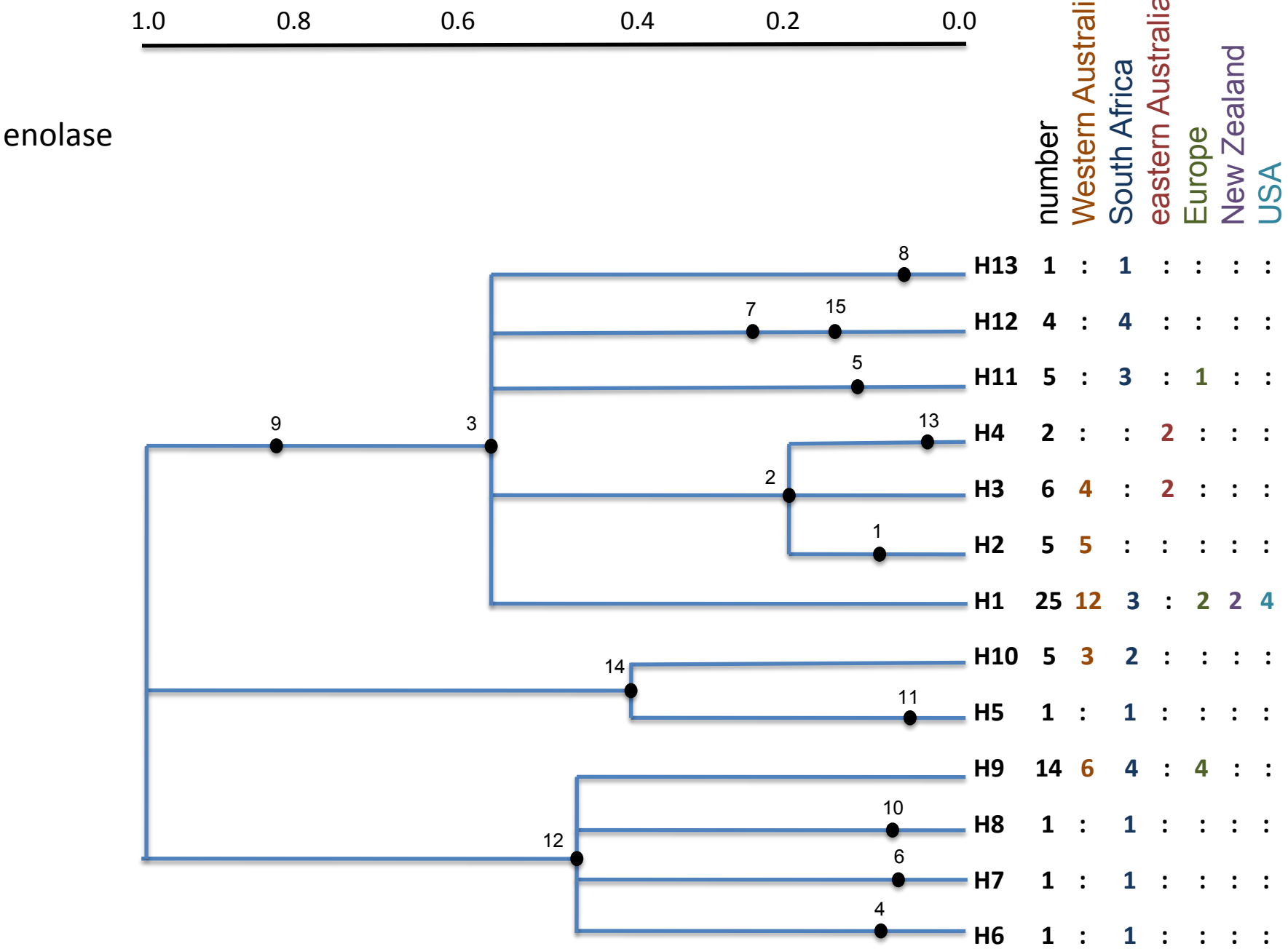
2
25
30


enolase
1.0
0.8
0.6
0.4
0.2
0.0
number
Western Australia
South Africa
eastern Australia
Europe
New Zealand
USA
8
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3
13
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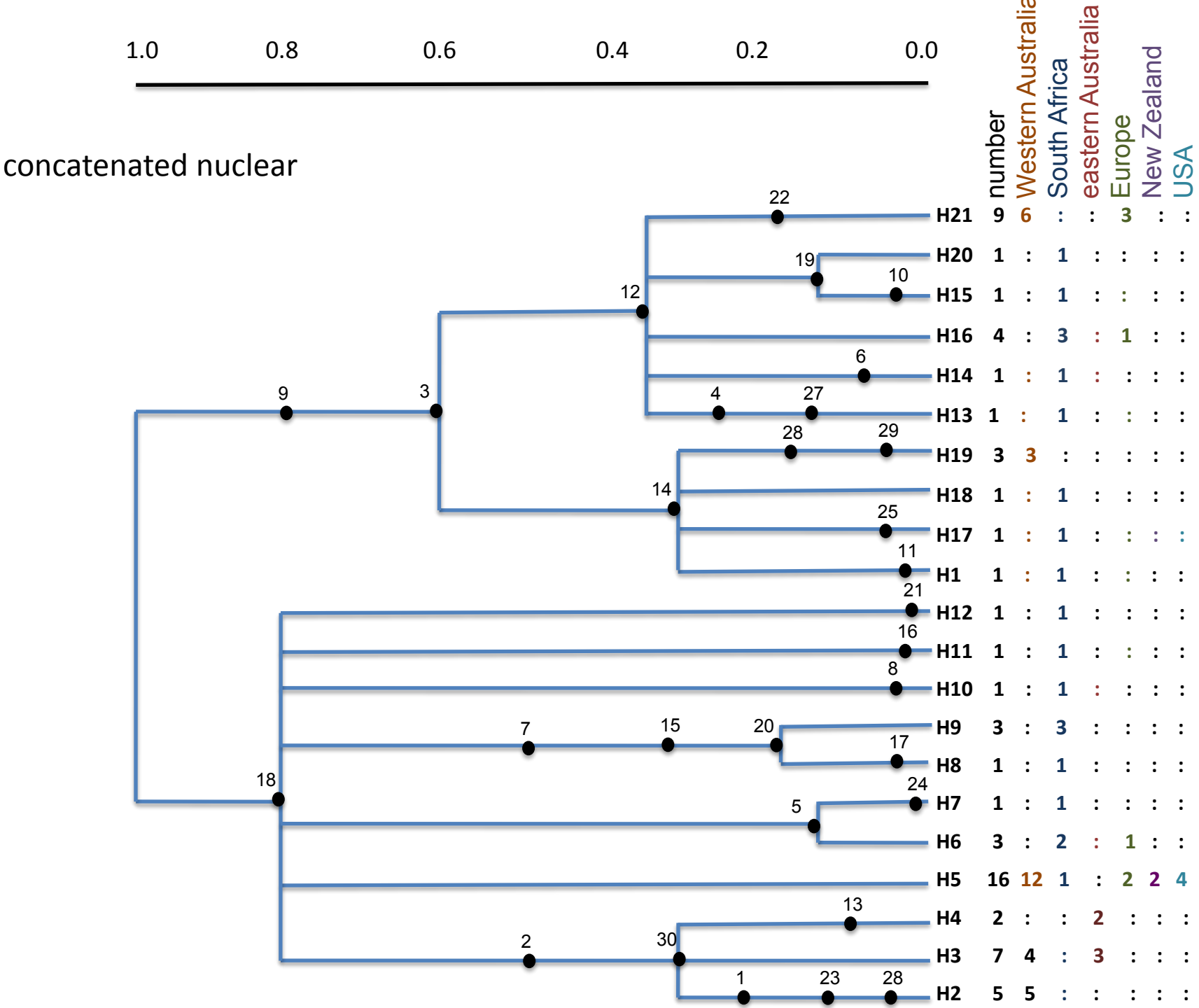
1
14
11
12
10
6
4
H13 1 : 1 : : : :
H12 4 : 4 : : : :
H11 5 : 3 : 1 : :
H4 2 : : 2 : : :
H3 6 4 : 2 : : :
H2 5 5 : : : : :
H1 25 12 3 : 2 2 4
H10 5 3 2 : : : :
H5 1 : 1 : : : :
H9 14 6 4 : 4 : :
H8 1 : 1 : : : :
H7 1 : 1 : : : :
H6 1 : 1 : : : :


1.0
0.8
0.6
0.4
0.2
0.0
concatenated nuclear
number
Western Australia
South Africa
eastern Australia
Europe
New Zealand
USA
H21 9 6 : : 3 : :
H20 1 : 1 : : : :
H15 1 : 1 : : : :
H16 4 : 3 : 1 : :
H14 1 : 1 : : : :
H13 1 : 1 : : : :
H19 3 3 : : : : :
H18 1 : 1 : : : :
H17 1 : 1 : : : :
H1 1 : 1 : : : :
H12 1 : 1 : : : :
H11 1 : 1 : : : :
H10 1 : 1 : : : :
H9 3 : 3 : : : :
H8 1 : 1 : : : :
H7 1 : 1 : : : :
H6 3 : 2 : 1 : :
H5 16 12 1 : 2 2 4
H4 2 : : 2 : : :
H3 7 4 : 3 : : :
H2 5 5 : : : : :
22
19
10
12
6
9
3
4
27
28
29
14
25
11
21
16
8
7
15
20
17
18
24
5
13
2
30
1
23
28

	l	*n*	*s*	*h*	*k*	$\pi \pm SE$ ($\times 10^{-3}$)	θw
Mitochondrial loci	**1072**	**70**	**32**	**22**	**3.769**	**3.61±0.23**	**6.648**
WA	1070	30	8	5	2.759	2.58±0.19	2.019
RSA	1044	21	21	16	4.608	4.41±0.40	6.008
Nuclear loci	**2140**	**70**	**37**	**21**	**6.505**	**3.40±0.20**	**7.963**
WA	2140	30	14	5	3.929	1.77±0.36	2.544
RSA	2140	21	27	16	7.170	3.35±0.24	7.725

l = length of sequence;
n = sample size;
s = number of segregating sites;
h = number of haplotypes;
k = mean number of pairwise nucleotide differences;
π = mean number of base differences per site;
θw = mean population mutation rate.
Mitochondrial loci = concatenated *cox*IGS and *nadh*1 sequence data;
Nuclear loci = concatenated *enolase*, *hsp*90, *ras*, and *asf*-like sequence data

- at the time of its description, *P. multivora* was virtually unknown outside Western Australia
- subsequently it is appearing more and more often in Europe
- also in Western Australia it has become the most common species isolated in the urban and peri-urban environment
- in South Africa, it is widely distributed and readily isolated from natural forest with no disease symptoms
- no unique isolates from Europe, USA and NZ, *P. multivora* appears to be introduced to these regions but to date dataset no large enough
- in coalescence analysis, more variable sites, more haplotypes and highest diversity among isolates from South Africa
- based on coalescence analysis, isolate diversity and biology we propose South Africa is the origin of *P. multivora*