Results

Of the 187 sequences included in this study, 52 ingroup sequences as well as two outgroup sequences were generated in a previous study (Grobler *et al*., 2006; Chapter 2). The Genbank accession numbers for these previously characterized specimens are AY762267-AY762320. An additional 135 sequences were generated in this study and are deposited in Genbank under accession numbers JF327506-JF327640. Of the 187 sequences used in this study, 131 represent unique haplotypes.

Nested clade analysis

A single haplotype network (Fig. 5), based on the 95 % connection probability (≤ 13 steps), was estimated by TCS 1.13 (Clement *et al*., 2000). From the nested design presented in Fig. 6, the total cladogram can be divided into two 6-step clades, three 5-step clades, and six 4-step clades at the higher clade level. The six 4-step clades separate from each other by more than five steps, representing missing intermediate haplotypes as indicated in Fig. 7. Nested clade 4-4 which consists of *E. kucheli* (Grobler *et al*., 2006) was considered basal to the other 4-step clades because time of coalescence of these individuals preceded that of the other clades (Grobler *et al*., 2006; Chapter 2), and therefore, all higher-step clades were designated with this in mind.

The results of the nested cladistic analysis of geographical distance for the mtDNA data set from the PEIA are shown in Fig. 8. The contingency analyses (Templeton *et al*., 1995) detected significant geographical associations with the total cladogram, a 6-step clade, two 5-step clades, only one 4-step clade, and a single 1-step clade (Table 1). Significant geographical structure was thus mainly indicated for the higher clade levels. With the exception of nested clade 1-96, no significance at the 1-, 2- and 3-step levels were found. One clade of each of the 4-, 3-, and 2-step clades also had a lower significant geographical association. Table 2 presents the chain of inferences followed when the inference key was applied to the statistical results given in Fig. 7 as well as the resulting inferences obtained.

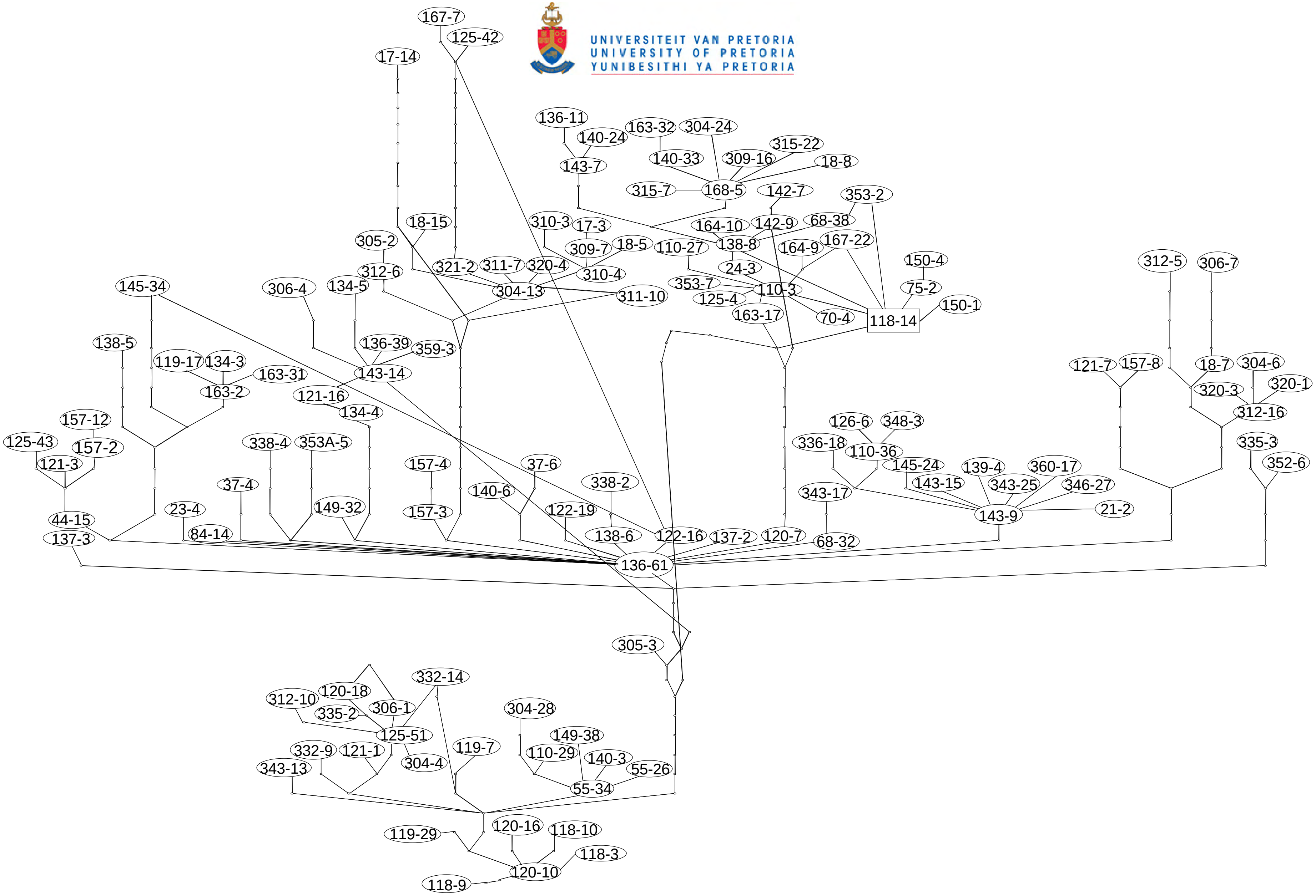


Fig. 5 Haplotype network based on 95% connection probability (≤ 13 steps) as estimated by TCS 1.13 (Clement et al., 2000).

Please find the figure on the disc in the envelope at the back

Fig. 6 Nested design according to previously described nesting rules of Templeton *et al*., 1987 and Crandall, 1996.

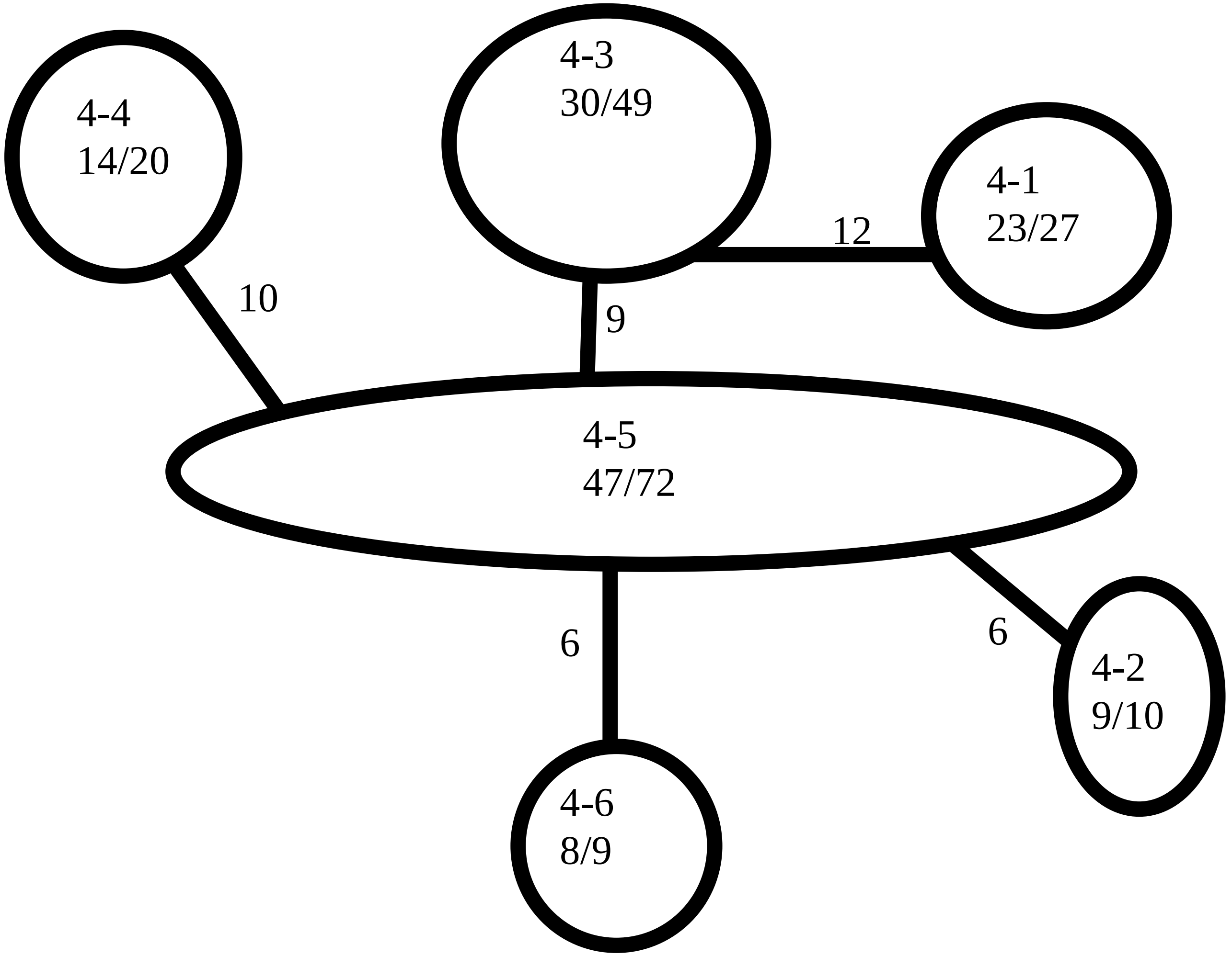


Fig. 7 Haplotype network of 187 *Ectemnorhinus* sequences. Sequences are grouped into six groups separated from each other by the number of missing haplotypes (as indicated on the lines). Within each circle is the designated name for the group followed by the number of unique haplotypes / total number of sequences / specimens characterized for each group.

Please find the figure on the disc in the envelope at the back

Fig. 8 Results of the nested clade analysis of the geographical distance for COI haplotypes of *Ectemnorhinus* weevils from the PEIA. Haplotypes (0-steps) are given at the top in bold. Interior haplotypes/clades are shaded. Higher level clade designations are indicated in bold as one moves down the figure. Boxed groupings indicate the nested structure. Following the number of any given clade is the clade (Dc) and nested clade (Dn) great circle distances. An 's' indicates that the distance is significantly small at the 5 % level and an "L" indicates that the distance is significantly large. For nested groupings that contain both tip and interior clades, the average differences of the distances between interior clades and tip clades within the nested group for clade distances, is indicated by the symbol '(T-1)c", with nested clade distances being indicated by the symbol '(T-1)n".

Table 1 Nested contingency analyses for geographical association showing the permutation chi-squared probabilities for geographical structure of the clades identified in Fig. 8 from 100 000 resamplings. Clades with a probability value less than 0.05 suggest significant geographical structure and are indicated with *. Clades with a probability value less than 0.1 are indicated with #.

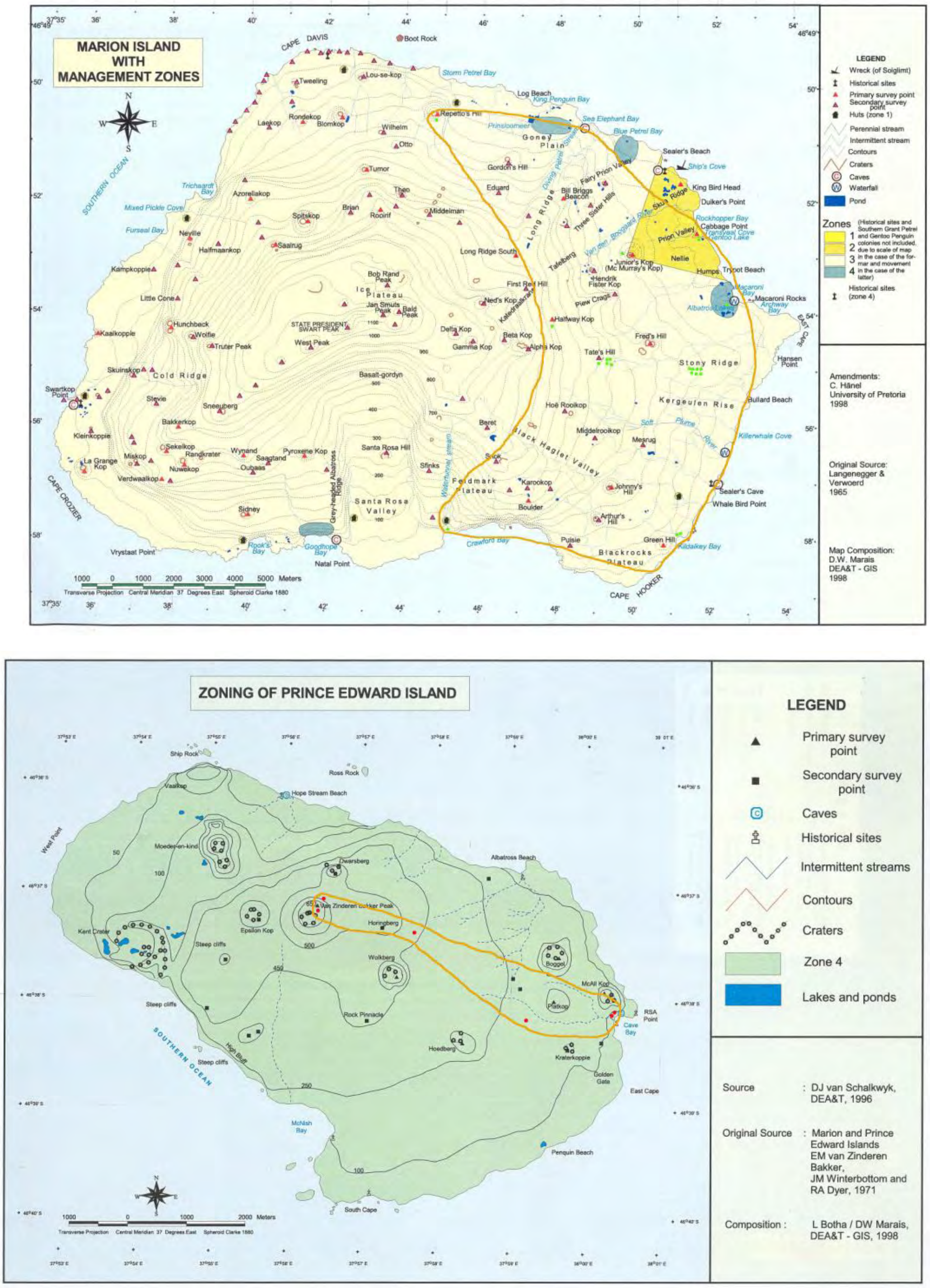
Clade	Permutational chi-square statistic	Probability
1-9	11.25	0.6860
1-12	1.3333	1.0000
1-14	15.0000	1.0000
1-15	2.0000	1.0000
1-17	2.0000	1.0000
1-18	34.0000	0.8300
1-20	3.0000	1.0000
1-34	2.0000	1.0000
1-38	0.7500	1.0000
1-43	10.0000	0.2010
1-56	2.0000	1.0000
1-60	1.3333	1.0000
1-67	10.0000	1.0000
1-71	75.4667	0.3210
1-79	2.0000	1.0000
1-80	5.9583	0.7680
1-81	10.0000	0.2900
1-82	2.0000	1.0000
1-83	34.0000	1.0000
1-85	2.0000	1.0000
1-87	3.0000	0.3220
1-89	21.3889	0.4830
1-91	5.0000	0.8370
1-92	2.0000	1.0000
1-93	3.0000	0.3340
1-96	62.2222	0.0410*
1-200	2.0000	1.0000
2-1	2.9167	0.6880
2-3	15.0000	1.0000
2-4	2.0000	1.0000
2-5	3.0000	1.0000
2-10	5.0000	0.4300
2-13	3.0000	1.0000
2-15	6.0000	0.3080
2-18	12.0000	0.0730#
2-19	4.0000	1.0000
2-20	12.0000	0.3810
2-22	17.0000	0.5780
2-23	2.0000	1.0000
2-27	10.0000	0.3380
2-29	3.2500	0.6120
2-31	18.0000	0.4910

Clade	Permutational chi-square statistic	Probability
2-33	153.3333	0.2680
2-34	30.6000	0.3640
2-35	11.2000	0.5500
2-36	4.9038	0.9120
2-37	11.0714	0.9880
3-2	1.2000	1.0000
3-3	13.3333	0.6430
3-4	19.2000	0.1400
3-6	13.9240	0.7950
3-7	35.1771	0.1100
3-8	0.6857	1.0000
3-9	29.8194	0.5160
3-10	20.0076	0.0950#
3-16	149.6400	0.4930
4-1	16.5515	0.2450
4-2	10.0000	0.1060
4-3	24.1412	0.1500
4-4	5.9649	0.8120
4-5	88.0677	0.0000*
4-6	3.9375	0.7870
5-1	100.0663	0.0020*
5-2	47.8767	0.0002*
6-1	71.2705	0.0000*
Total Cladogram	101.4970	0.0000*

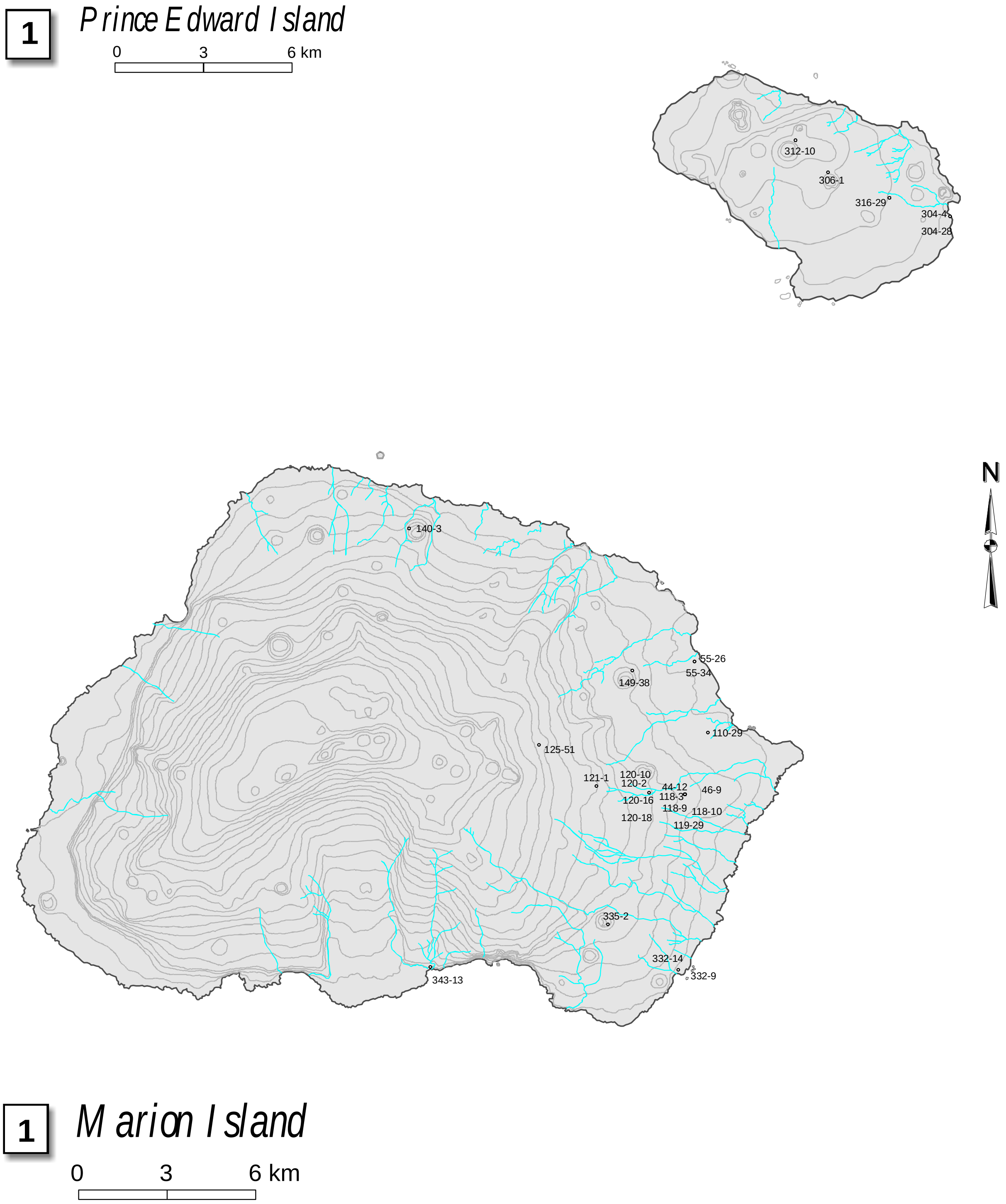
Table 2 Inference chain for the results of the *Ectemnorhinus* phylogeography as indicated by the nested clade analysis from the results given in Fig. 8 and Table 1. Only the clades that resulted in a rejection of the null hypothesis, i.e. that there are no significant relationships between genetic variation and respective geographical locations of haplotypes, are included. Clades marked with # were not significant at the 0.05 % level but were significant at the 0.1 % level.

Clade	Chain of inference	Inverence
1-96	1-2-3-5-6-7	Insufficient genetic resolution to discriminate between range expansion / colonization and restricted dispersal / gene flow. Restricted gene flow / dispersal but with some long distance dispersal.
2-18#	1- 2 – 11 - 12	Continuous range expansion
3-10#	1- 2 – 11 – 17 -	Inconclusive outcome
4-5	1-2-11-17-	Inconclusive outcome
5-1	1-2-11-12	Contiguous range expansion,
5-2	1-2-11-17-	Inconclusive outcome
6-1	1-2-11-17-4-	Restricted gene flow with isolation by distance

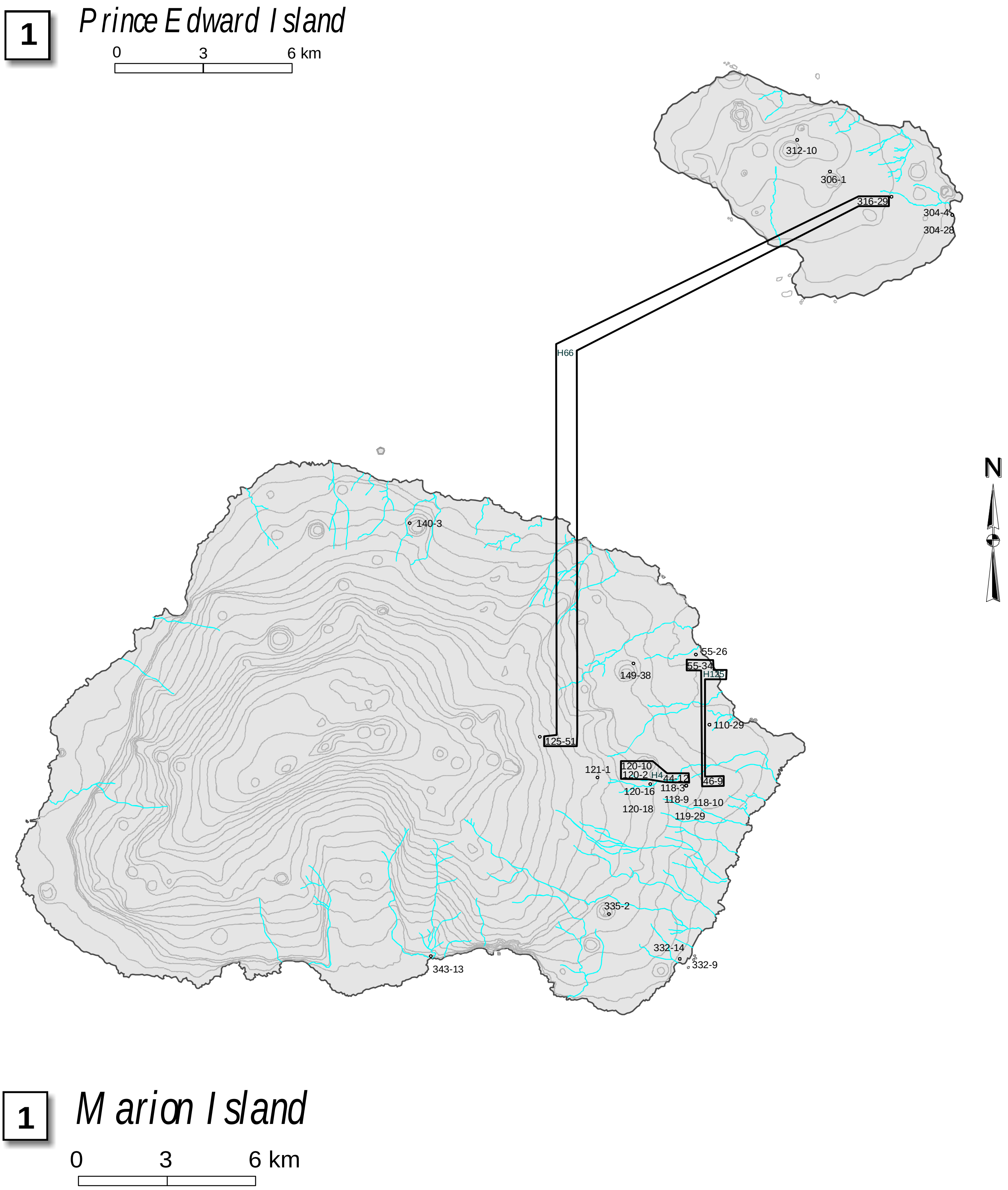
In order to gain further insight into the geographical structuring, clades were mapped onto the islands according to the sampling localities of the constituent haplotypes. Because of the very large dataset and the fact that the 4-step clades separate from each other by more than three missing haplotypes (Fig. 7) the nested clade diagram was partitioned into the six different 4-step clades to ensure manageable mapping and result presentation. The different maps for the individuals falling in each 4-step clade are presented in Figs. 8-13 with each being divided into six parts.



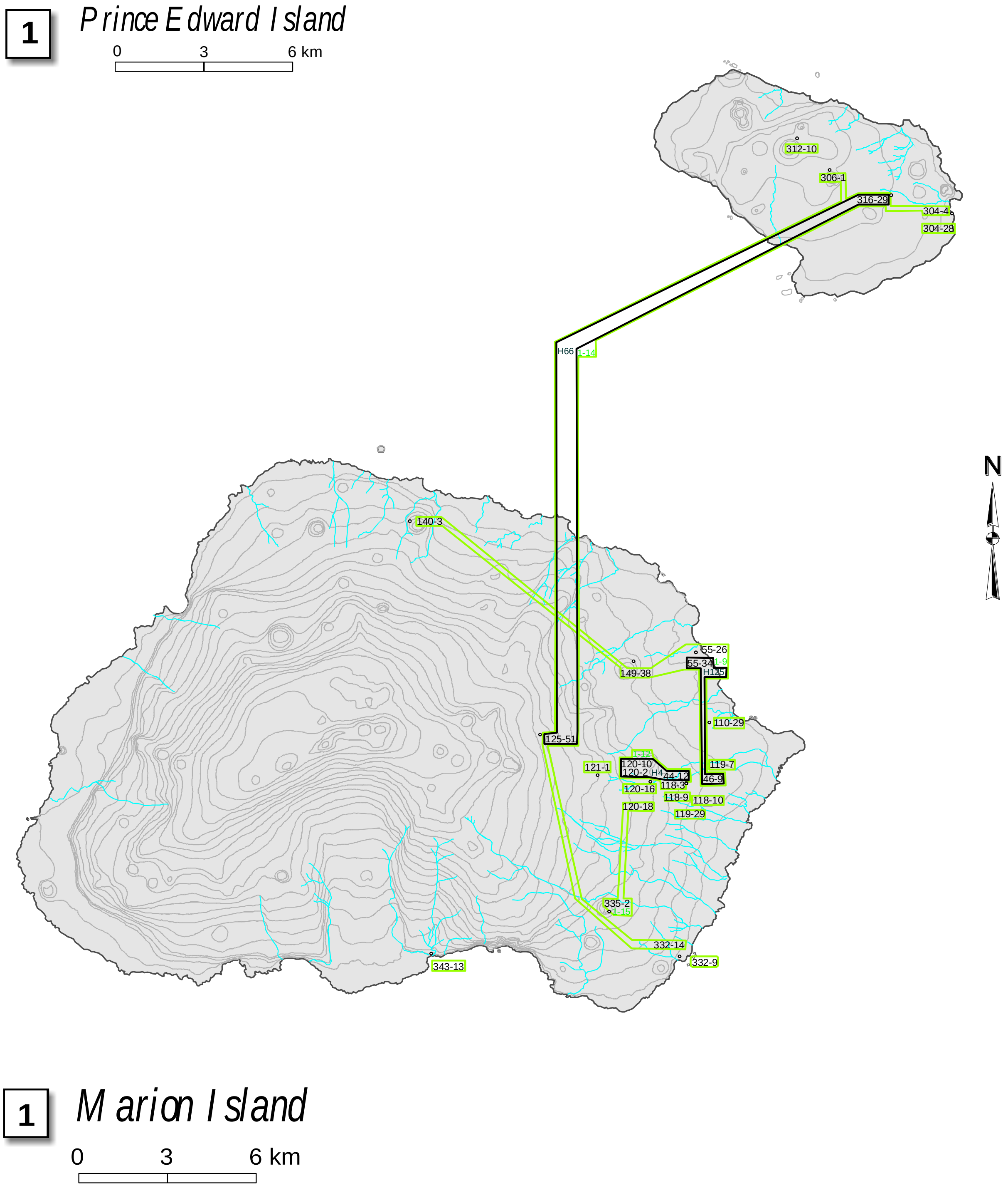
(a)


1
Prince Edward Island
0
3
6 km
312-10
306-1
316-29
304-4
304-28
N
140-3
55-26
55-34
149-38
110-29
125-51
121-1
120-10
120-2
44-12
118-3
46-9
120-16
118-9
118-10
120-18
119-29
335-2
332-14
332-9
343-13
1
Marion Island
0
3
6 km

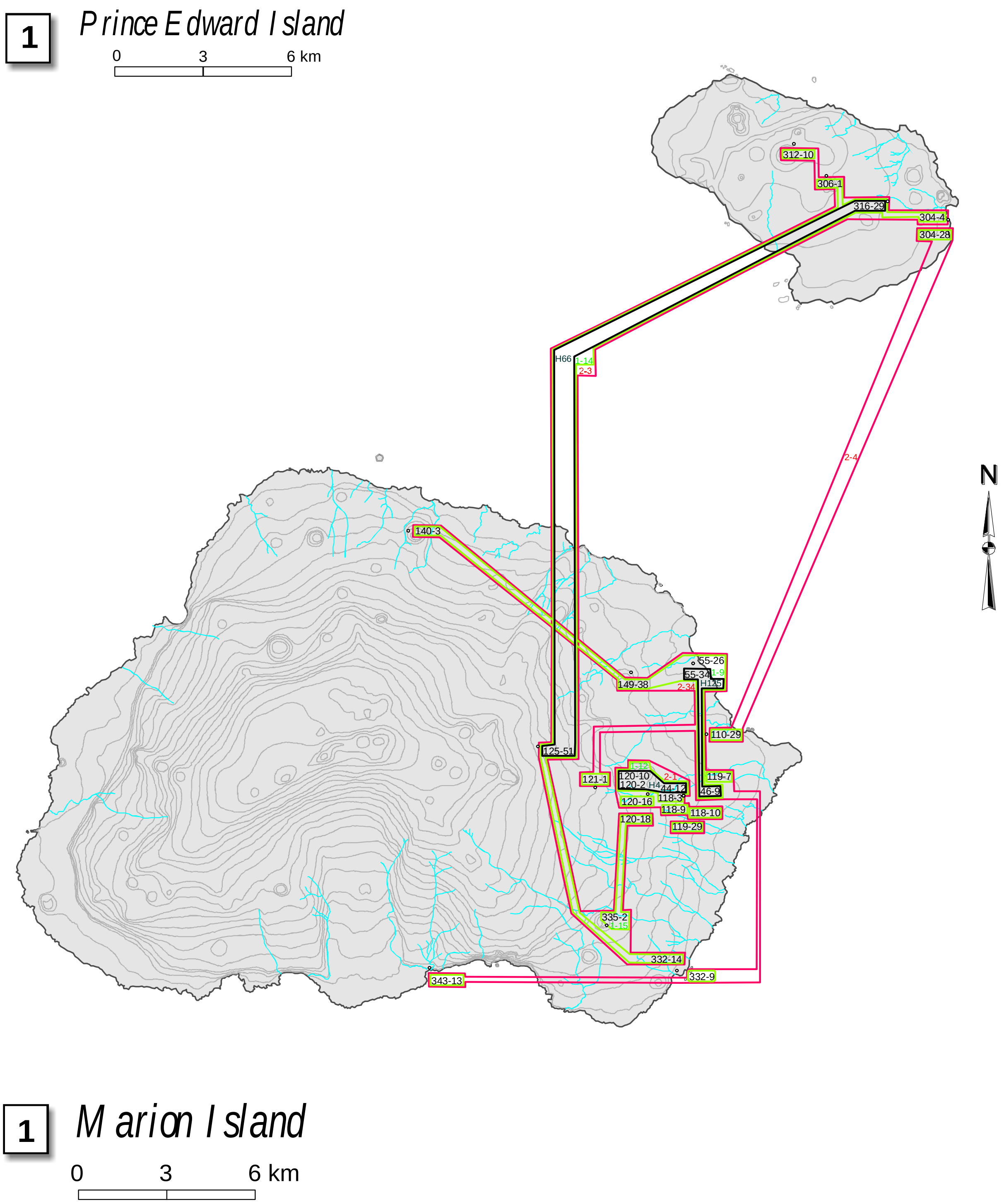
(b)


1
Prince Edward Island
0
3
6 km
312-10
306-1
316-29
304-4
304-28
H66
N
140-3
55-26
55-34
H125
149-38
110-29
125-51
121-1
120-10
120-2
H4
44-12
46-9
120-16
118-3
118-9
118-10
120-18
119-29
335-2
332-14
332-9
343-13
1
Marion Island
0
3
6 km

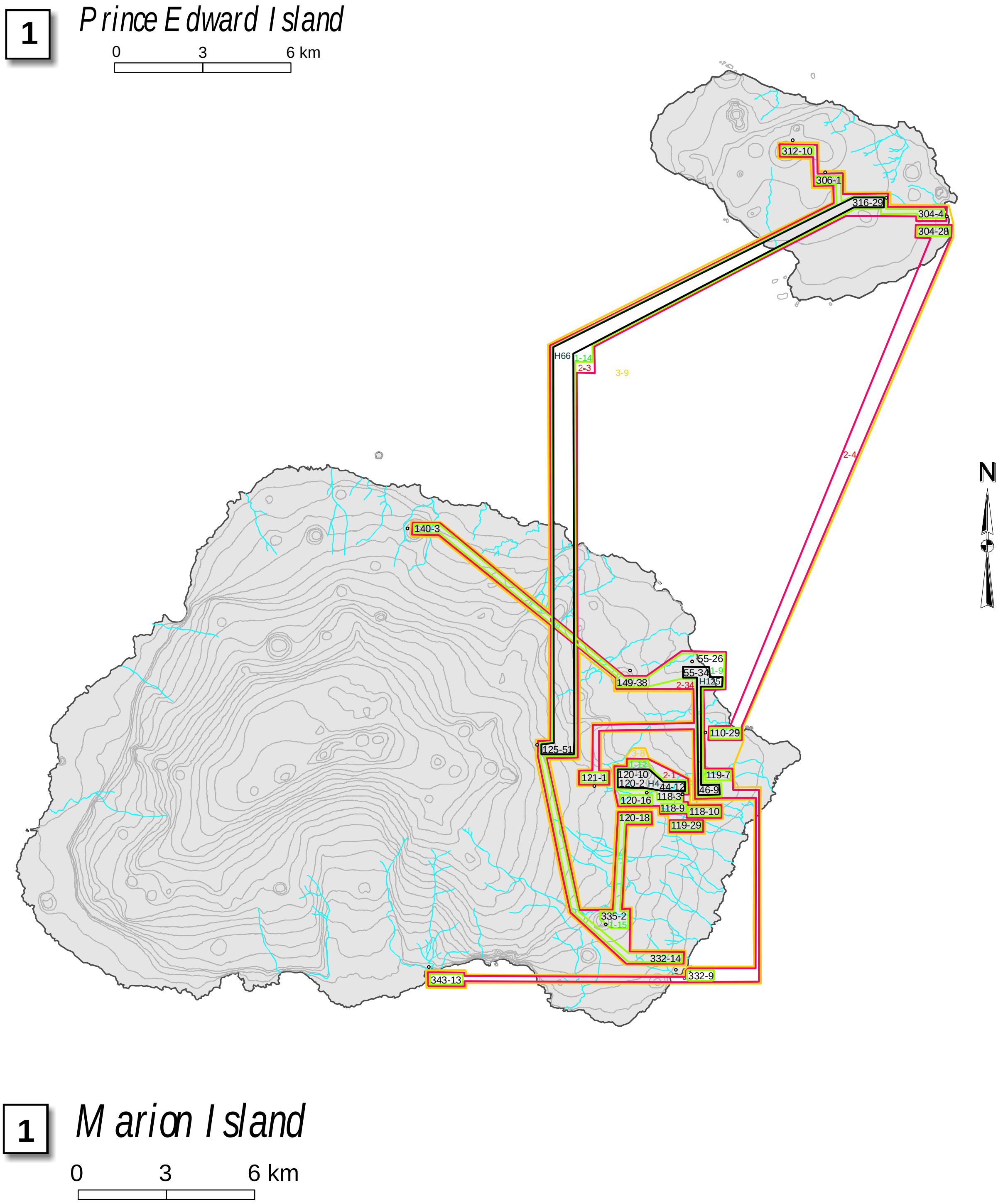
(c)


1
Prince Edward Island
0
3
6 km
312-10
306-1
316-29
304-4
304-28
H66
1-14
N
140-3
55-26
55-34
1-9
H125
149-38
110-29
125-51
1-12
121-1
120-10
120-2
H4
44-12
119-7
46-9
120-16
118-3
118-9
118-10
120-18
119-29
335-2
1-15
332-14
332-9
343-13
1
Marion Island
0
3
6 km

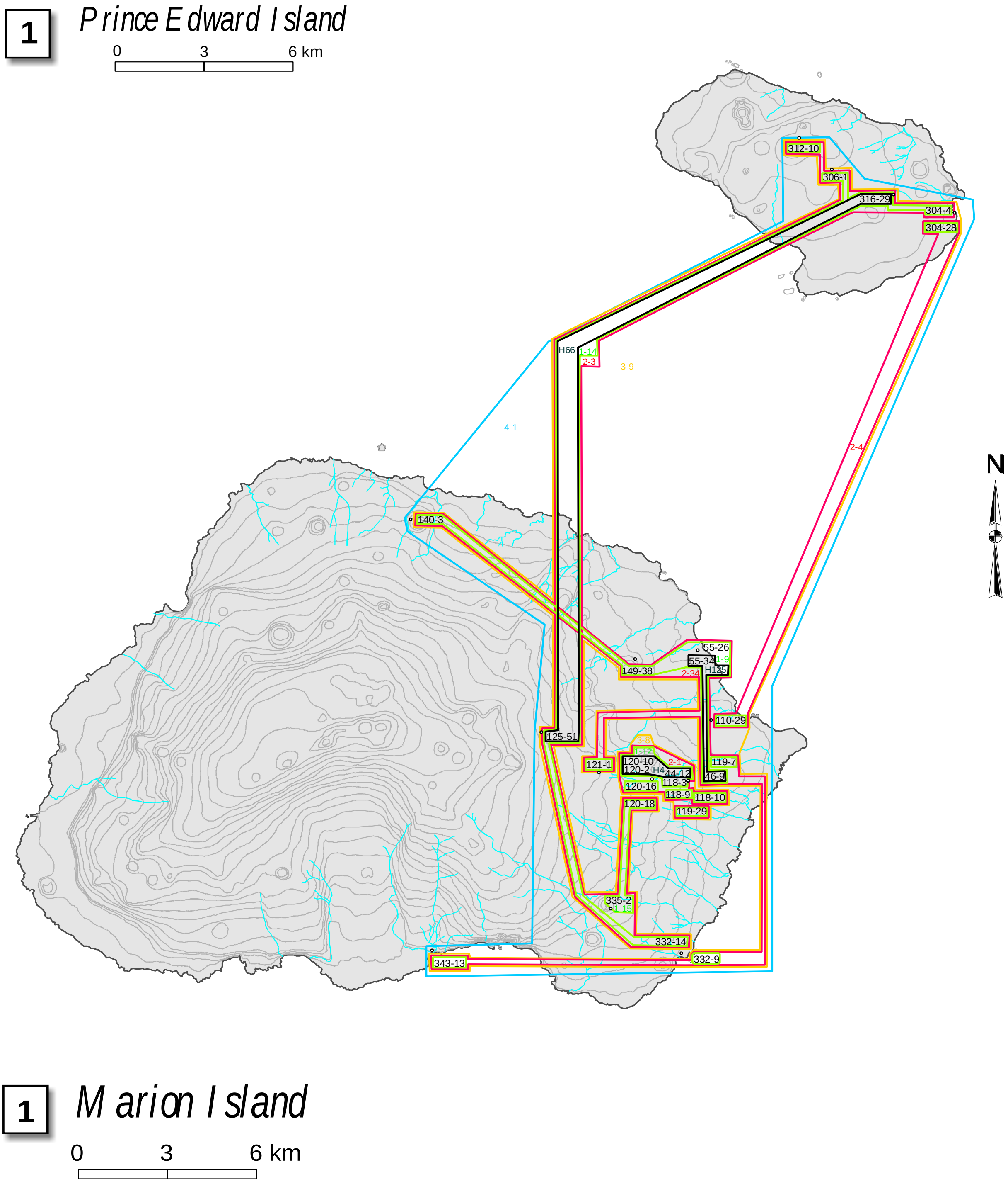
(d)


1
Prince Edward Island
0
3
6 km
312-10
306-1
316-29
304-4
304-28
H66
1-14
2-3
2-4
N
140-3
149-38
55-26
55-34
1-9
H125
2-34
110-29
125-51
121-1
1-12
120-10
120-2
H4
2-1
44-12
119-7
46-9
120-16
118-3
118-9
118-10
120-18
119-29
335-2
1-15
332-14
343-13
332-9
1
Marion Island
0
3
6 km

(e)

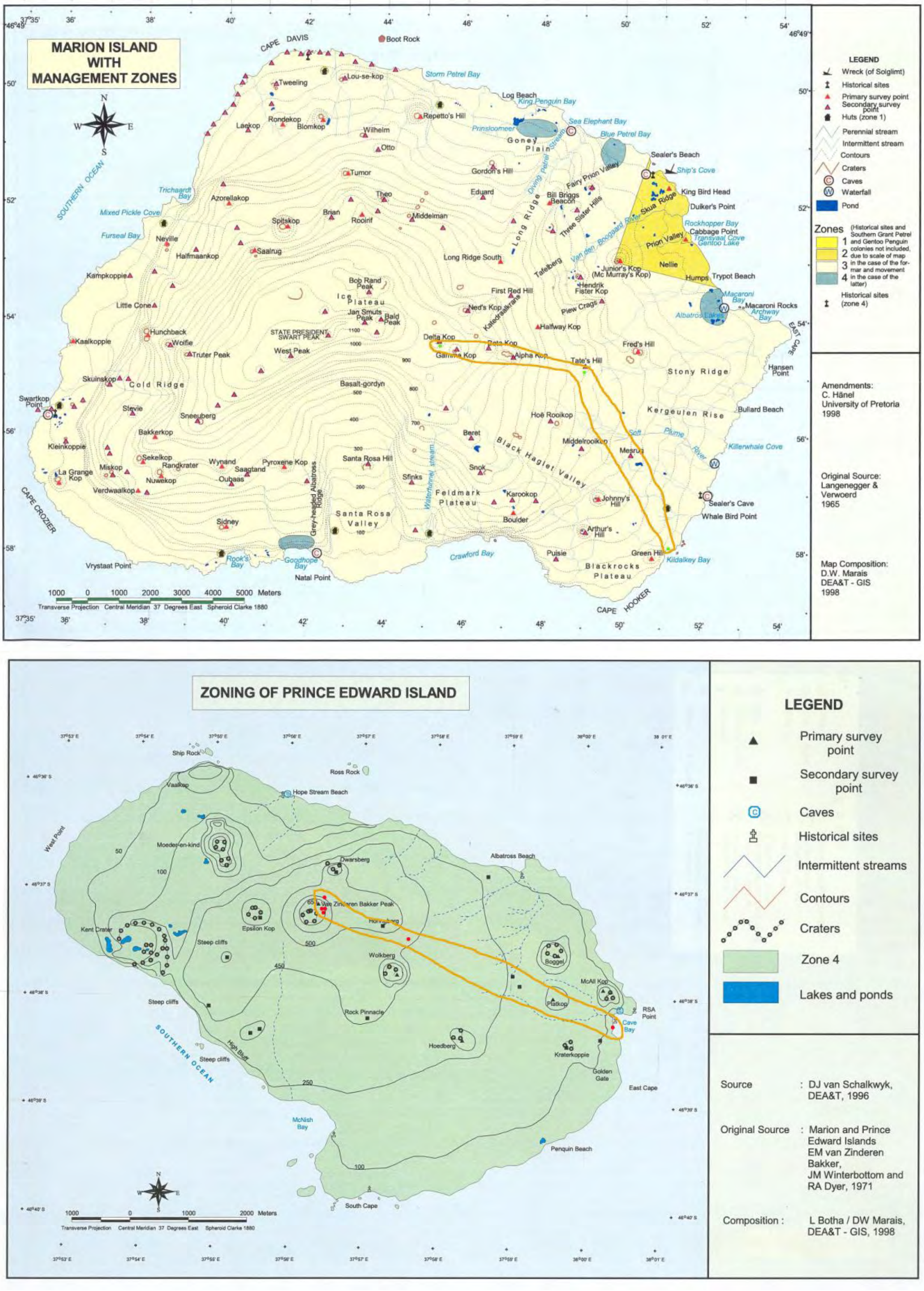

1
Prince Edward Island
0
3
6 km
312-10
306-1
316-29
304-4
304-28
H66
1-14
2-3
3-9
2-4
N
140-3
55-26
55-34
1-9
H125
149-38
2-34
110-29
125-51
121-1
120-10
120-2
H4
44-12
2-1
119-7
46-9
120-16
118-3
118-9
118-10
120-18
119-29
335-2
1-15
332-14
343-13
332-9
1
Marion Island
0
3
6 km

(f)

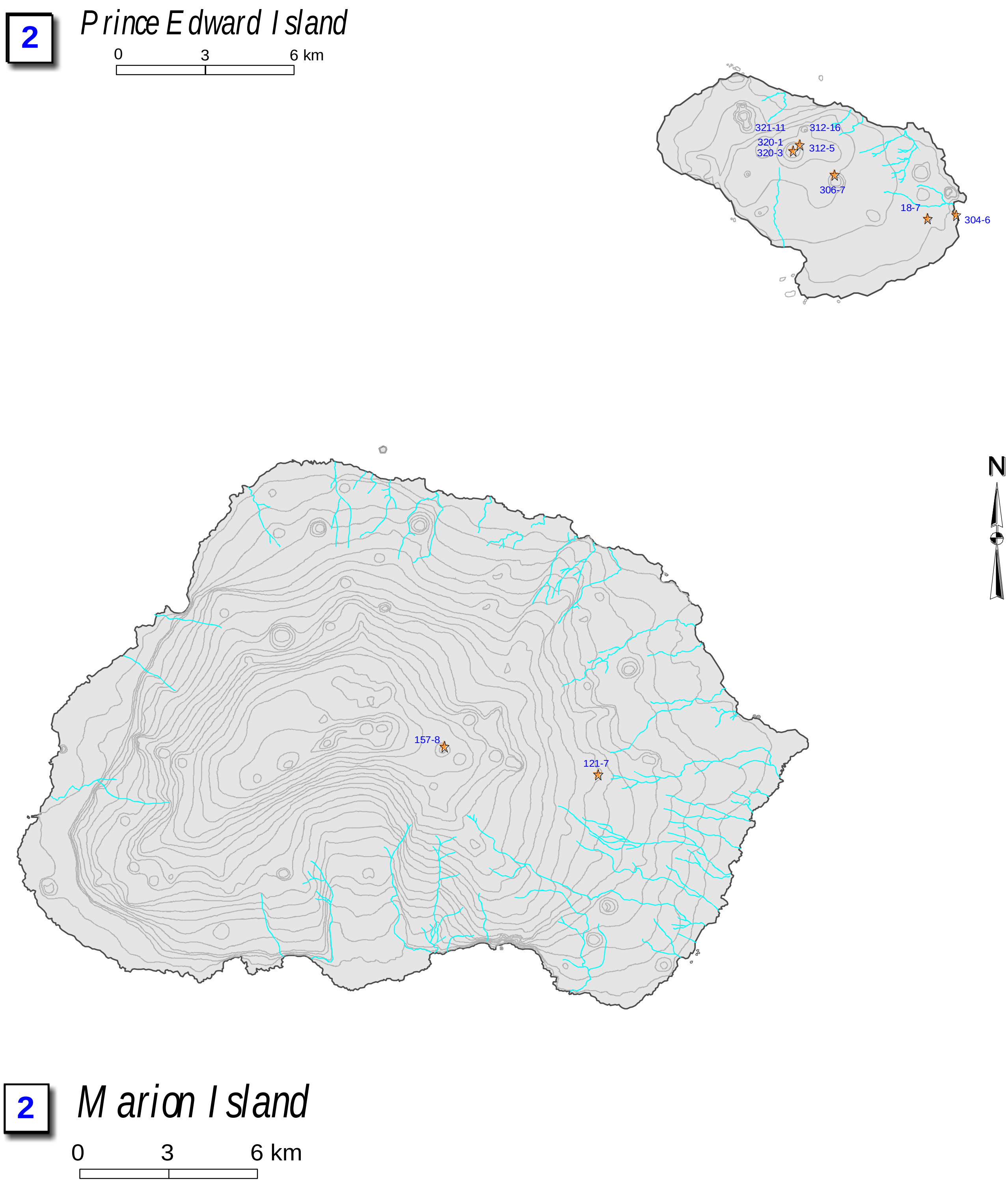


(g)

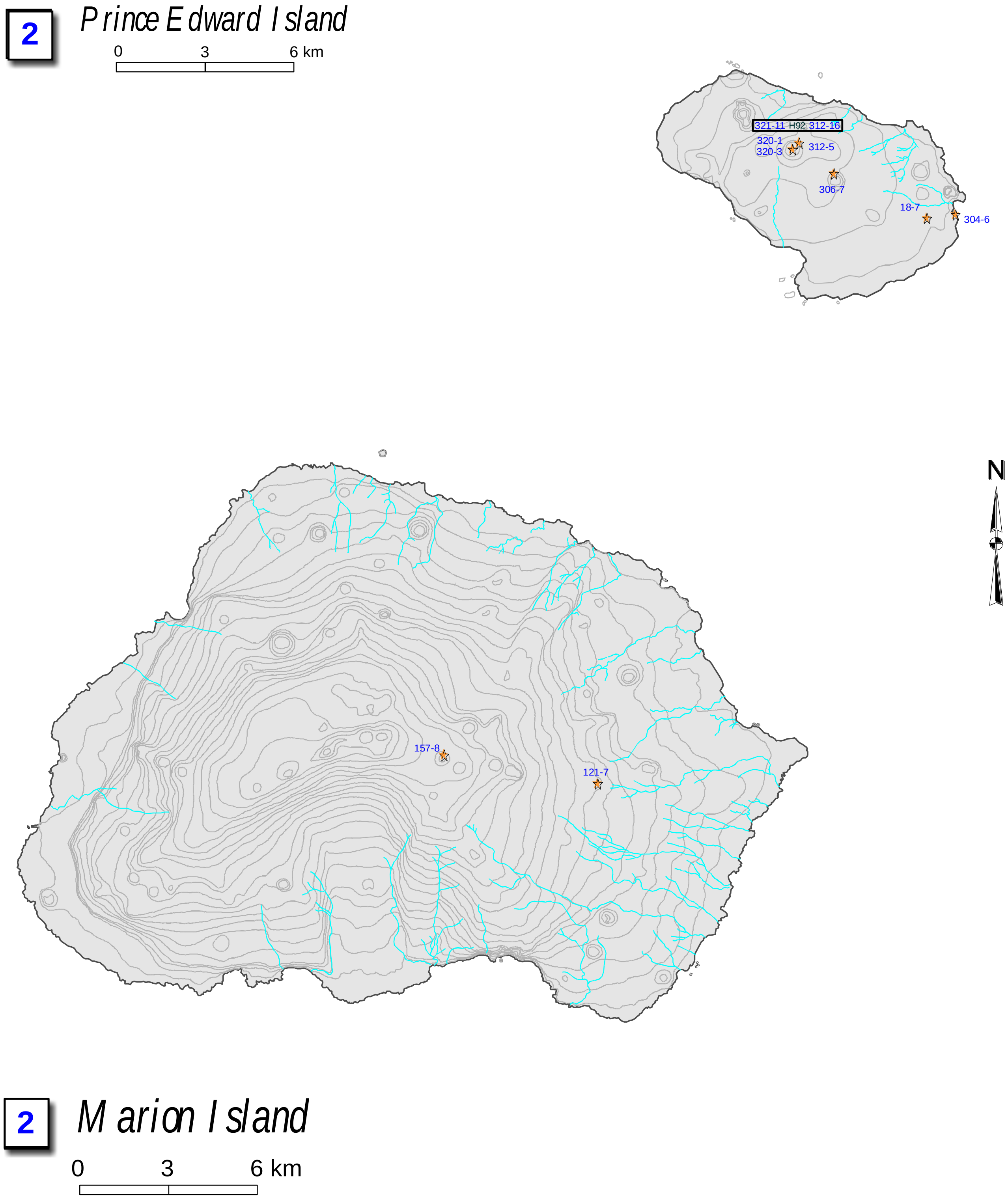
Fig. 9 *Ectemnorhinus* individuals that group into 4-step clade 4-1 mapped onto the islands according to a) sampling localities with place names for references, samples on Marion Island are indicated in green while those on Prince Edward Island are indicated in red b) sampling localities as used in the nested design c) those that share the same haplotypes nested into 0-step clades, the d) 1-step clades, e) 2-step clades f) 3 step clades and finally g) the complete 4-1 clade as depicted in Fig. 5.


MARION ISLAND WITH MANAGEMENT ZONES
LEGEND
Wreck (of Solglimt)
Historical sites
Primary survey point
Secondary survey point
Huts (zone 1)
Perennial stream
Intermittent stream
Contours
Craters
Caves
Waterfall
Pond
Zones (Historical sites and Southern Grant Petrel and Gentoo Penguin colonies not included, due to scale of map in the case of the former and movement in the case of the latter)
1
2
3
4
Historical sites (zone 4)
Amendments: C. Hänel University of Pretoria 1998
Original Source: Langenegger & Verwoerd 1965
Map Composition: D.W. Marais DEA&T - GIS 1998
CAPE DAVIS
Boot Rock
Storm Petrel Bay
Log Beach
King Penguin Bay
Sea Elephant Bay
Blue Petrel Bay
Goney Plain
Sealer's Beach
Ship's Cove
King Bird Head
Duiker's Point
Rockhopper Bay
Cabbage Point
Transvaal Cove
Gentoo Lake
Prion Valley
Skua Ridge
Nellie
Humps
Trypot Beach
Macaroni Bay
Macaroni Rocks
Archway Bay
Albatross Lakes
EAST CAPE
Hansen Point
Stony Ridge
Kerguelen Rise
Bullard Beach
Killerwhale Cove
Sealer's Cave
Whale Bird Point
Kildalkey Bay
Green Hill
Blackrocks Plateau
CAPE HOOKER
Crawford Bay
Natal Point
Goodhope Bay
Rook's Bay
Vrystaat Point
CAPE CROZIER
SOUTHERN OCEAN
Trichaardt Bay
Mixed Pickle Cove
Furseal Bay
Swartkop Point
Tweeling
Lou-se-kop
Repetto's Hill
Rondekop
Blomkop
Wilhelm
Otto
Tumor
Gordon's Hill
Theo
Eduard
Middelman
Bill Briggs Beacon
Long Ridge
Three Sister Hills
Fairy Prion Valley
Van den Boogaard River
Azorellakop
Spitskop
Brian
Rooirif
Neville
Halfmaankop
Saalrug
Kampkoppie
Long Ridge South
Tafelberg
Junior's Kop (Mc Murray's Kop)
Hendrik Fister Kop
Bob Rand Peak
Ice Plateau
Jan Smuts Peak
Bald Peak
First Red Hill
Ned's Kop
Katedraalkrans
Piew Crags
Halfway Kop
Little Cone
Hunchback
Wolfie
Kaalkoppie
Truter Peak
STATE PRESIDENT SWART PEAK
West Peak
Delta Kop
Gamma Kop
Beta Kop
Alpha Kop
Tate's Hill
Fred's Hill
Skuinskop
Cold Ridge
Basalt-gordyn
Stevie
Sneeuberg
Hoë Rooikop
Bakkerkop
Beret
Soft Plume River
Middelrooikop
Mesrug
Black Haglet Valley
Kleinkoppie
Sekelkop
Randkrater
Wynand
Saagtand
Pyroxene Kop
Santa Rosa Hill
Sfinks
Snok
La Grange Kop
Miskop
Nuwekop
Oubaas
Verdwaalkop
Grey-headed Albatross Ridge
Waterhunnel stream
Feldmark Plateau
Karookop
Johnny's Hill
Santa Rosa Valley
Sidney
Boulder
Arthur's Hill
Puisie
Prinsloomeer
Diving Petrel Stream
1000 0 1000 2000 3000 4000 5000 Meters
Transverse Projection Central Meridian 37 Degrees East Spheroid Clarke 1880
ZONING OF PRINCE EDWARD ISLAND
LEGEND
Primary survey point
Secondary survey point
Caves
Historical sites
Intermittent streams
Contours
Craters
Zone 4
Lakes and ponds
Source : DJ van Schalkwyk, DEA&T, 1996
Original Source : Marion and Prince Edward Islands EM van Zinderen Bakker, JM Winterbottom and RA Dyer, 1971
Composition : L Botha / DW Marais, DEA&T - GIS, 1998
Ship Rock
Ross Rock
Vaalkop
Hope Stream Beach
West Point
Moeder-en-kind
Dwarsberg
Albatross Beach
Van Zinderen Bakker Peak
Hornsberg
Kent Crater
Epsilon Kop
Steep cliffs
Wolkberg
Boggel
McAll Kop
Platkop
RSA Point
Cave Bay
Rock Pinnacle
Hoedberg
Kraterkoppie
Golden Gate
East Cape
High Bluff
SOUTHERN OCEAN
McNish Bay
Penguin Beach
South Cape
1000 0 1000 2000 Meters
Transverse Projection Central Meridian 37 Degrees East Spheroid Clarke 1880

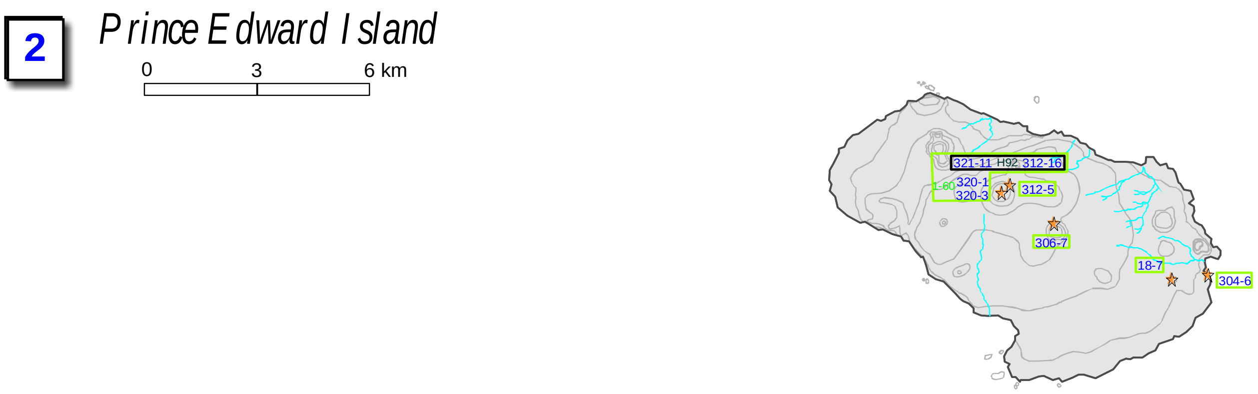
(a)

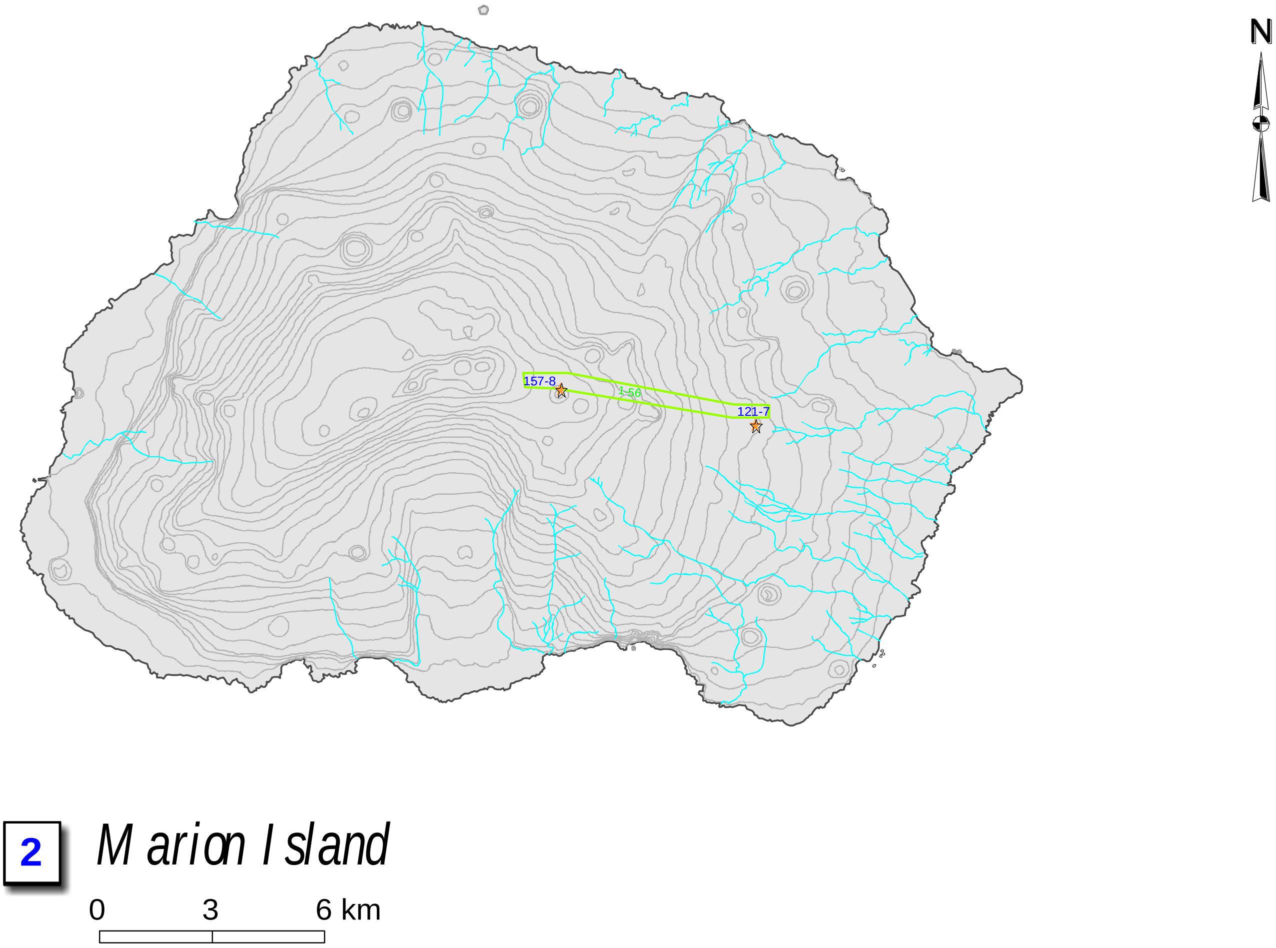

2
Prince Edward Island
0
3
6 km
321-11
312-16
320-1
320-3
312-5
306-7
18-7
304-6
N
157-8
121-7
2
Marion Island
0
3
6 km

(b)

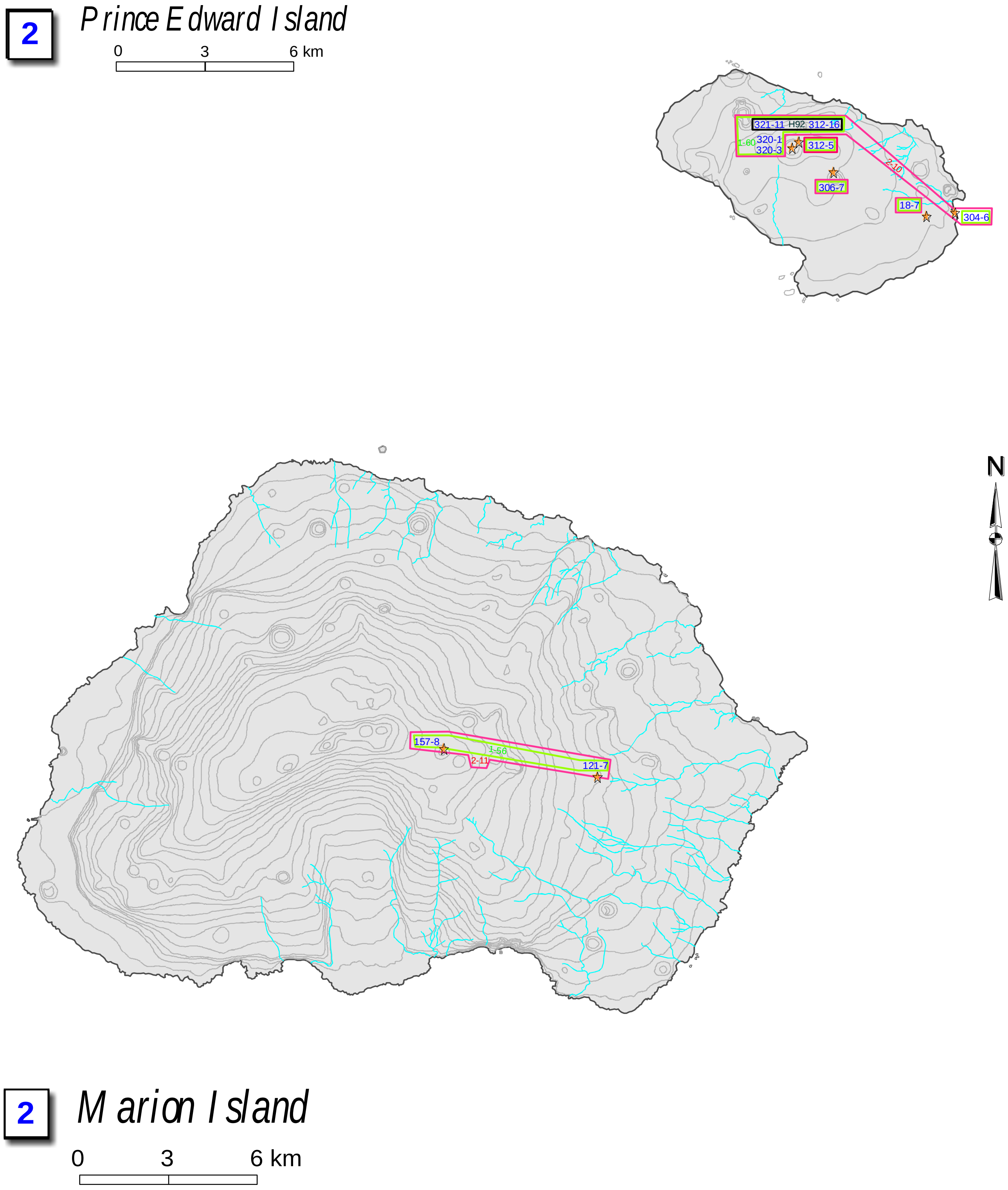

2
Prince Edward Island
0
3
6 km
321-11 H92 312-16
320-1
320-3
312-5
306-7
18-7
304-6
N
157-8
121-7
2
Marion Island
0
3
6 km

(c)

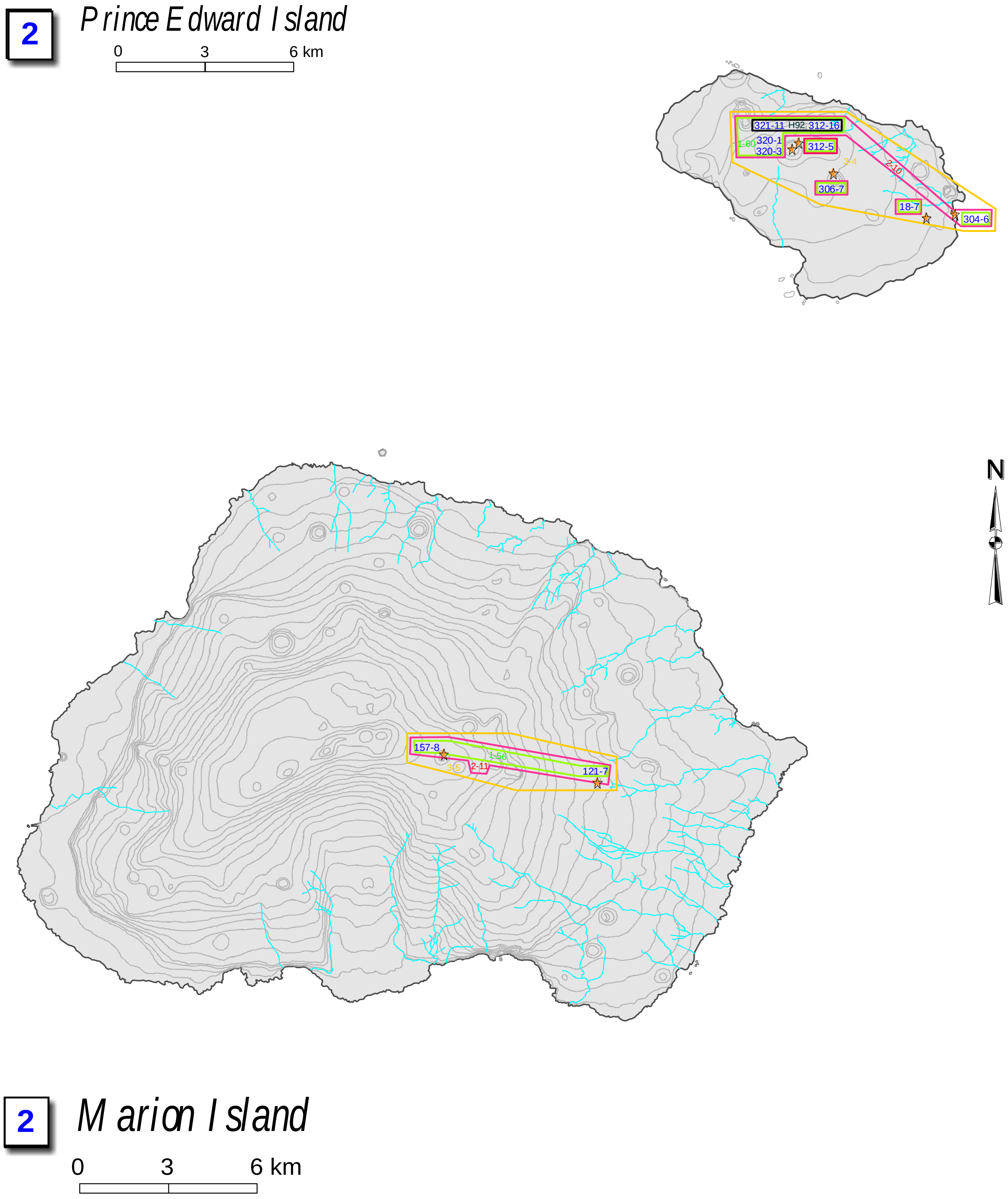

2
Prince Edward Island
0
3
6 km
321-11
H92
312-16
1-60
320-1
320-3
312-5
306-7
18-7
304-6


N
157-8
1-56
121-7
2
Marion Island
0
3
6 km

(d)


2
Prince Edward Island
0
3
6 km
321-11
H92
312-16
1-60
320-1
320-3
312-5
2-10
306-7
18-7
304-6
N
157-8
1-56
2-11
121-7
2
Marion Island
0
3
6 km

(e)


2
Prince Edward Island
0
3
6 km
321-11
H92
312-16
1-60
320-1
320-3
312-5
3-4
2-10
306-7
18-7
304-6
N
157-8
1-56
3-5
2-11
121-7
2
Marion Island
0
3
6 km

(f)

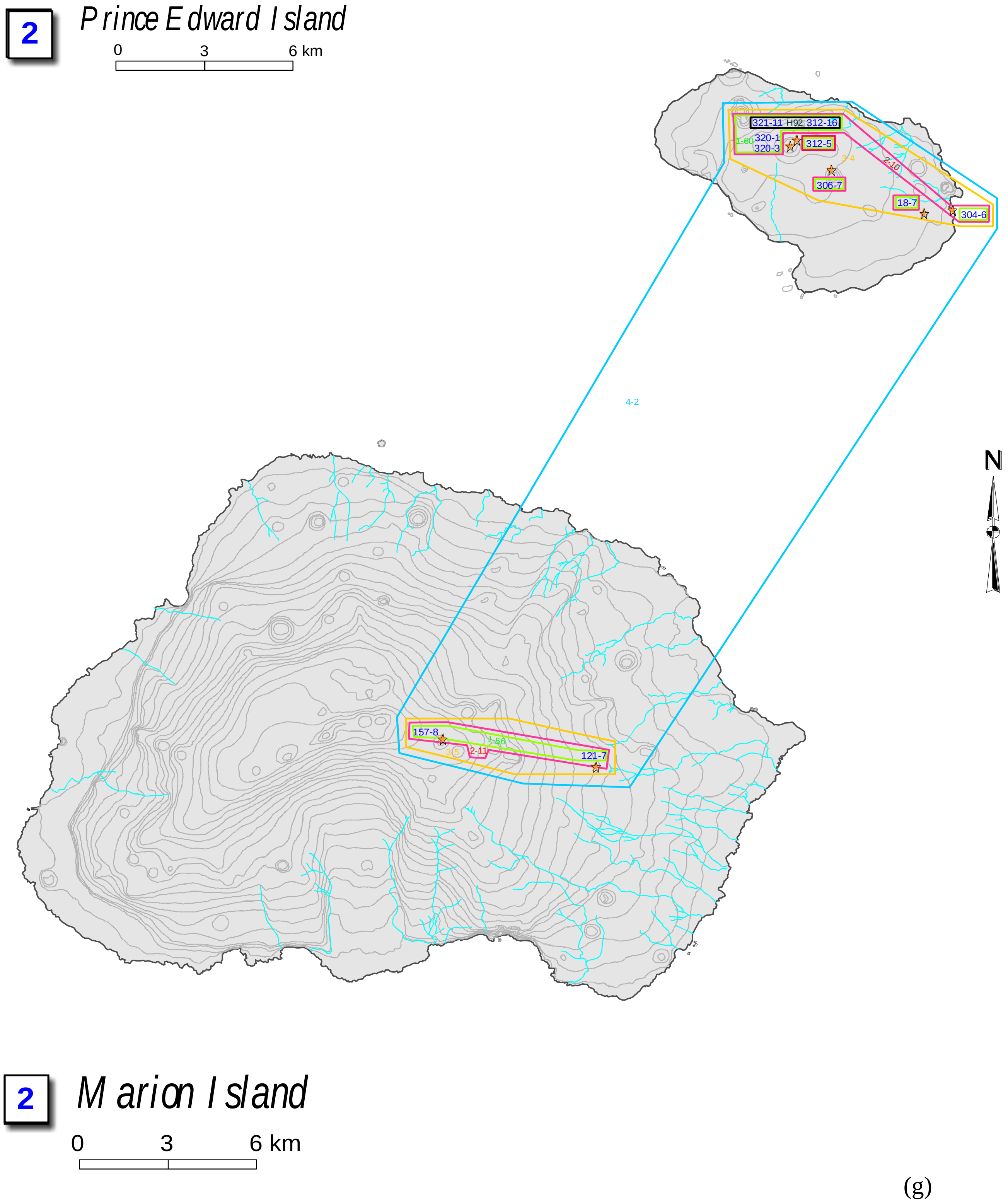
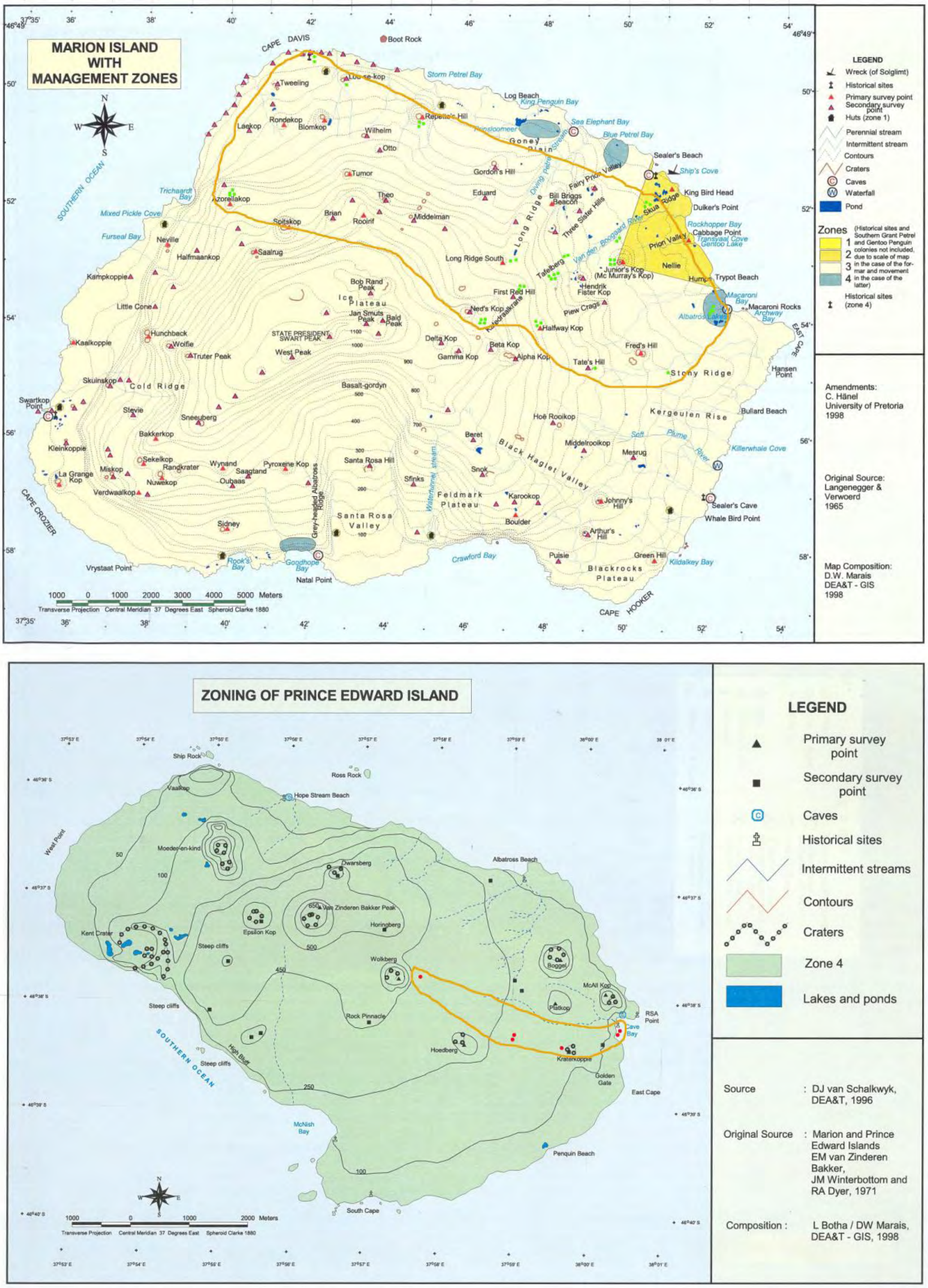
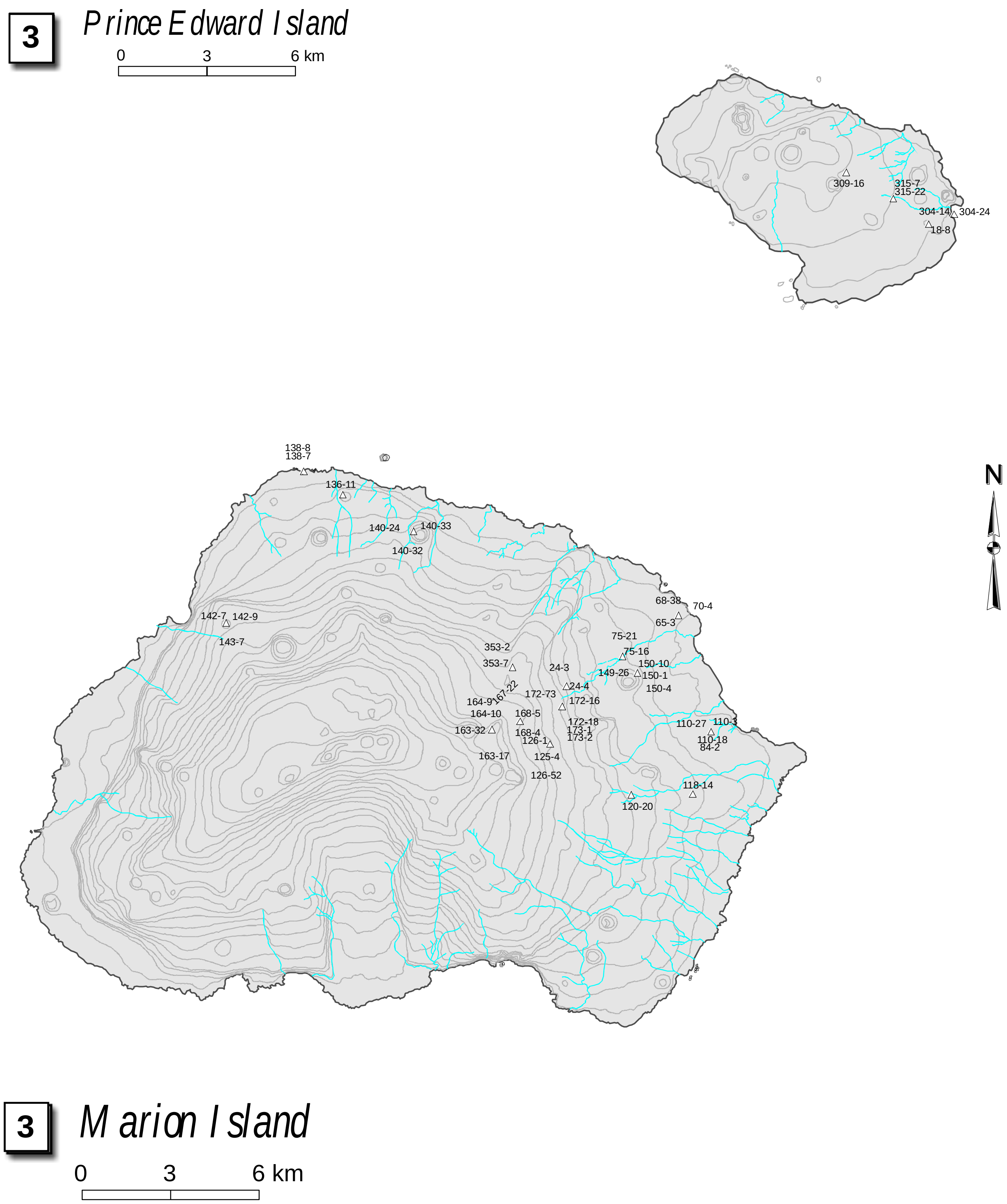


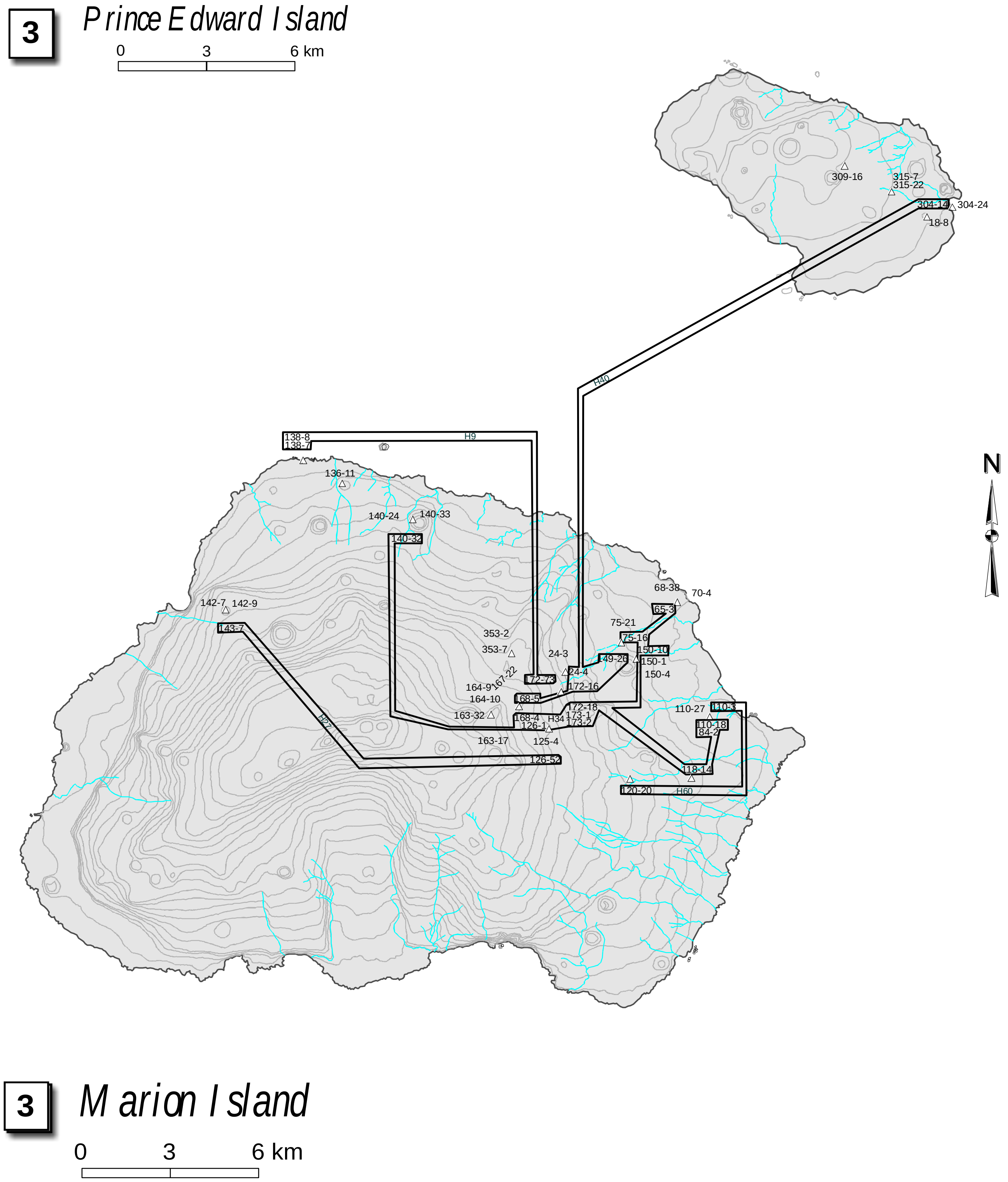
Fig. 10 *Ectemnorhinus* individuals that group into 4-step clade 4-2 mapped onto the islands according to a) sampling localities with place names for references, samples on Marion Island are indicated in green while those on Prince Edward Island are indicated in red b) sampling localities as used in the nested design c) those that share the same haplotypes nested into 0-step clades, the d) 1-step clades, e) 2-step clades f) 3 step clades and finally g) the complete 4-2 clade as depicted in Fig. 5.


MARION ISLAND WITH MANAGEMENT ZONES
LEGEND
Wreck (of Solglimt)
Historical sites
Primary survey point
Secondary survey point
Huts (zone 1)
Perennial stream
Intermittent stream
Contours
Craters
Caves
Waterfall
Pond
Zones
1
2
3
4
(Historical sites and Southern Grant Petrel and Gentoo Penguin colonies not included, due to scale of map in the case of the formar and movement in the case of the latter)
Historical sites (zone 4)
Amendments: C. Hänel University of Pretoria 1998
Original Source: Langenegger & Verwoerd 1965
Map Composition: D.W. Marais DEA&T - GIS 1998
CAPE DAVIS
Boot Rock
Storm Petrel Bay
Log Beach
King Penguin Bay
Sea Elephant Bay
Blue Petrel Bay
Sealer's Beach
Ship's Cove
King Bird Head
Duiker's Point
Rockhopper Bay
Cabbage Point
Transvaal Cove
Gentoo Lake
Trypot Beach
Macaroni Bay
Macaroni Rocks
Archway Bay
EAST CAPE
Hansen Point
Bullard Beach
Killerwhale Cove
Sealer's Cave
Whale Bird Point
Kildalkey Bay
CAPE HOOKER
Crawford Bay
Natal Point
Goodhope Bay
Rook's Bay
Vrystaat Point
CAPE CROZIER
Swartkop Point
SOUTHERN OCEAN
Trichardt Bay
Mixed Pickle Cove
Furseal Bay
Tweeling
Rondekop
Blomkop
Laekop
Wilhelm
Otto
Repetto's Hill
Goney Plain
Tumor
Azorellakop
Theo
Middelman
Brian
Rooirif
Spitskop
Neville
Halfmaankop
Saalrug
Kampkoppie
Little Cone
Hunchback
Wolfie
Kaalkoppie
Truter Peak
Skuinskop
Cold Ridge
Stevie
Sneeuberg
Bakkerkop
Kleinkoppie
Sekelkop
Randkrater
La Grange Kop
Miskop
Nuwekop
Verdwaalkop
Wynand
Saagtand
Oubaas
Pyroxene Kop
Sidney
Santa Rosa Hill
Santa Rosa Valley
Grey-headed Albatross Ridge
Sfinks
Waterfunnel stream
Feldmark Plateau
Karookop
Boulder
Snok
Beret
Black Haglet Valley
Middelrooikop
Mesrug
Johnny's Hill
Arthur's Hill
Puisie
Green Hill
Blackrocks Plateau
Ice Plateau
Bob Rand Peak
Jan Smuts Peak
Bald Peak
STATE PRESIDENT SWART PEAK
West Peak
Basalt-gordyn
Delta Kop
Gamma Kop
Beta Kop
Alpha Kop
Tate's Hill
Fred's Hill
Stony Ridge
Kerguelen Rise
Hoë Rooikop
Halfway Kop
Ned's Kop
First Red Hill
Piew Crags
Hendrik Fister Kop
Junior's Kop (Mc Murray's Kop)
Tafelberg
Nellie
Prion Valley
Skua Ridge
Long Ridge
Long Ridge South
Three Sister Hills
Van den Boogaard River
Bill Briggs Beacon
Fairy Prion Valley
Gordon's Hill
Eduard
Diving petrel stream
Albatross Lakes
Hump
1000 0 1000 2000 3000 4000 5000 Meters
Transverse Projection Central Meridian 37 Degrees East Spheroid Clarke 1880
ZONING OF PRINCE EDWARD ISLAND
LEGEND
Primary survey point
Secondary survey point
Caves
Historical sites
Intermittent streams
Contours
Craters
Zone 4
Lakes and ponds
Source : DJ van Schalkwyk, DEA&T, 1996
Original Source : Marion and Prince Edward Islands EM van Zinderen Bakker, JM Winterbottom and RA Dyer, 1971
Composition : L Botha / DW Marais, DEA&T - GIS, 1998
Ship Rock
Ross Rock
Hope Stream Beach
Vaalkop
West Point
Moeder-en-kind
Dwarsberg
Albatross Beach
Epsilon Kop
Van Zinderen Bakker Peak
Horingberg
Kent Crater
Steep cliffs
Wolkberg
Boggel
McAll Kop
Platkop
RSA Point
Cave Bay
Rock Pinnacle
Hoedberg
Kraterkoppie
Golden Gate
East Cape
High Bluff
SOUTHERN OCEAN
McNish Bay
Penguin Beach
South Cape
1000 0 1000 2000 Meters
Transverse Projection Central Meridian 37 Degrees East Spheroid Clarke 1880

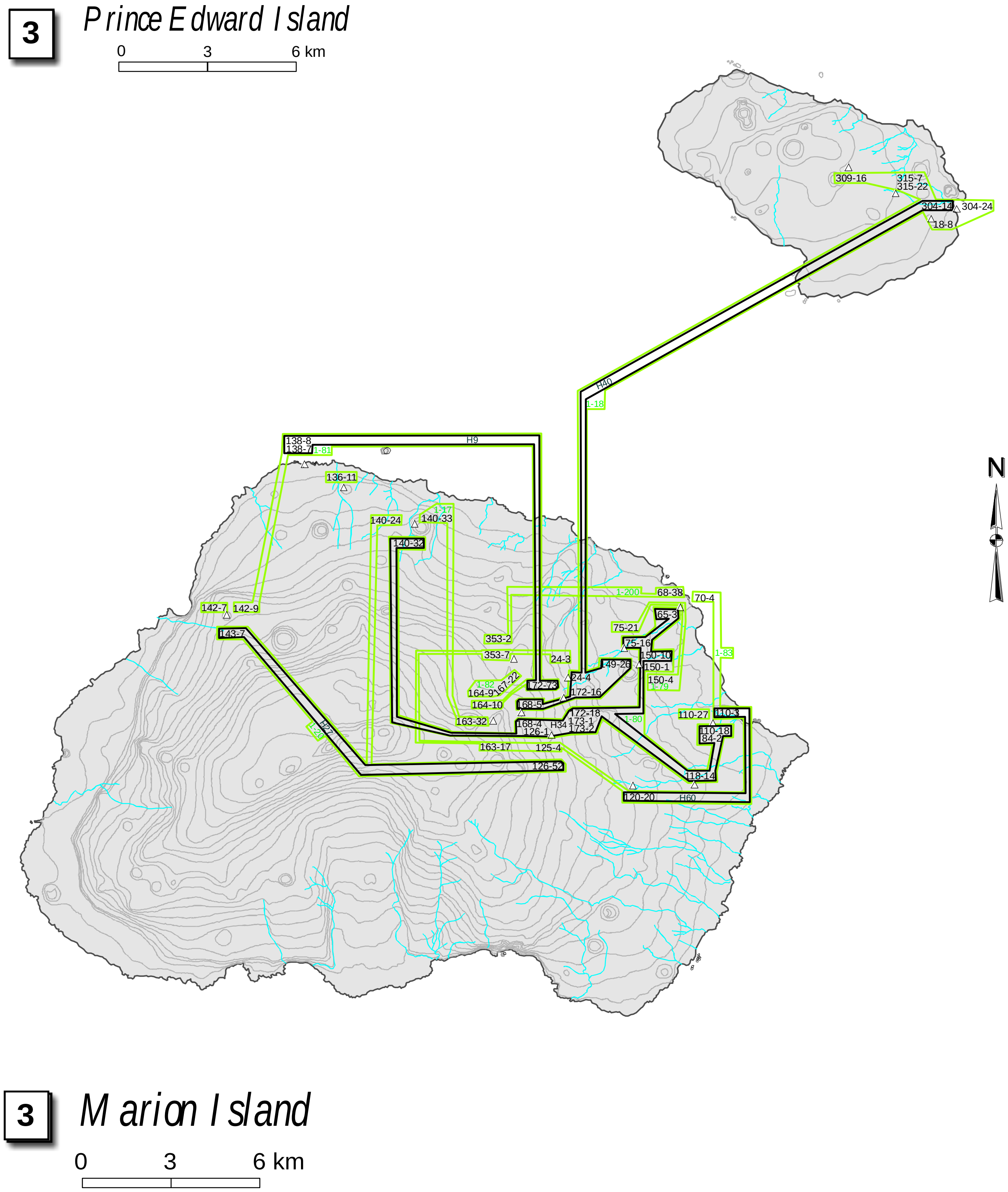
(a)


3
Prince Edward Island
0
3
6 km
309-16
315-7
315-22
304-14
304-24
18-8
138-8
138-7
136-11
140-24
140-33
140-32
142-7
142-9
143-7
68-38
70-4
65-3
75-21
75-16
150-10
150-1
150-4
149-26
353-2
353-7
24-3
24-4
167-22
172-73
172-16
164-9
164-10
168-5
163-32
168-4
126-1
172-18
173-1
173-2
163-17
125-4
126-52
110-27
110-3
110-18
84-2
118-14
120-20
N
3
Marion Island
0
3
6 km

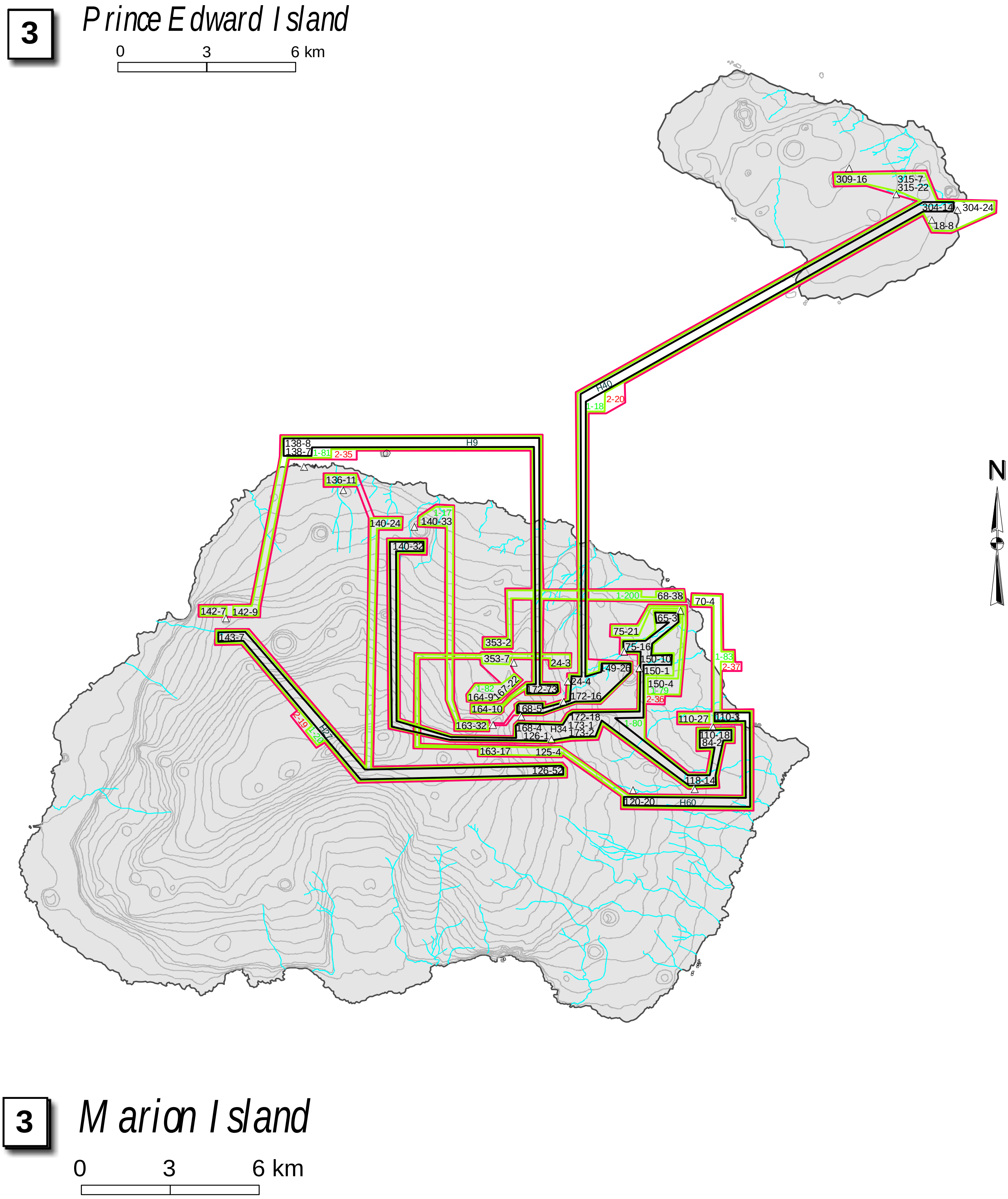
(b)


3
Prince Edward Island
0
3
6 km
309-16
315-7
315-22
304-14
304-24
18-8
H40
N
138-8
138-7
H9
136-11
140-24
140-33
140-32
68-38
70-4
65-3
142-7
142-9
143-7
75-21
75-16
353-2
353-7
24-3
150-10
150-1
149-26
150-4
24-4
172-73
167-22
164-9
172-16
164-10
168-5
172-18
110-27
110-3
163-32
168-4
H34
173-1
173-2
126-1
110-18
184-2
H27
163-17
125-4
126-52
118-14
120-20
H60
3
Marion Island
0
3
6 km

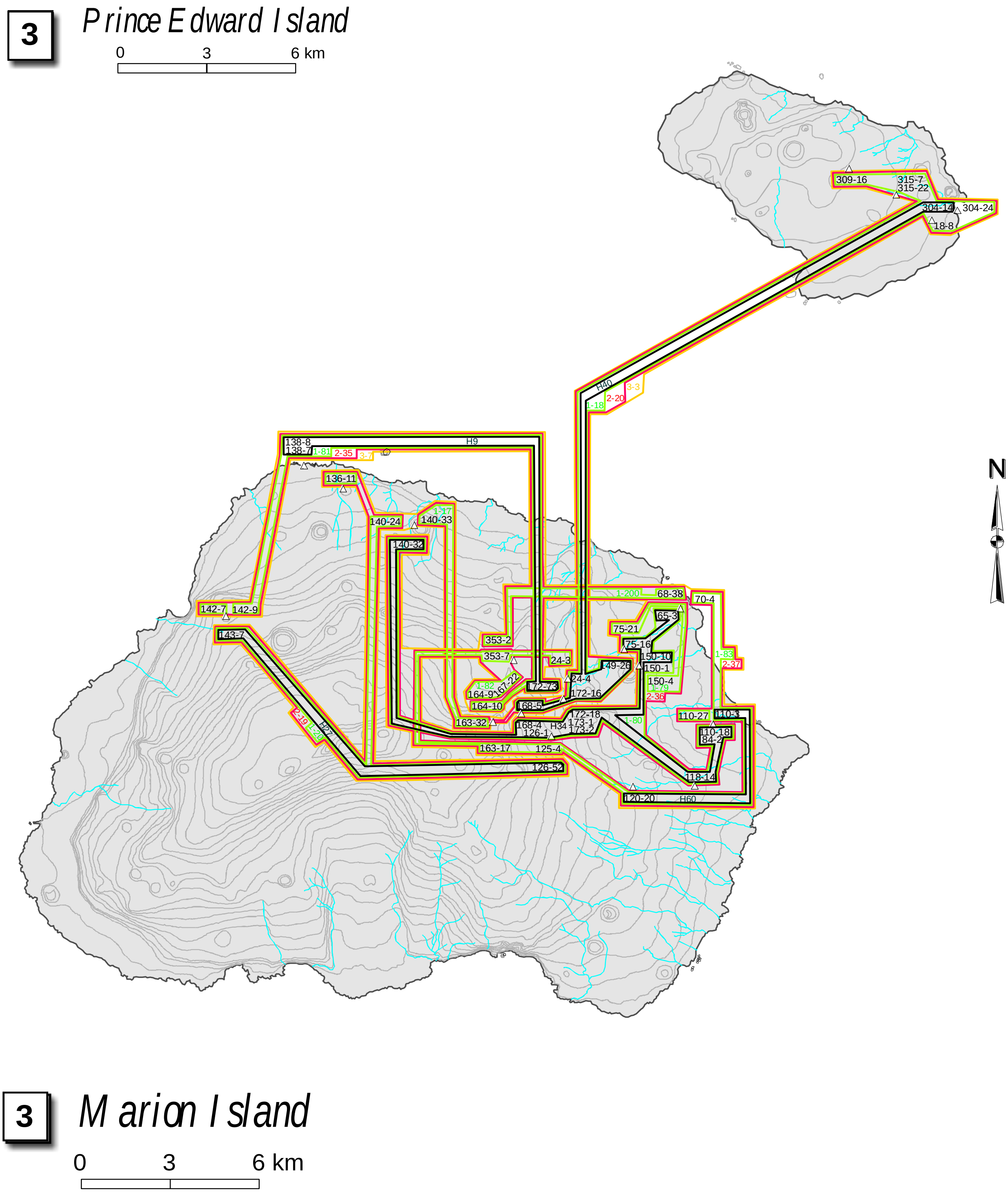
(c)


3
Prince Edward Island
0
3
6 km
309-16
315-7
315-22
304-14
304-24
18-8
H40
1-18
N
138-8
138-7
1-81
H9
136-11
140-24
1-17
140-33
140-32
142-7
142-9
143-7
H27
1-20
1-200
68-38
70-4
65-3
75-21
75-16
353-2
353-7
24-3
149-26
150-10
150-1
1-83
150-4
1-79
24-4
1-82
167-22
172-73
164-9
172-16
164-10
168-5
172-18
173-1
173-2
H34
168-4
126-1
163-32
1-80
110-27
110-3
110-18
84-2
163-17
125-4
126-52
118-14
120-20
H60
3
Marion Island
0
3
6 km

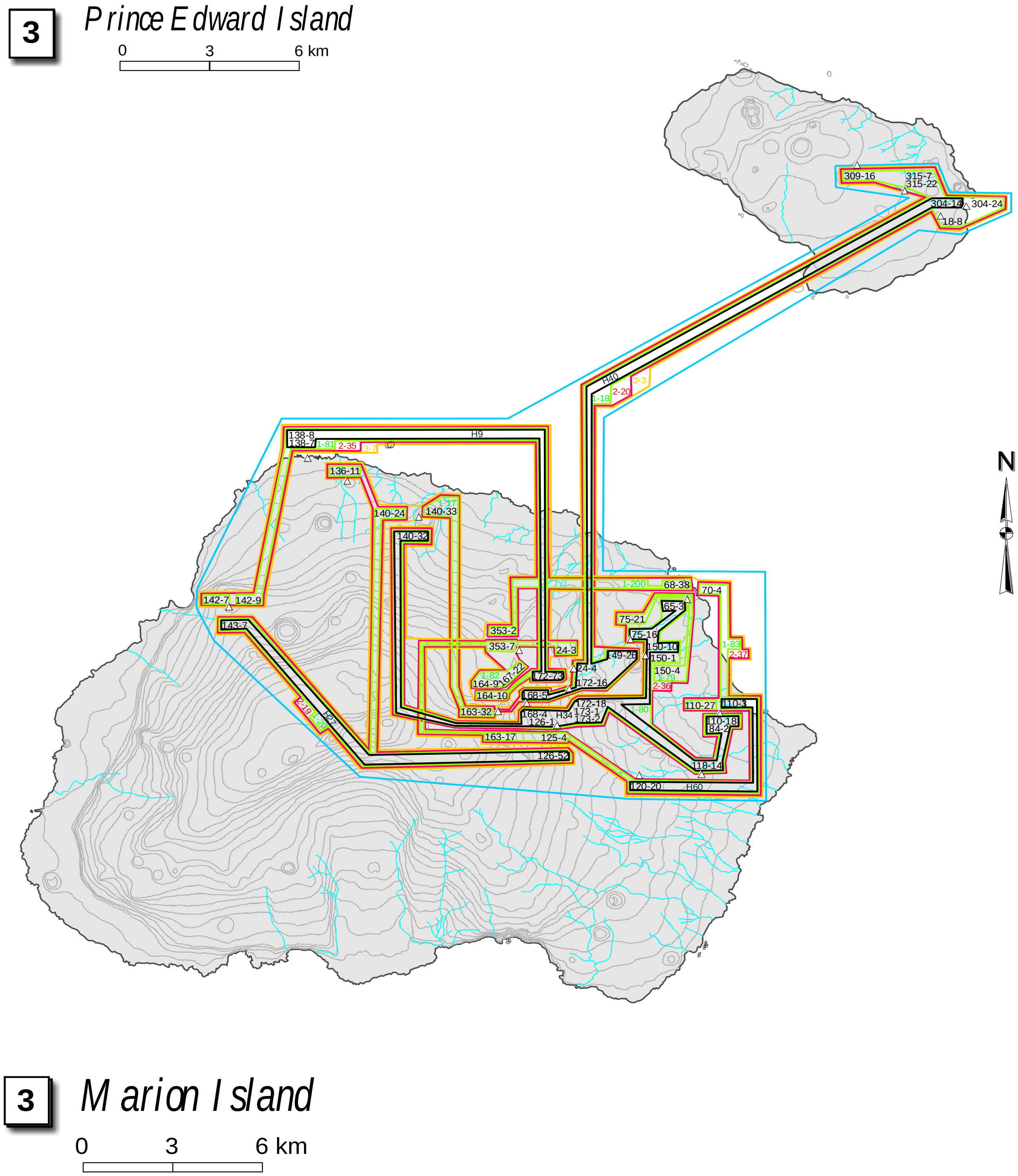
(d)


3
Prince Edward Island
0
3
6 km
309-16
315-7
315-22
304-14
304-24
18-8
H40
2-20
1-18
138-8
138-7
1-81
2-35
H9
136-11
140-24
1-17
140-33
140-32
142-7
142-9
143-7
1-200
68-38
70-4
65-3
75-21
75-16
353-2
353-7
24-3
149-26
150-10
150-1
1-83
2-37
150-4
1-79
2-36
24-4
172-16
172-73
1-82
164-9
167-22
164-10
168-5
163-32
172-18
173-1
173-2
168-4
H34
126-1
1-80
110-27
110-3
110-18
84-2
2-19
1-20
H27
163-17
125-4
126-52
118-14
120-20
H60
N
3
Marion Island
0
3
6 km

(e)


3
Prince Edward Island
0
3
6 km
309-16
315-7
315-22
304-14
304-24
18-8
H40
3-3
2-20
1-18
138-8
138-7
1-81
2-35
H9
136-11
140-24
140-33
1-17
140-32
142-7
142-9
143-7
2-19
1-21
H27
1-200
68-38
70-4
65-3
75-21
75-16
353-2
353-7
24-3
49-26
150-10
150-1
150-4
1-79
2-36
1-83
2-37
1-82
164-9
167-22
172-73
24-4
172-16
164-10
168-5
163-32
168-4
H34
126-1
172-18
173-1
173-2
1-80
110-27
110-3
110-18
84-2
163-17
125-4
126-52
118-14
120-20
H60
N
3
Marion Island
0
3
6 km

(f)



(g)

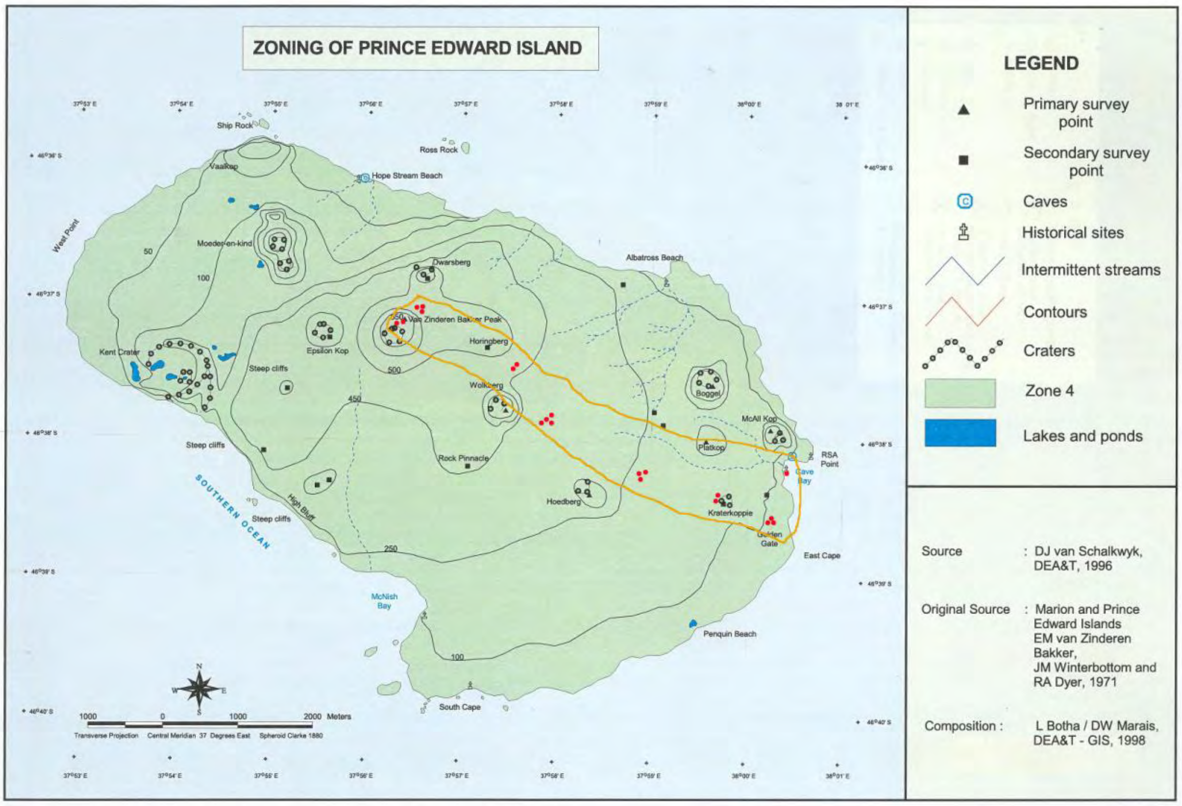
Fig. 11 *Ectemnorhinus* individuals that group into 4-step clade 4-3 mapped onto the islands according to a) sampling localities with place names for references, samples on Marion Island are indicated in green while those on Prince Edward Island are indicated in red b) sampling localities as used in the nested design c) those that share the same haplotypes nested into 0-step clades, the d) 1-step clades, e) 2-step clades f) 3 step clades and finally g) the complete 4-3 clade as depicted in Fig. 5.

MARION ISLAND WITH MANAGEMENT ZONES

Amendments:
C. Hänel
University of Pretoria
1998

Original Source:
Langenegger &
Verwoerd
1965

Map Composition:
D.W. Marais
DEA&T - GIS
1998



ZONING OF PRINCE EDWARD ISLAND

Source : DJ van Schalkwyk, DEA&T, 1996

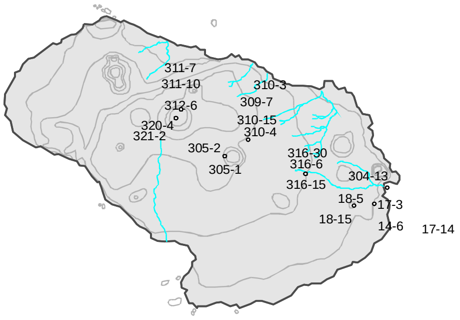
Original Source : Marion and Prince Edward Islands EM van Zinderen Bakker, JM Winterbottom and RA Dyer, 1971

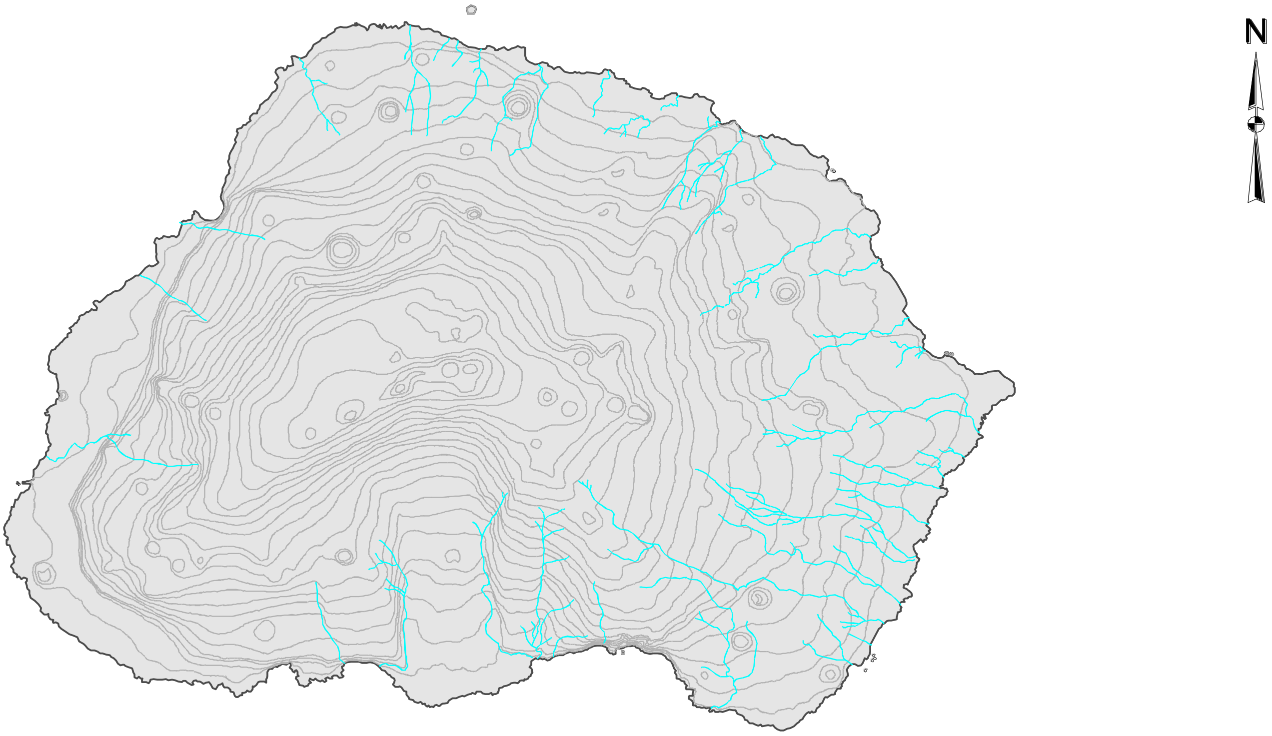
Composition : L Botha / DW Marais, DEA&T - GIS, 1998

(a)

4 *Prince Edward Island*

0 3 6 km

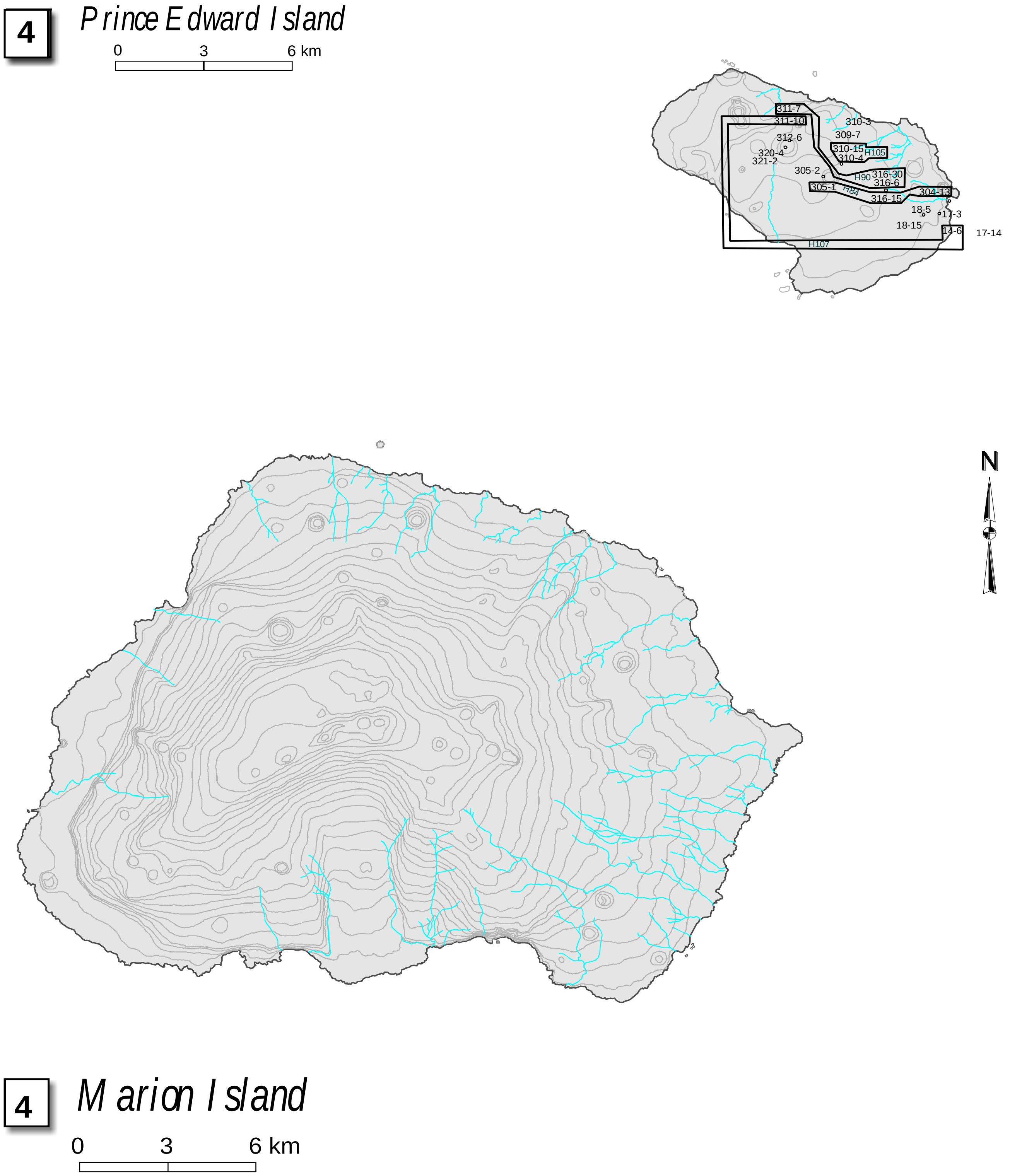




4 *Marion Island*

0 3 6 km

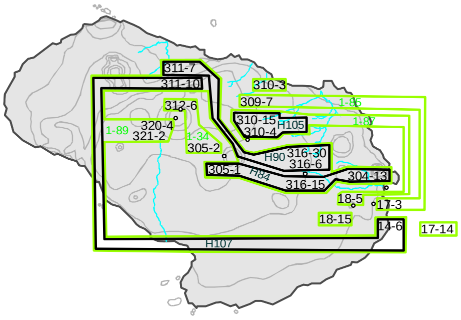
(b)

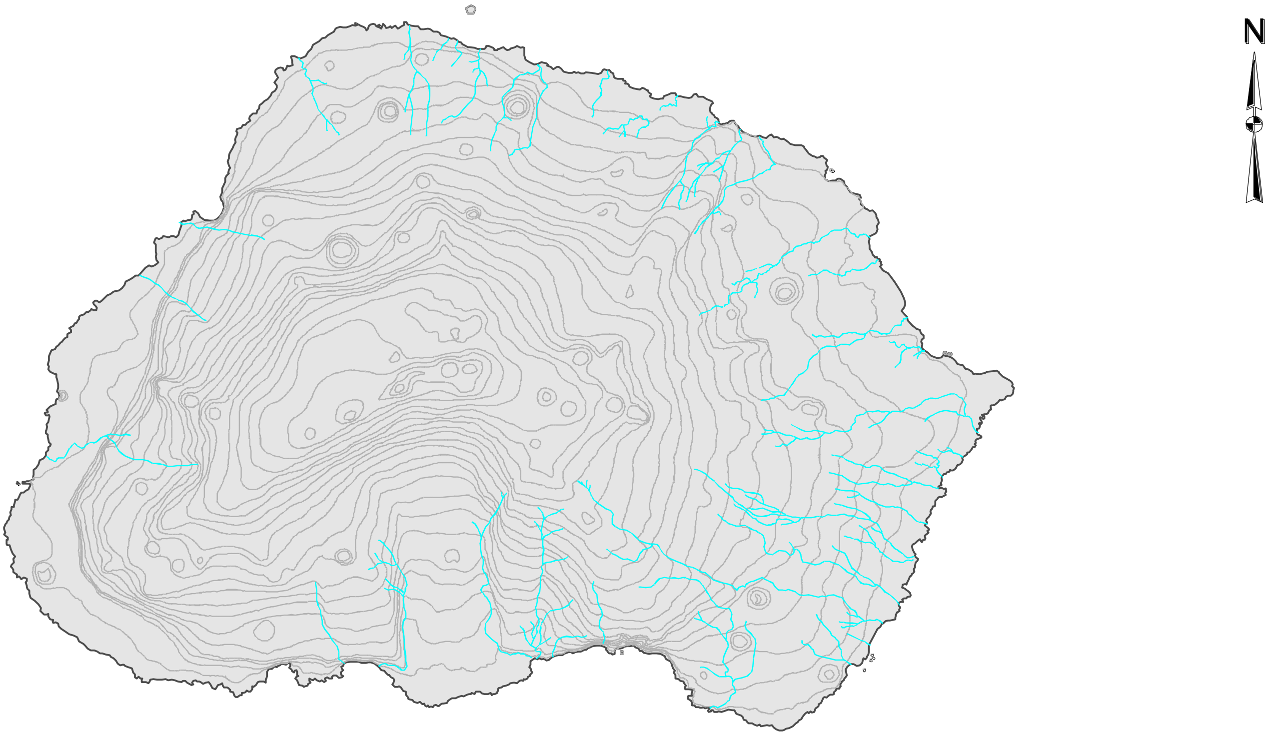

4
Prince Edward Island
0
3
6 km
311-7
311-10
310-3
309-7
312-6
320-4
321-2
310-15
H105
310-4
305-2
H90
316-30
316-6
305-1
H84
304-13
316-15
18-5
17-3
18-15
14-6
17-14
H107
N
4
Marion Island
0
3
6 km

(c)

4 *Prince Edward Island*

0 3 6 km

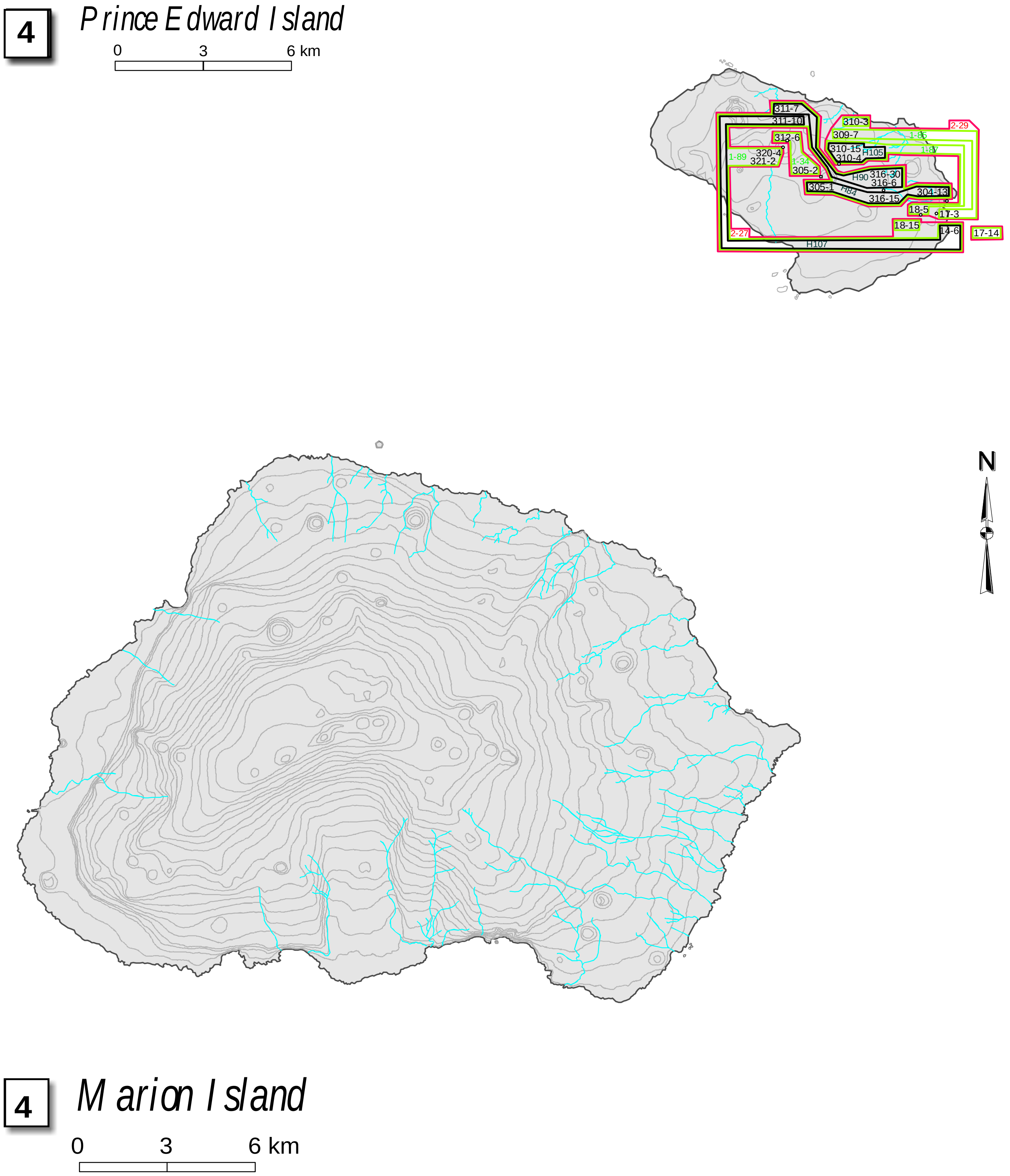




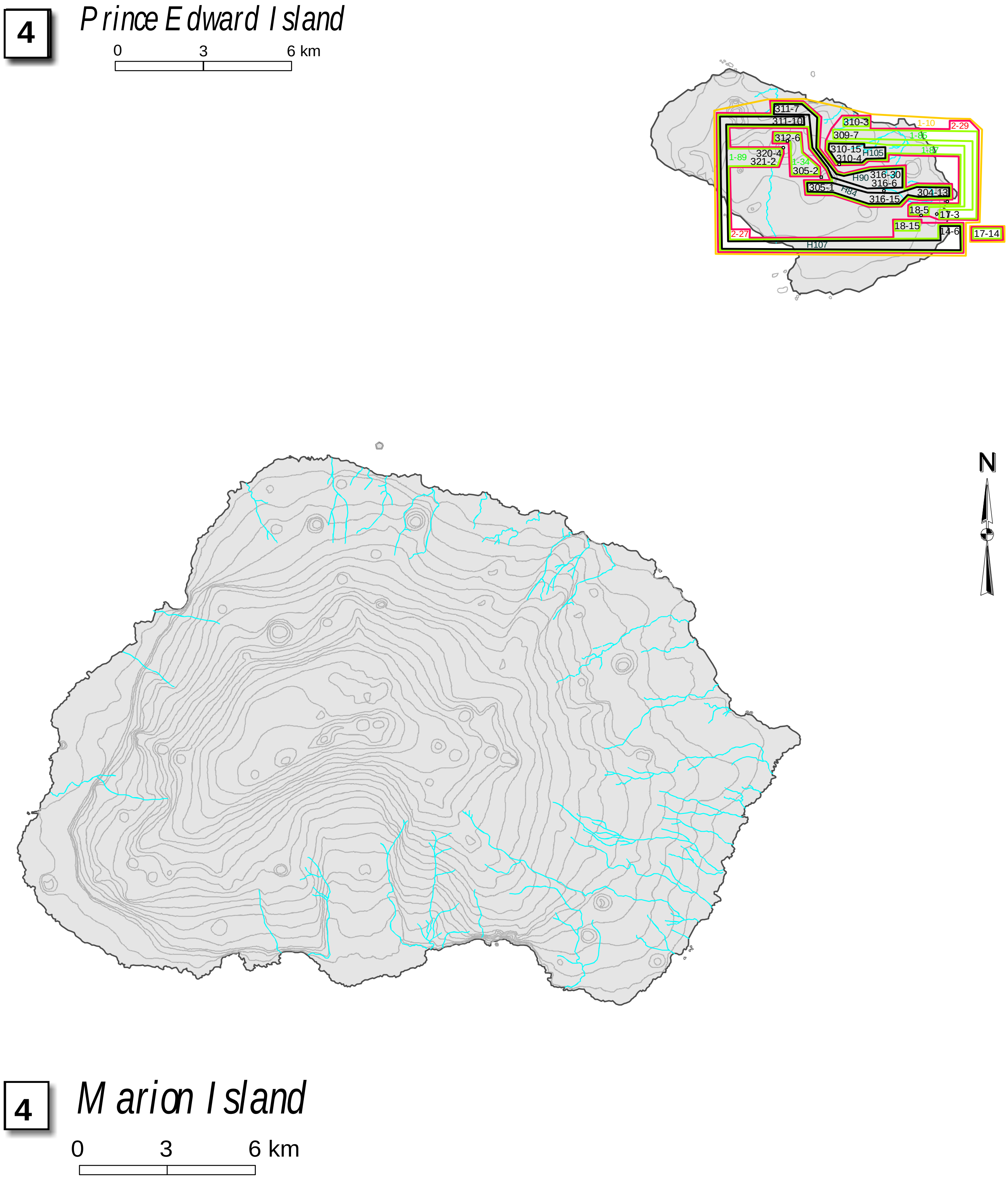
4 *Marion Island*

0 3 6 km

(d)


4
Prince Edward Island
0
3
6 km
311-7
311-10
310-3
2-29
309-7
1-85
312-6
1-89
320-4
321-2
1-34
305-2
310-15
H105
310-4
1-87
H90
316-30
316-6
305-1
H84
316-15
304-13
18-5
17-3
18-15
14-6
17-14
2-27
H107
N
4
Marion Island
0
3
6 km

(e)


4
Prince Edward Island
0
3
6 km
311-7
311-10
310-3
1-10
2-29
309-7
1-85
312-6
310-15
H105
1-87
320-4
1-89
321-2
310-4
1-34
305-2
H90
316-30
316-6
305-1
H84
304-13
316-15
18-5
17-3
18-15
14-6
17-14
2-27
H107
N
4
Marion Island
0
3
6 km

(f)

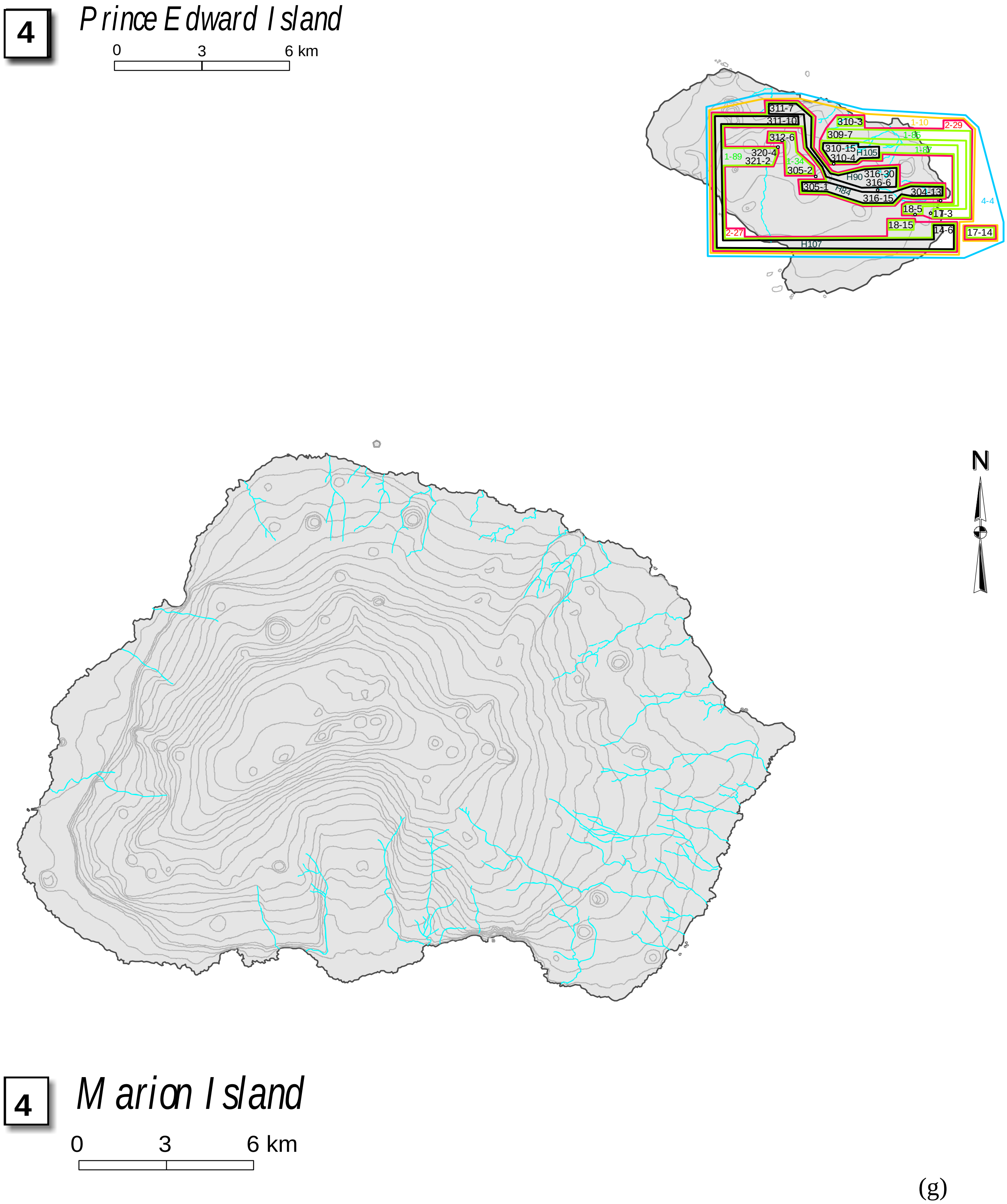
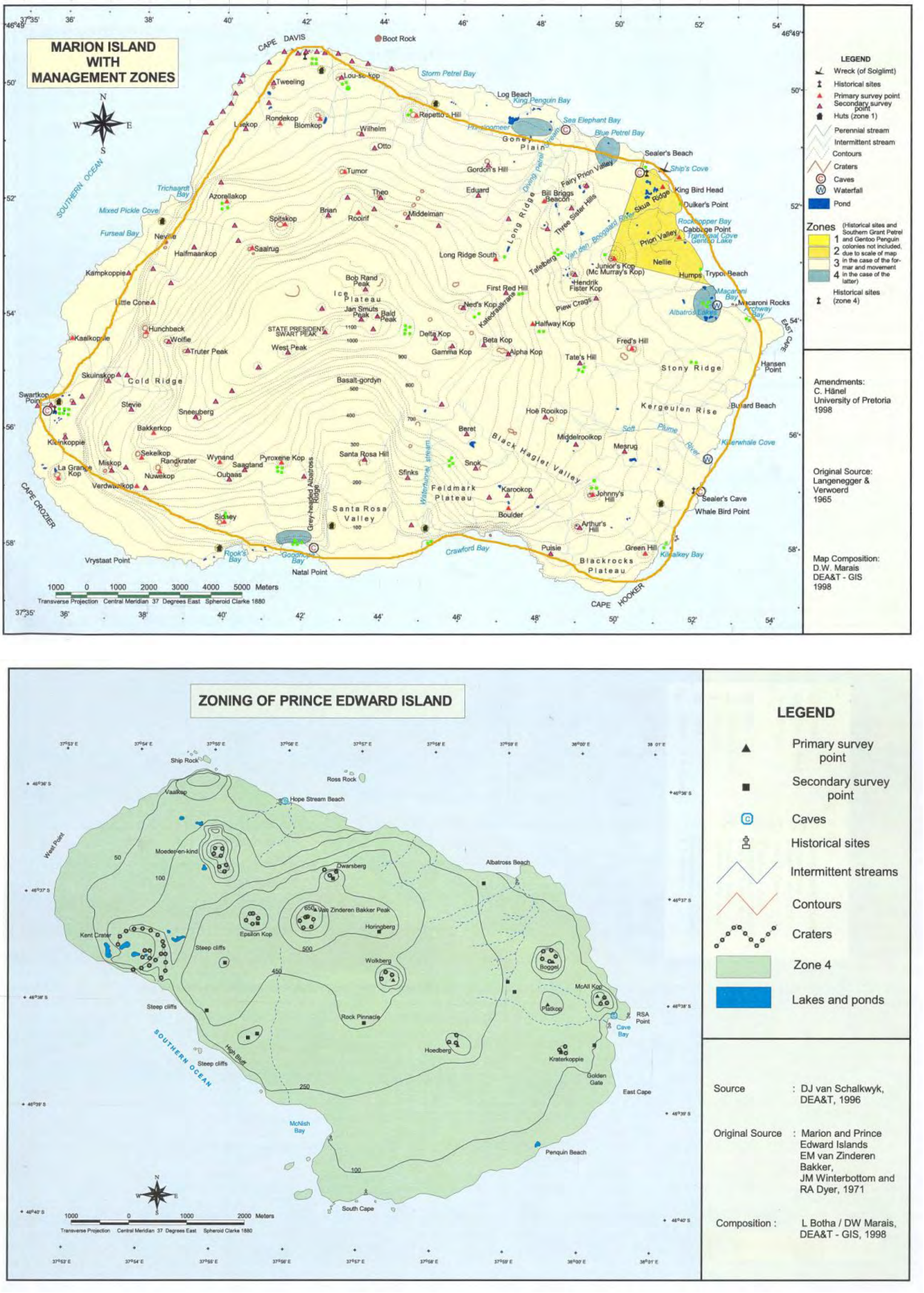


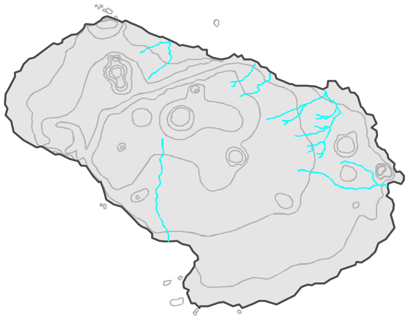
Fig. 12 *Ectemnorhinus* individuals that group into 4-step clade 4-4 mapped onto the islands according to a) sampling localities with place names for references, samples on Marion Island are indicated in green while those on Prince Edward Island are indicated in red b) sampling localities as used in the nested design c) those that share the same haplotypes nested into 0-step clades, the d) 1-step clades, e) 2-step clades f) 3 step clades and finally g) the complete 4-4 clade as depicted in Fig. 5.

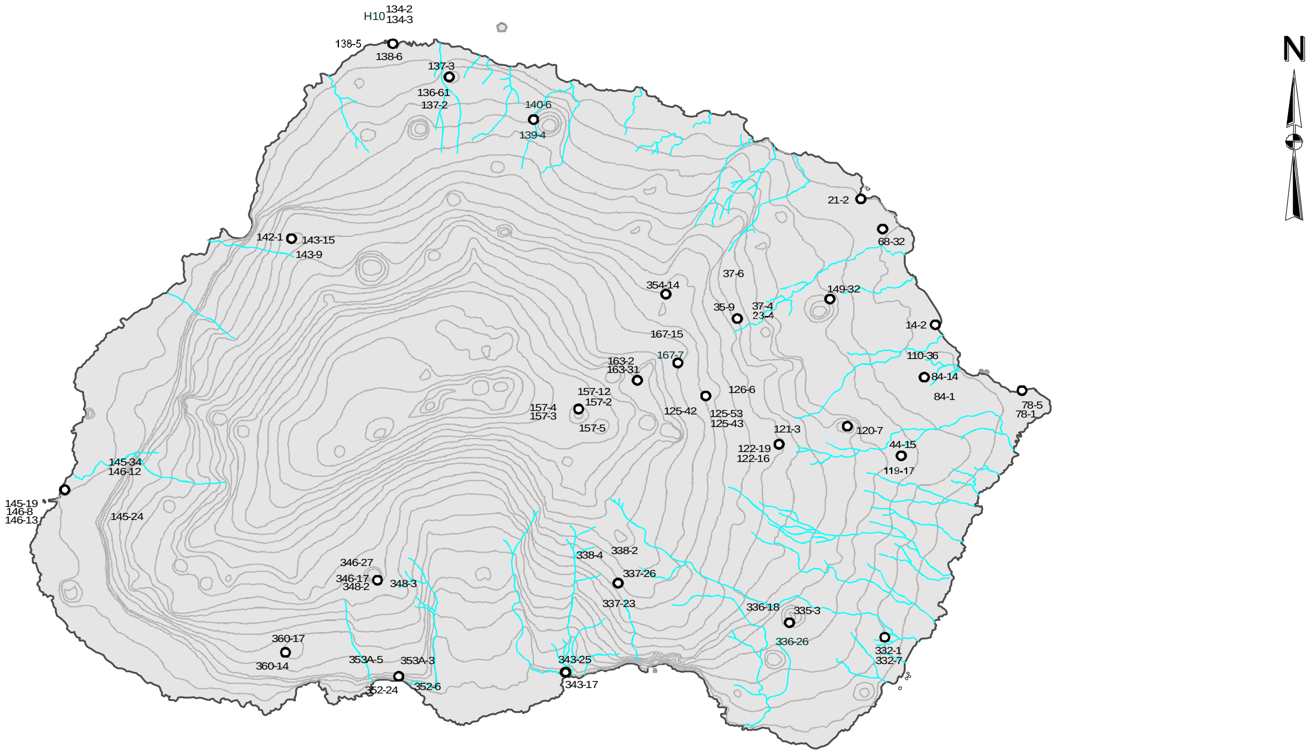

MARION ISLAND WITH MANAGEMENT ZONES
LEGEND
Wreck (of Solglimt)
Historical sites
Primary survey point
Secondary survey point
Huts (zone 1)
Perennial stream
Intermittent stream
Contours
Craters
Caves
Waterfall
Pond
Zones
1
2
3
4
(Historical sites and Southern Grant Petrel and Gentoo Penguin colonies not included, due to scale of map in the case of the formar and movement in the case of the latter)
Historical sites (zone 4)
Amendments: C. Hänel University of Pretoria 1998
Original Source: Langenegger & Verwoerd 1965
Map Composition: D.W. Marais DEA&T - GIS 1998
CAPE DAVIS
Boot Rock
Storm Petrel Bay
Log Beach
King Penguin Bay
Sea Elephant Bay
Blue Petrel Bay
Sealer's Beach
Ship's Cove
King Bird Head
Duiker's Point
Rockhopper Bay
Cabbage Point
Transvaal Cove
Gentoo Lake
Nellie
Trypot Beach
Macaroni Bay
Macaroni Rocks
Archway Bay
EAST CAPE
Hansen Point
Bullard Beach
Killerwhale Cove
Sealer's Cave
Whale Bird Point
Killalkey Bay
Green Hill
Blackrocks Plateau
CAPE HOOKER
Crawford Bay
Natal Point
Goodhope Bay
Rook's Bay
Vrystaat Point
CAPE CROZIER
Swartkop Point
SOUTHERN OCEAN
Trichardt Bay
Mixed Pickle Cove
Furseal Bay
Ice Plateau
STATE PRESIDENT SWART PEAK
Santa Rosa Valley
Feldmark Plateau
Black Haglet Valley
Kerguelen Rise
Stony Ridge
Long Ridge
Goney Plain
Cold Ridge
Grey-headed Albatross Ridge
1000 0 1000 2000 3000 4000 5000 Meters
Transverse Projection Central Meridian 37 Degrees East Spheroid Clarke 1880
ZONING OF PRINCE EDWARD ISLAND
LEGEND
Primary survey point
Secondary survey point
Caves
Historical sites
Intermittent streams
Contours
Craters
Zone 4
Lakes and ponds
Source : DJ van Schalkwyk, DEA&T, 1996
Original Source : Marion and Prince Edward Islands EM van Zinderen Bakker, JM Winterbottom and RA Dyer, 1971
Composition : L Botha / DW Marais, DEA&T - GIS, 1998
Ship Rock
Ross Rock
Hope Stream Beach
Vaalkop
West Point
Moeder-en-kind
Albatross Beach
Dwarsberg
Van Zinderen Bakker Peak
Horingberg
Epsilon Kop
Kent Crater
Steep cliffs
Wolkberg
Boggel
McAll Kop
Platkop
RSA Point
Cave Bay
Rock Pinnacle
Hoedberg
Kraterkoppie
Golden Gate
East Cape
High Bluff
SOUTHERN OCEAN
McNish Bay
Penguin Beach
South Cape
1000 0 1000 2000 Meters
Transverse Projection Central Meridian 37 Degrees East Spheroid Clarke 1880

(a)

5 Prince Edward Island

0 3 6 km



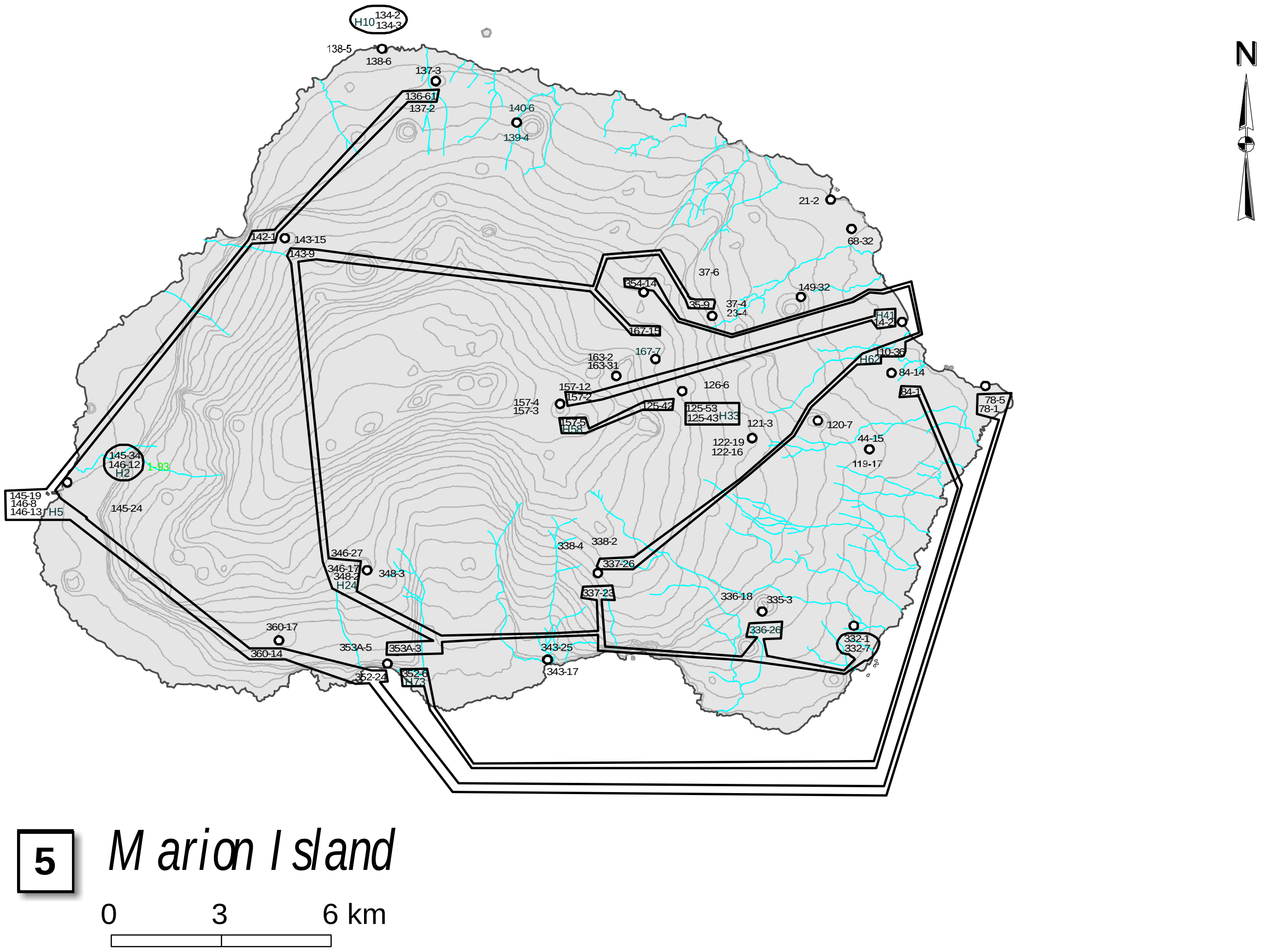


5 Marion Island

0 3 6 km

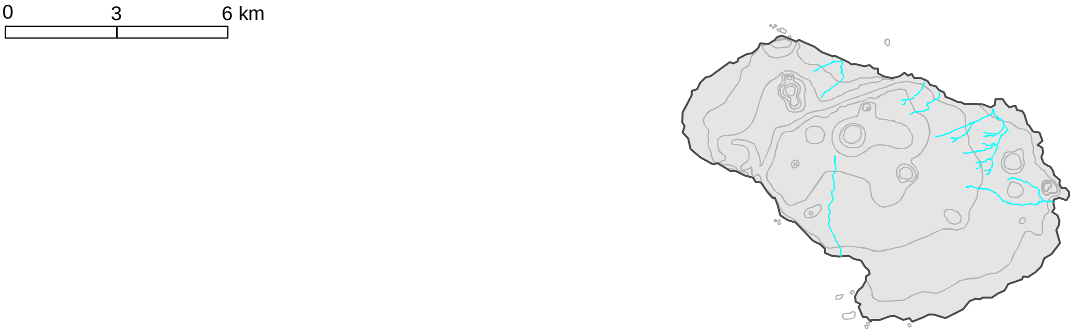
(b)

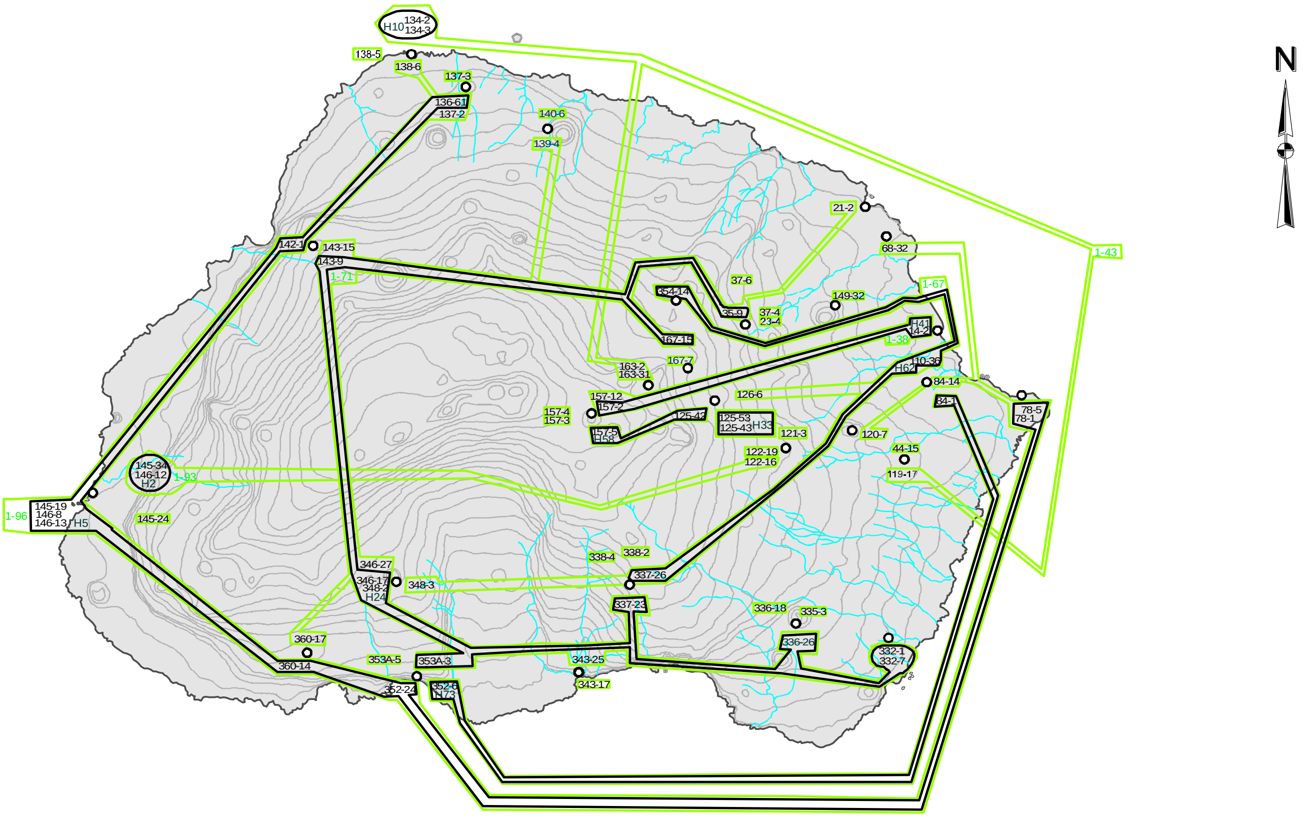

5
Prince Edward Island
0
3
6 km


N
H10
134-2
134-3
138-5
138-6
137-3
136-61
137-2
140-6
139-4
21-2
68-32
142-1
143-15
143-9
37-6
354-14
149-32
35-9
37-4
23-4
H41
14-2
167-15
167-7
163-2
163-31
110-36
H62
84-14
157-12
157-2
126-6
84-1
78-5
78-1
157-4
157-3
125-42
125-53
125-43
H33
157-5
H58
121-3
120-7
122-19
122-16
44-15
119-17
145-34
146-12
H2
1-93
145-19
146-8
146-13
H5
145-24
338-2
338-4
337-26
346-27
346-17
348-2
H24
348-3
337-23
336-18
335-3
336-26
360-17
360-14
353A-5
353A-3
343-25
343-17
332-1
332-7
352-24
352-6
H73
5
Marion Island
0
3
6 km

(c)

5 *Prince Edward Island*





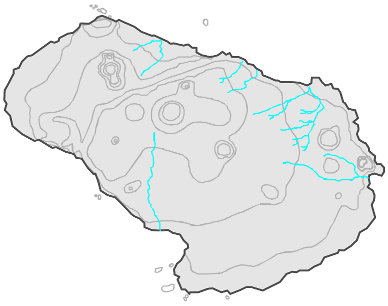
5 *Marion Island*

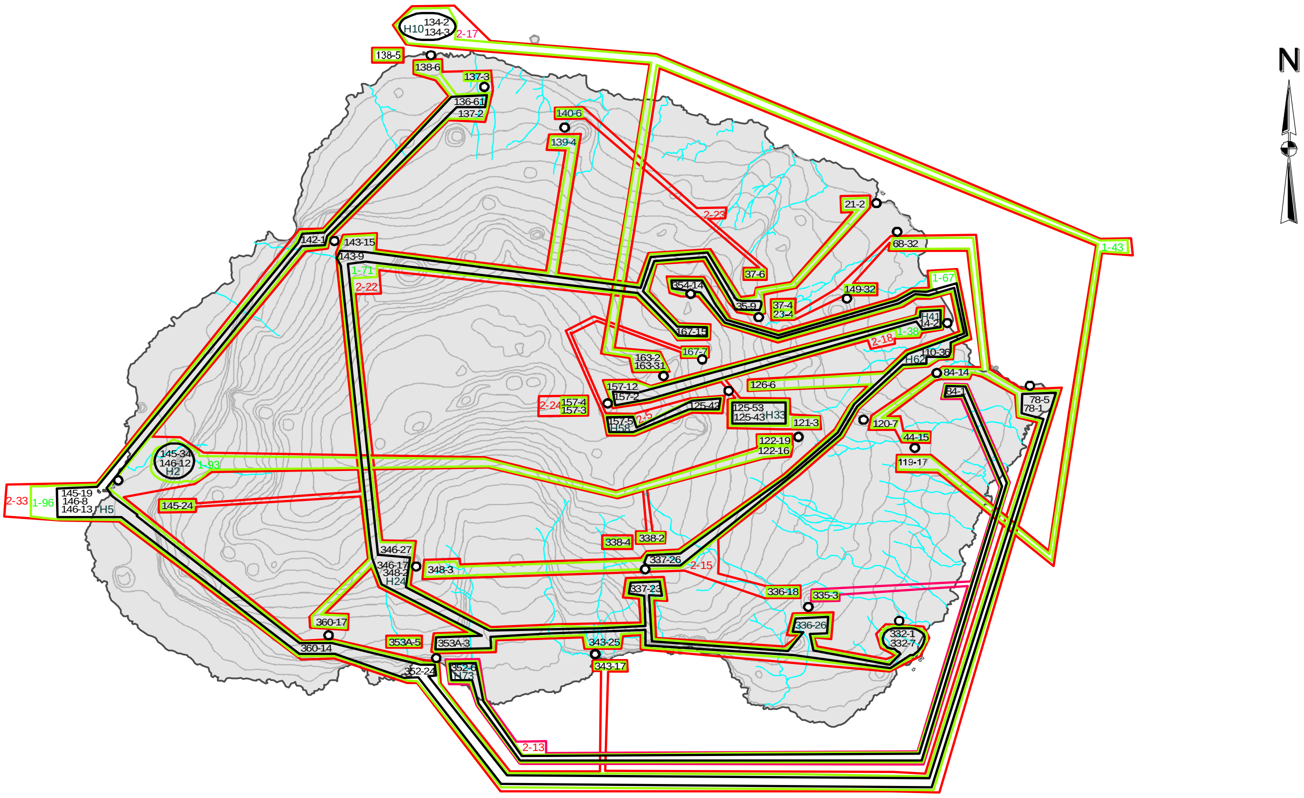
0 3 6 km

(d)

5 *Prince Edward Island*

0 3 6 km

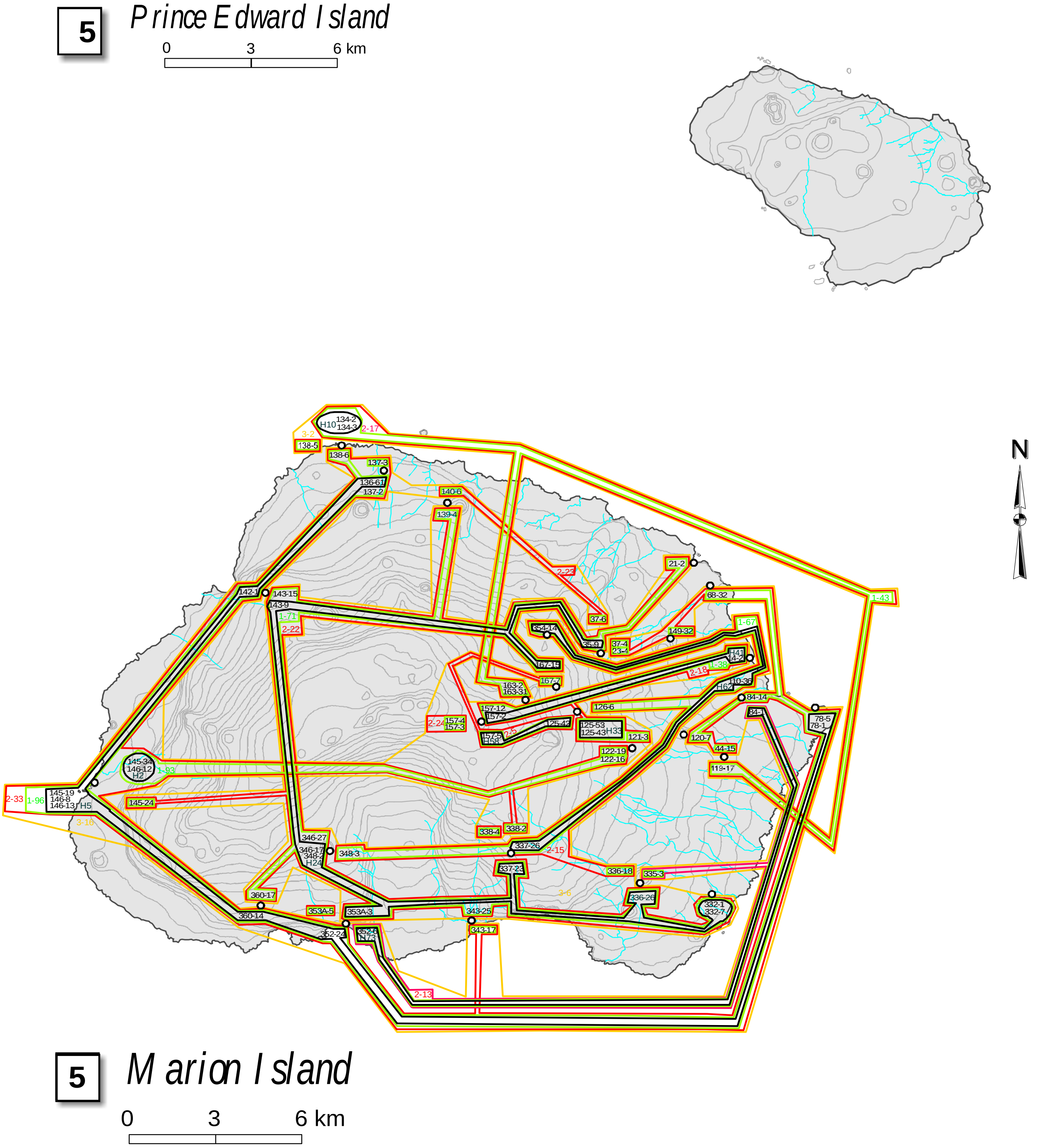




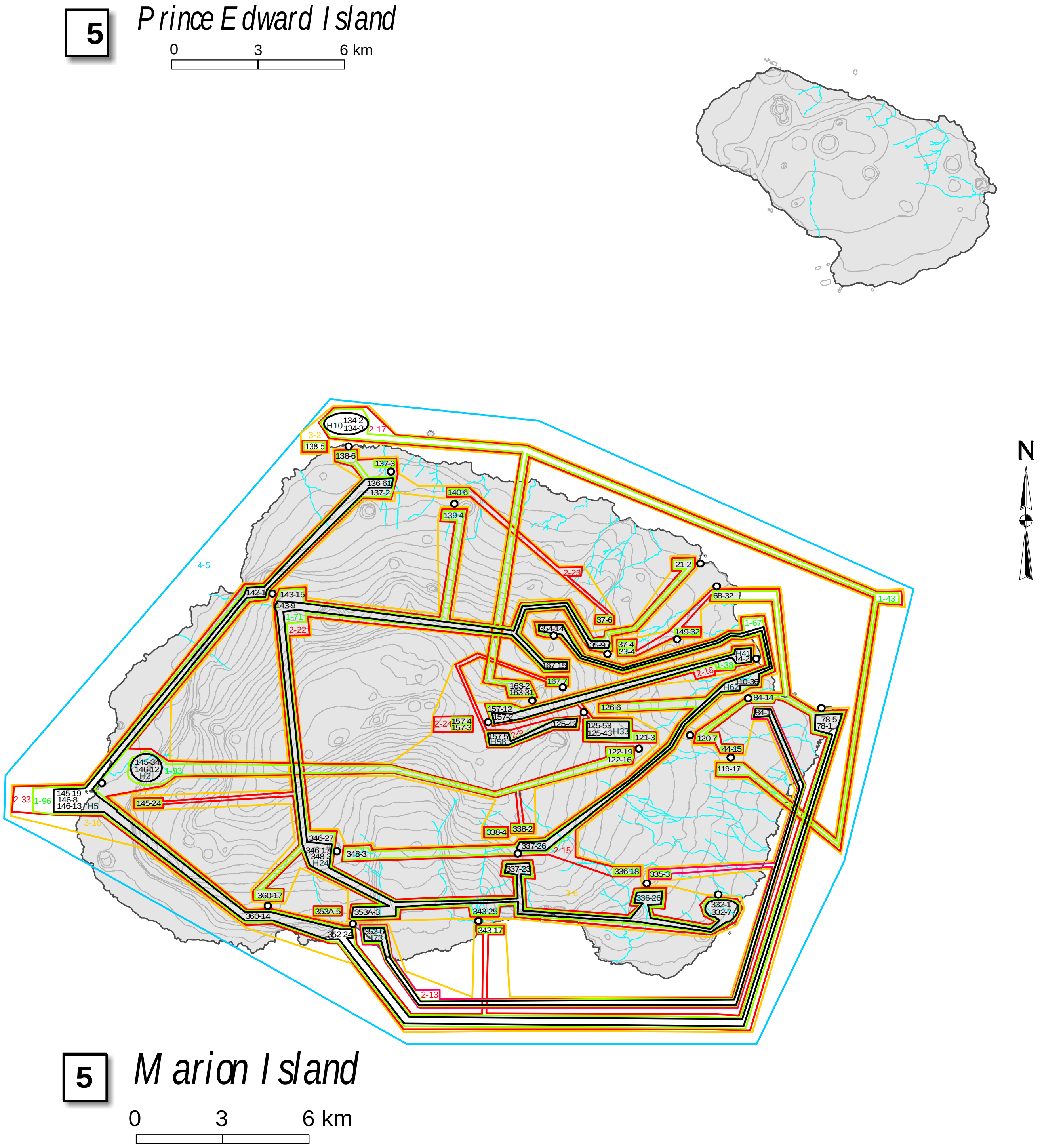
5 *Marion Island*

0 3 6 km

(e)


5
Prince Edward Island
0
3
6 km
N
H10
134-2
134-3
2-17
3-2
138-5
138-6
137-3
136-61
137-2
140-6
139-4
2-23
21-2
68-32
1-43
142-1
143-15
143-9
1-71
2-22
37-6
354-14
149-32
1-67
35-9
37-4
23-4
H41
14-2
2-18
1-39
167-15
167-7
163-2
163-31
H62
110-36
84-14
126-6
157-12
157-2
2-24
157-4
157-3
125-42
84-1
78-5
78-1
157-8
H58
2-5
125-53
125-43
H33
121-3
120-7
122-19
122-16
44-15
145-34
146-12
H2
1-93
119-17
2-33
1-96
145-19
146-8
146-13
H5
145-24
3-10
338-4
338-2
346-27
337-26
2-15
346-17
348-4
H24
348-3
337-23
336-18
335-3
3-6
360-17
336-26
332-1
332-7
353A-5
353A-3
343-25
360-14
352-24
352-6
H72
343-17
2-13
5
Marion Island
0
3
6 km

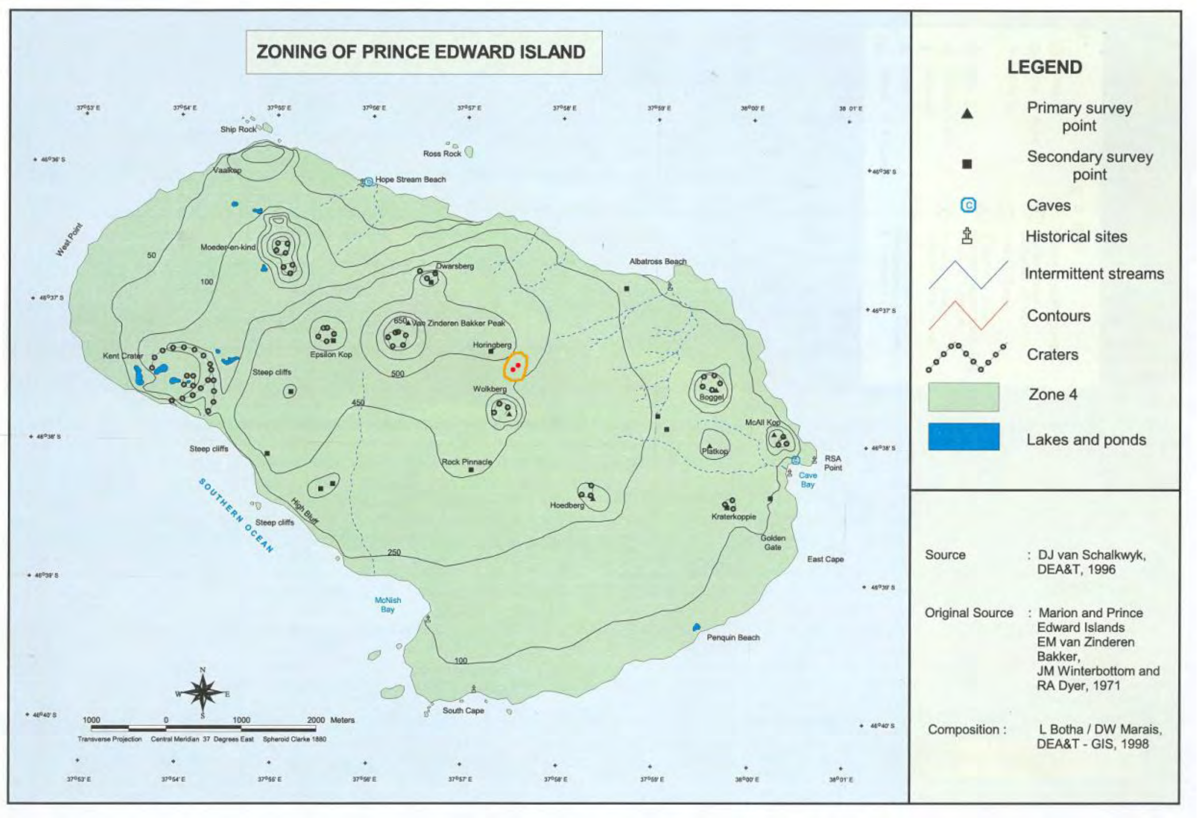
(f)



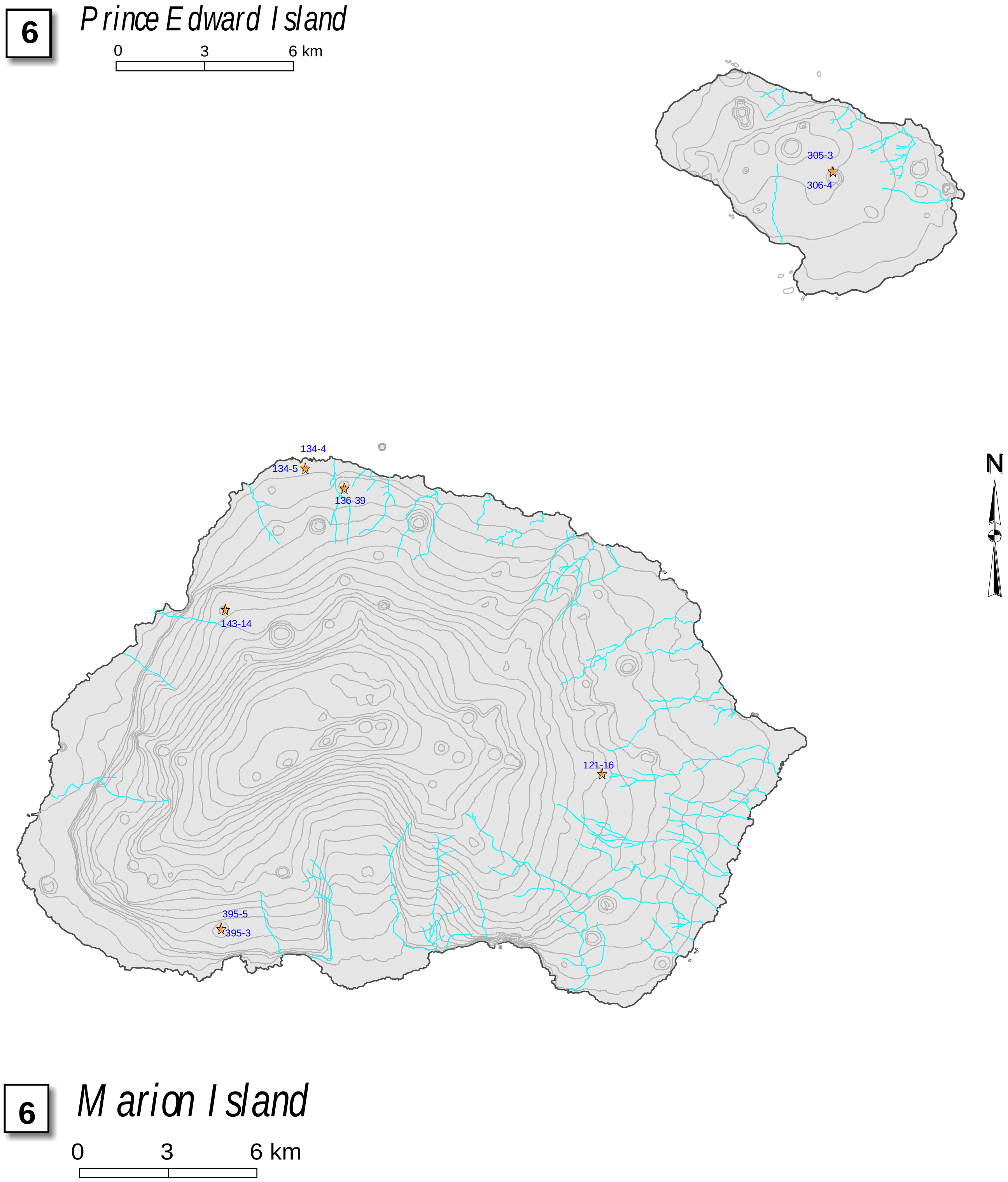
(g)

Fig. 13 *Ectemnorhinus* individuals that group into 4-step clade 4-5 mapped onto the islands according to a) sampling localities with place names for references, samples on Marion Island are indicated in green while those on Prince Edward Island are indicated in red b) sampling localities as used in the nested design c) those that share the same haplotypes nested into 0-step clades, the d) 1-step clades, e) 2-step clades f) 3 step clades and finally g) the complete 4-5 clade as depicted in Fig. 5.

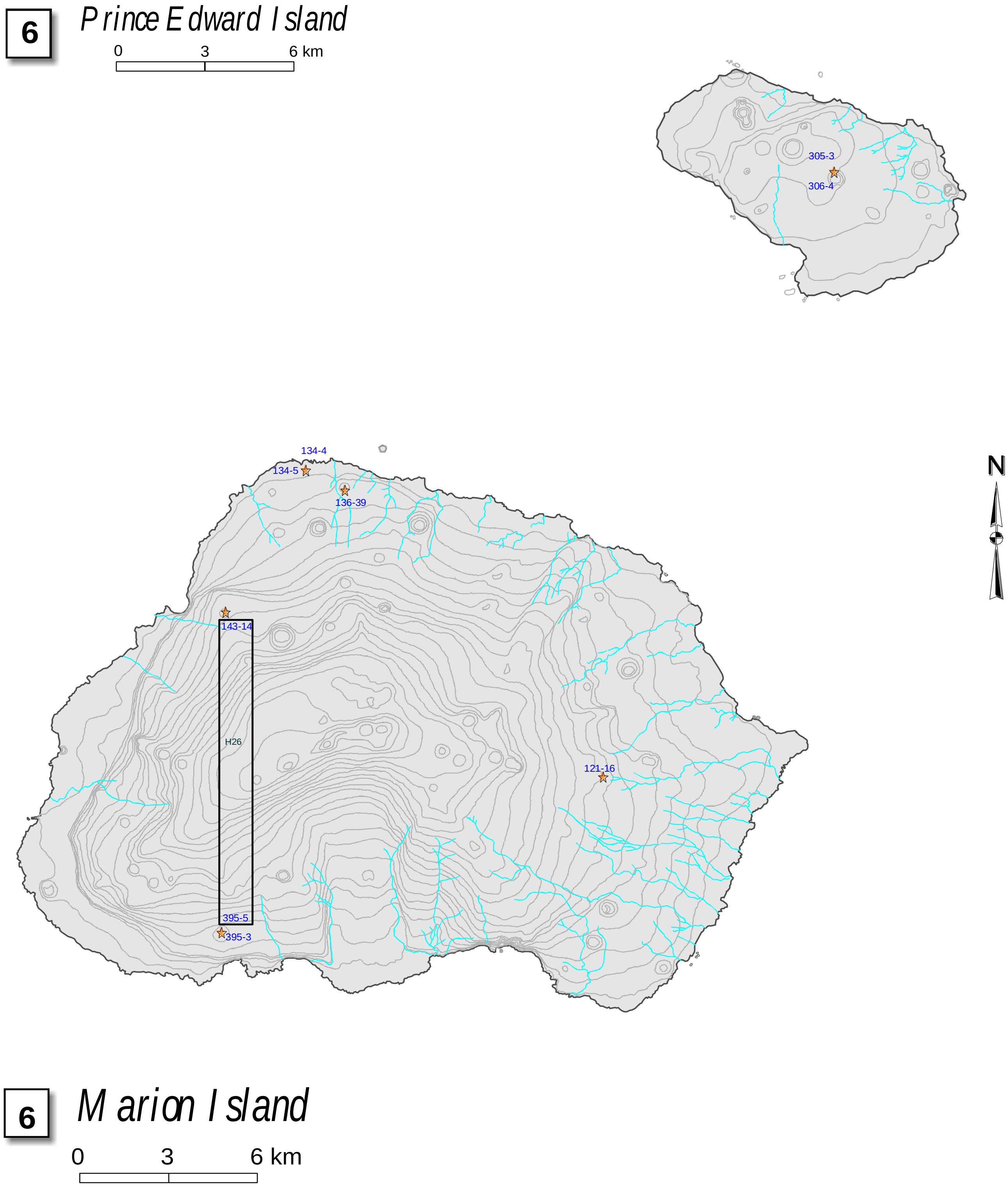

MARION ISLAND WITH MANAGEMENT ZONES
LEGEND
Wreck (of Solglimt)
Historical sites
Primary survey point
Secondary survey point
Huts (zone 1)
Perennial stream
Intermittent stream
Contours
Craters
Caves
Waterfall
Pond
Zones
1
2
3
4
(Historical sites and Southern Grant Petrel and Gentoo Penguin colonies not included, due to scale of map in the case of the former and movement in the case of the latter)
Historical sites (zone 4)
Amendments: C. Hänel University of Pretoria 1998
Original Source: Langenegger & Verwoerd 1965
Map Composition: D.W. Marais DEA&T - GIS 1998
CAPE DAVIS
Boot Rock
Storm Petrel Bay
Log Beach
King Penguin Bay
Sea Elephant Bay
Blue Petrel Bay
Sealer's Beach
Ship's Cove
King Bird Head
Duiker's Point
Rockhopper Bay
Cabbage Point
Transvaal Cove
Gentoo Lake
Prion Valley
Nellie
Humps
Trypot Beach
Macaroni Bay
Macaroni Rocks
Archway Bay
EAST CAPE
Hansen Point
Stony Ridge
Bullard Beach
Kergeulen Rise
Killerwhale Cove
Sealer's Cave
Whale Bird Point
Kildalkey Bay
Green Hill
Blackrocks Plateau
CAPE HOOKER
Crawford Bay
Natal Point
Goodhope Bay
Rook's Bay
Vrystaat Point
CAPE CROZIER
Swartkop Point
Kaalkoppie
Kampkoppie
Furseal Bay
Mixed Pickle Cove
Trichaardt Bay
SOUTHERN OCEAN
Ice Plateau
STATE PRESIDENT SWART PEAK
Feldmark Plateau
Santa Rosa Valley
Black Haglet Valley
Long Ridge
Goney Plain
Cold Ridge
Tweeling
Rondekop
Blomkop
Wilhelm
Otto
Repetto's Hill
Tumor
Theo
Middelman
Spitskop
Saalrug
Bob Rand Peak
Jan Smuts Peak
Bald Peak
West Peak
Delta Kop
Beta Kop
Alpha Kop
Tate Hill
Hoë Rugkop
Basalt-gordyn
Santa Rosa Hill
Pyroxene Kop
Sfinks
Snok
Karookop
Boulder
Johnny's Hill
Arthur's Hill
Pulsie
Fred's Hill
Mesrug
Middelrooikop
Sneeuberg
Stevie
Bakkerkop
Kleinkoppie
Sekelkop
Randkrater
Wynand
Saagtand
Oubaas
Nuwekop
Miskop
La Grange Kop
Verdwaalkop
Skuinskop
Little Cone
Hunchback
Wolfie
Truter Peak
Halfmaankop
Neville
Azorellakop
Long Ridge South
First Red Hill
Ned's Kop
Halfway Kop
Piew Crags
Hendrik Fister Kop
Junior's Kop (Mc Murray's Kop)
Tafelberg
Bill Briggs Beacon
Three Sister Hills
Fairy Prion Valley
Skua Ridge
Grey-headed Albatross Ridge
Waterfunnel stream
Gordon's Hill
Eduard
Brian
Rooirif
Prinsloomeer
Albatross Lakes
Meters
Transverse Projection Central Meridian 37 Degrees East Spheroid Clarke 1880


ZONING OF PRINCE EDWARD ISLAND
LEGEND
Primary survey point
Secondary survey point
Caves
Historical sites
Intermittent streams
Contours
Craters
Zone 4
Lakes and ponds
Source : DJ van Schalkwyk, DEA&T, 1996
Original Source : Marion and Prince Edward Islands EM van Zinderen Bakker, JM Winterbottom and RA Dyer, 1971
Composition : L Botha / DW Marais, DEA&T - GIS, 1998
Ship Rock
Ross Rock
Hope Stream Beach
Vaalkop
West Point
Moeder-en-kind
Dwarsberg
Albatross Beach
Van Zinderen Bakker Peak
Epsilon Kop
Horingberg
Kent Crater
Steep cliffs
Wolkberg
Boggel
McAll Kop
Platkop
RSA Point
Cave Bay
Rock Pinnacle
Hoedberg
Kraterkoppie
Golden Gate
East Cape
High Bluff
SOUTHERN OCEAN
McNish Bay
Penguin Beach
South Cape
Meters
Transverse Projection Central Meridian 37 Degrees East Spheroid Clarke 1880

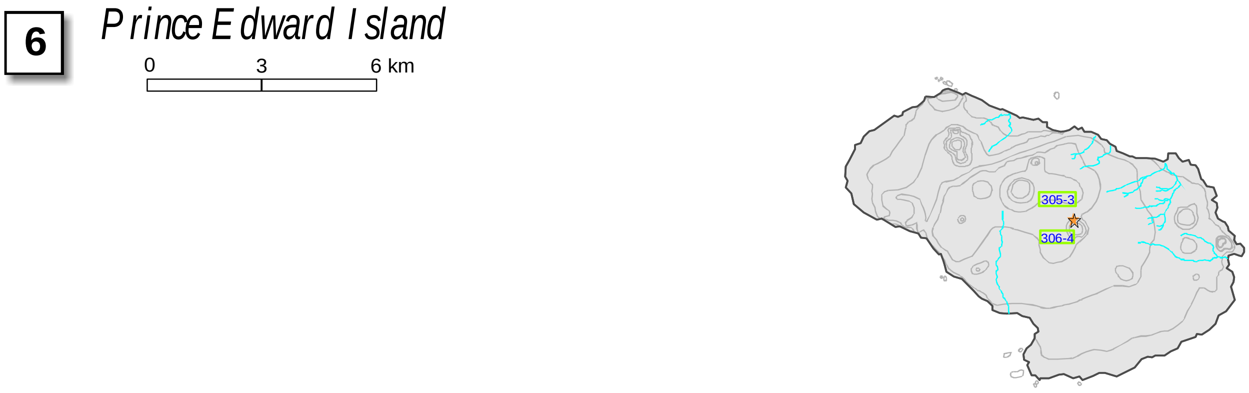
(a)

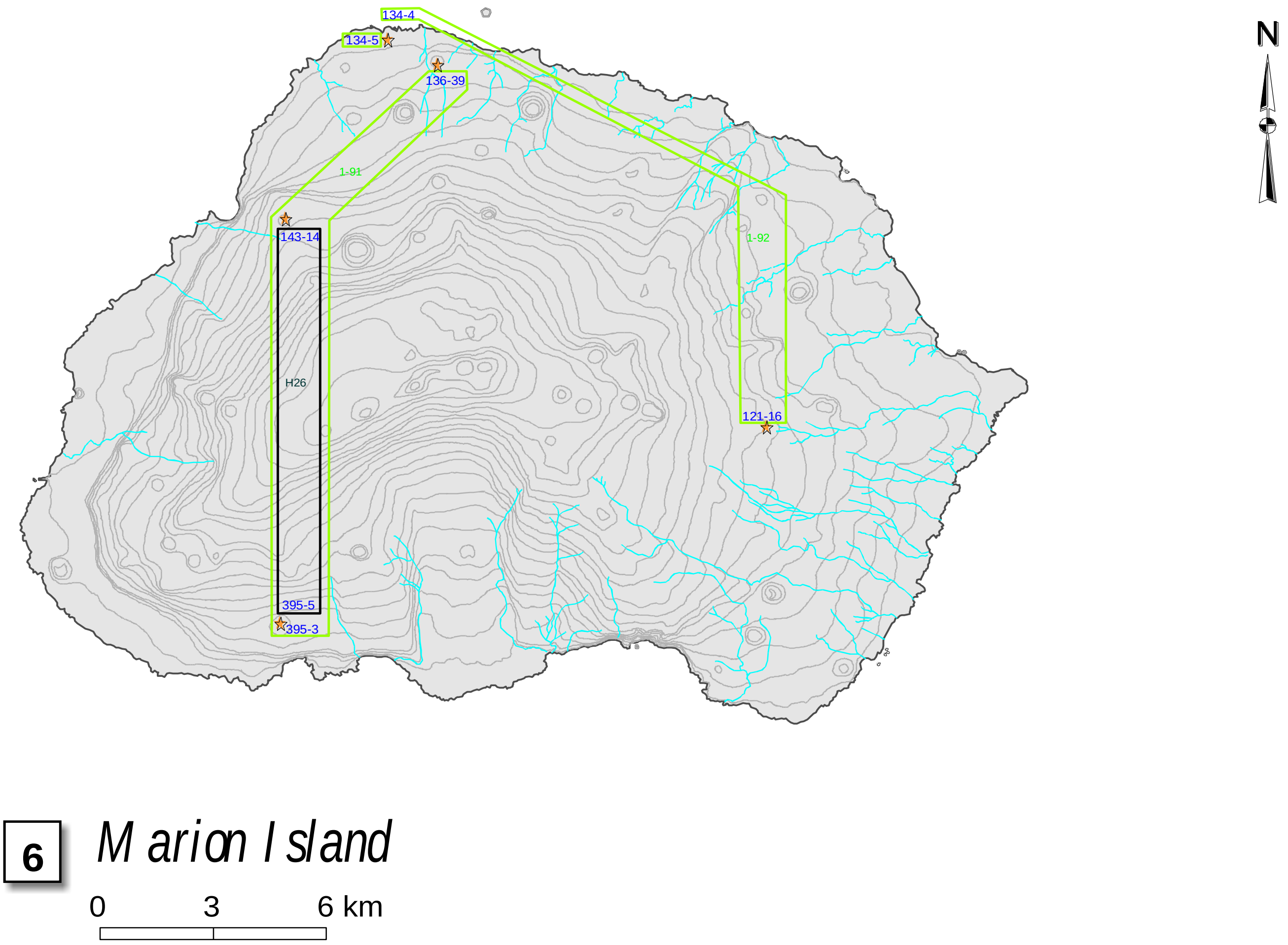

6
Prince Edward Island
0
3
6 km
305-3
306-4
N
134-4
134-5
136-39
143-14
121-16
395-5
395-3
6
Marion Island
0
3
6 km

(b)

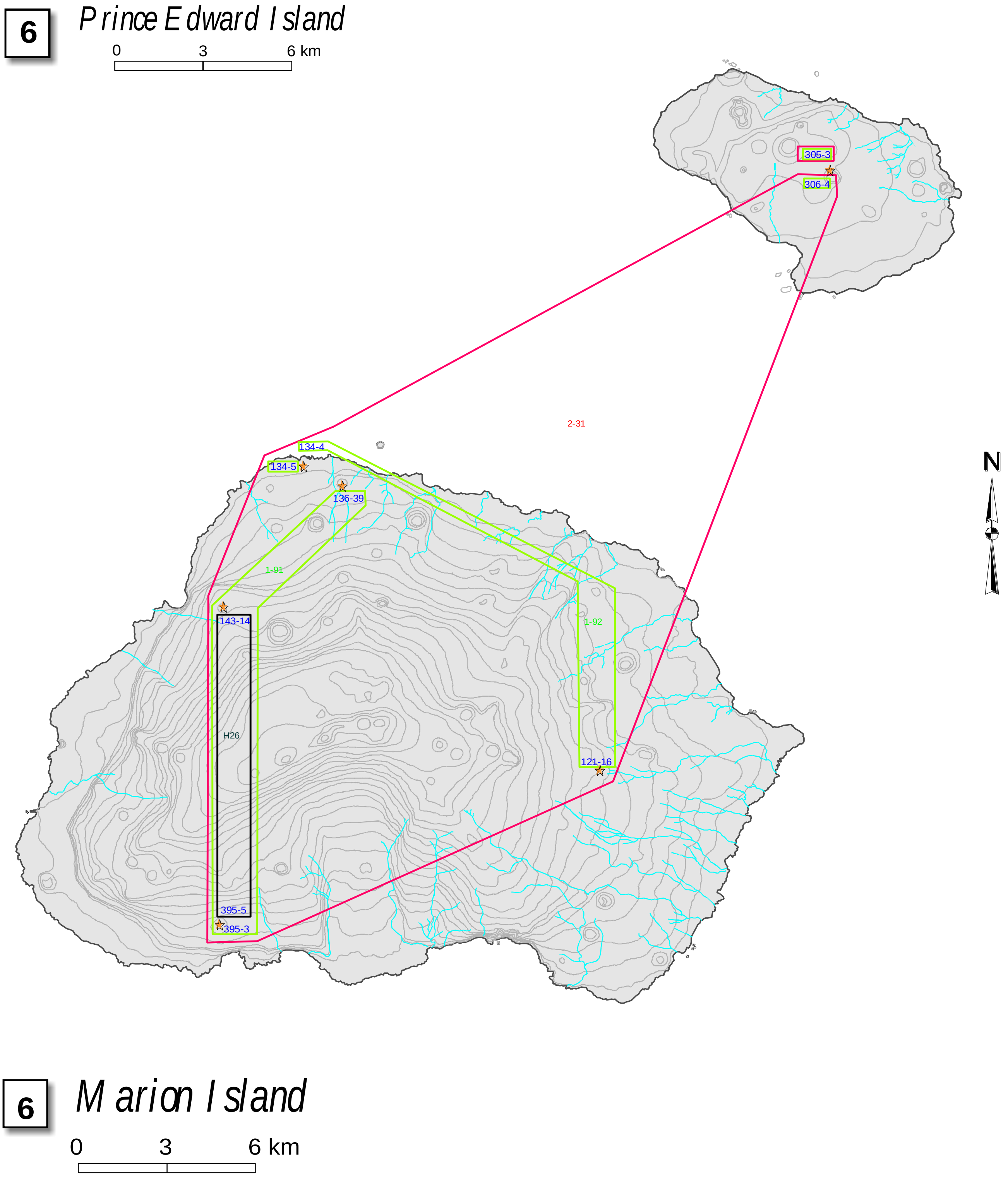

6
Prince Edward Island
0
3
6 km
305-3
306-4
134-4
134-5
136-39
143-14
H26
395-5
395-3
121-16
N
6
Marion Island
0
3
6 km

(c)

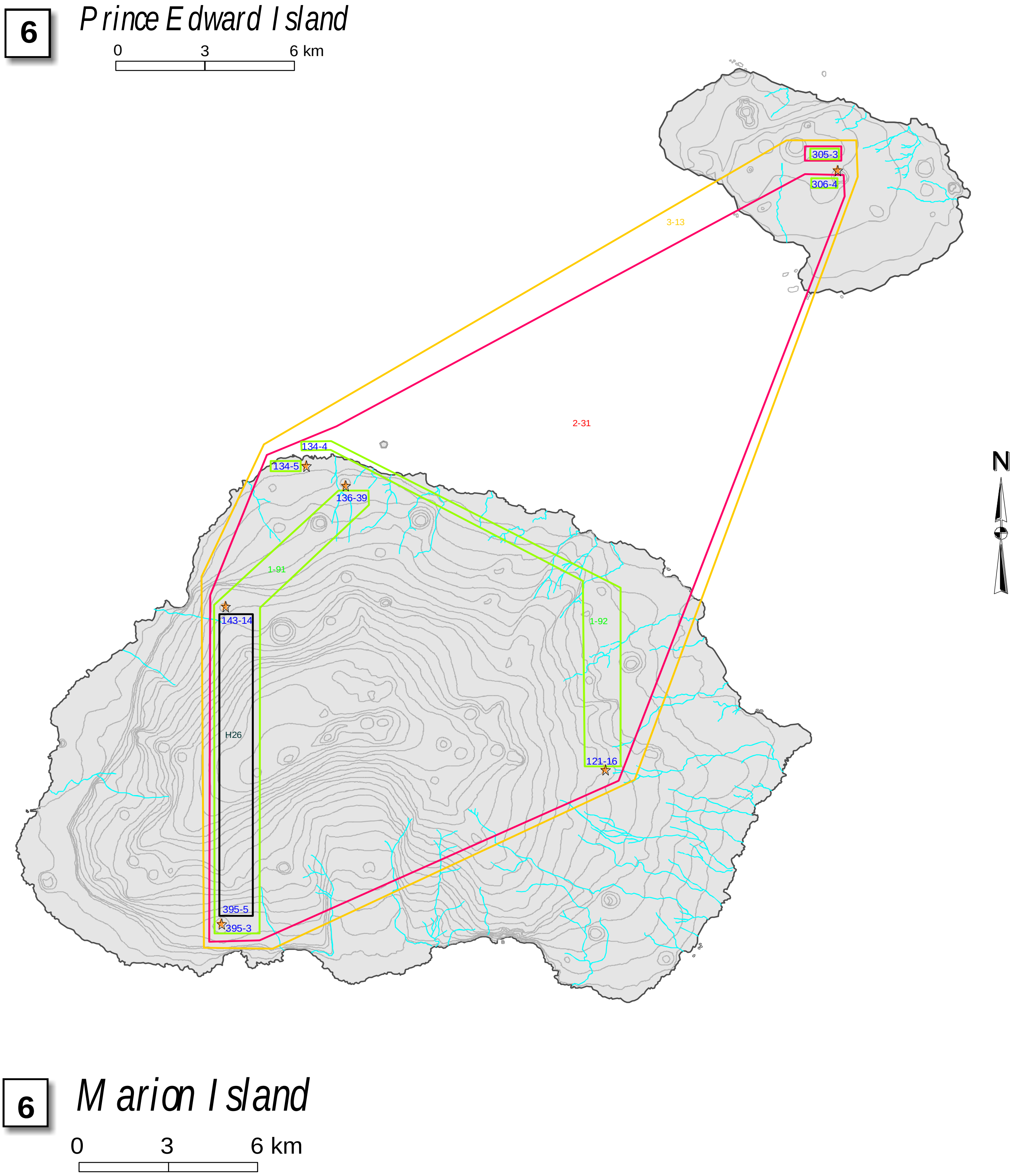

6
Prince Edward Island
0
3
6 km
305-3
306-4


134-4
134-5
136-39
1-91
143-14
H26
1-92
121-16
395-5
395-3
N
6
Marion Island
0
3
6 km

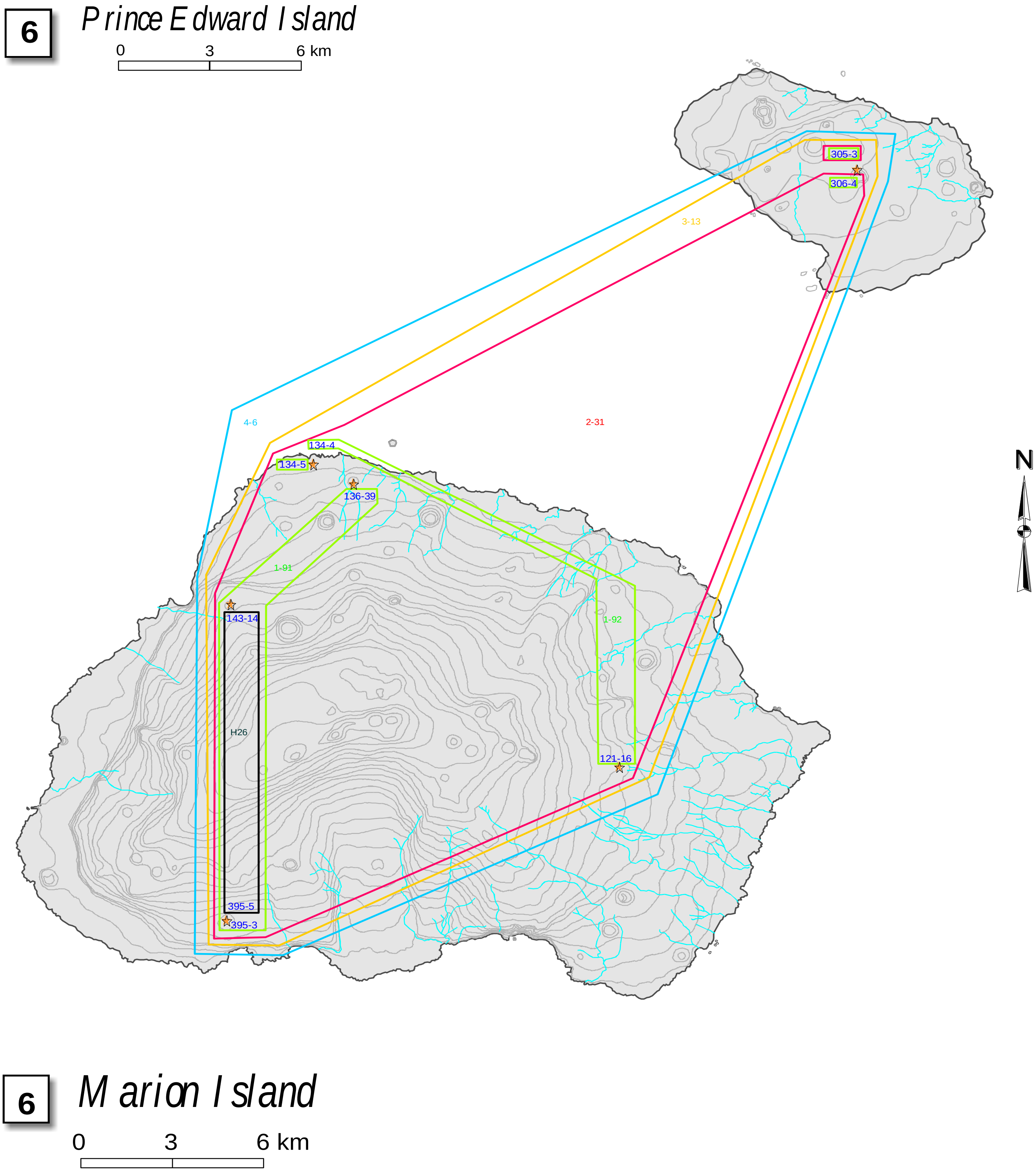
(d)


6
Prince Edward Island
0
3
6 km
305-3
306-4
2-31
N
134-4
134-5
136-39
1-91
143-14
H26
1-92
121-16
395-5
395-3
6
Marion Island
0
3
6 km

(e)


6
Prince Edward Island
0
3
6 km
305-3
306-4
3-13
2-31
134-4
134-5
136-39
1-91
143-14
H26
1-92
121-16
395-5
395-3
N
6
Marion Island
0
3
6 km

(f)



(g)

Fig. 14 *Ectemnorhinus* individuals that group into 4-step clade 4-6 mapped onto the islands according to a) sampling localities with place names for references, samples on Marion Island are indicated in green while those on Prince Edward Island are indicated in red b) sampling localities as used in the nested design c) those that share the same haplotypes nested into 0-step clades, the d) 1-step clades, e) 2-step clades f) 3 step clades and finally g) the complete 4-6 clade as depicted in Fig. 5.

Fig. 9a shows that the individuals included in nested clade 4-1 are located mainly to the eastern part of MI with some individuals occurring on PEI. Although 23 haplotypes were detected in clade 4-1 only three are represented by more than one individual (Fig. 9b) and only one of these haplotypes is shared between the two islands. These individuals group into 15 one-step clades (Fig. 9c), five two-step clades (Fig. 9d) and two 3-step clades (Fig. 9e). Nested clade 4-2 consists of just ten individuals the vast majority of which were collected from PEI (Fig. 10a). Within these ten individuals, nine different haplotypes were identified, with the two individuals sharing a haplotype occurring on PEI (Fig. 10b). The individuals that make up nested clade 4-2 group into six nested one-step clades (Fig. 10c), five nested 2-step clades (Fig. 10d) and two nested 3-step clades (Fig. 10e). It is important to note that the 3-step clades also separate the MI individuals from the PEI individuals. Nested clade 4-3 consists of 49 individuals that map mainly to the north-eastern side of MI, again with a few individuals occurring on PEI (Fig. 11a). In Fig. 11b, 30 different haplotypes are apparent with haplotype H34 occurring in 13 individuals. The nested design unfolds further into 12 one-step clades (Fig 11c), five two-step clades (Fig 11d) and two three-step clades (Fig. 11e). Fig. 12a shows that all 20 *E. kucheli* (Grobler *et al*., 2006) individuals of nested clade 4-4 map to PEI while Fig. 12b shows that they represent 14 different haplotypes. Seven 1-step clades (Fig. 12c), four 2-step clades (Fig. 12d) and two 3-step clades (Fig. 12e) all combine into nested clade 4-4 (Fig. 11f). Fig. 13a shows that nested clade 4-5 maps to the whole of MI and as the largest of the 4-step clades, consists of 72 individuals. Nested clade 4-5 has no representatives on PEI and the individuals therein can be grouped into 47 different haplotypes (Fig. 13b), 29 1-step clades (Fig. 13c), 12 2-step clades (Fig. 13d) and three 3-step clades (Fig. 13e). Four of the nine individuals making up nested clade 4-6 map to the north-western side of MI, two to the south-western side of MI, one to the central eastern side of MI and the last two to PEI (Fig. 14a). Only one of the eight haplotypes that occurred in more than one individual was shown to link the individuals from the north-western side of MI to those of the south-western side of MI (Fig. 14b). The remaining subclades of nested clade 4-6 consist of five one-step clades (Fig. 14c), two 2-step clades (Fig. 14d) and a single 3-step clade (Fig 14e).

Phylogenetic analyses

Table 3 shows the jModel Test results obtained for the whole data set, the two islands individually, as well as the different 4-step nested clades. Two phylogenetic trees containing all the individuals that are represented in the nested clade analyses are presented. Fig. 15 shows the tree obtained from the Minimum Evolution analyses while Fig. 16 shows the tree obtained from the Bayesian analyses. All the four-step nested clades are retained in the trees, except nested clade 4-2 and nested clade 4-5, which were each divided into ‘a’ and ‘b’ subclades. Individuals grouping in nested clades 4-1, 4-3 and 4-4 also group together in both trees with high levels of support. Individuals grouping together in nested clade 4-6 also group together in both trees. Although clade 4-6 does not have high bootstrap support in the Minimum Evolution tree (Fig. 15), it has 93 % support in the Bayesian tree (Fig. 16). Clade 4-2 in the nested design shows that sequences 121-7 and 157-8 (clade 2b) are from MI while the rest of the sequences (clade 2a) are from PEI and that the individuals from the different islands separates from each other even at the 3-step level (Fig. 10e). Both clades 2a and 2b have high levels of support in both trees (Figs. 15& 16). Nested clade 4-5 separates in both the Minimum Evolution (Fig. 15) and the Bayesian trees (Fig. 16) into clades 4-5a and 4-5b. Although neither clades 4-5a nor 4-5b have bootstrap support of more than 50% in the Minimum Evolution tree (Fig. 15), clade 4-5a has 94 % support and clade 4-5b has 85 % support in the Bayesian tree (Fig.16). The nested design (Fig. 6) shows that individuals grouping in clade 4-5b separate from those grouping in clade 4-5a by at least six missing haplotypes. Other 3-step nested clades are also easily recognisable in the trees. As the minimum evolution tree did not recover any of the internal nodes with high levels of support, this analysis gave no information about the relationship between the major clades. The Bayesian analyses (Fig. 16) on the other hand, clarifies the relationship between the major clades, where individuals grouping together in nested clade 4-4 are basal to the rest of the tree, as suggested by Grobler *et al*. (2006), and all the other clades also group together with 95% support.

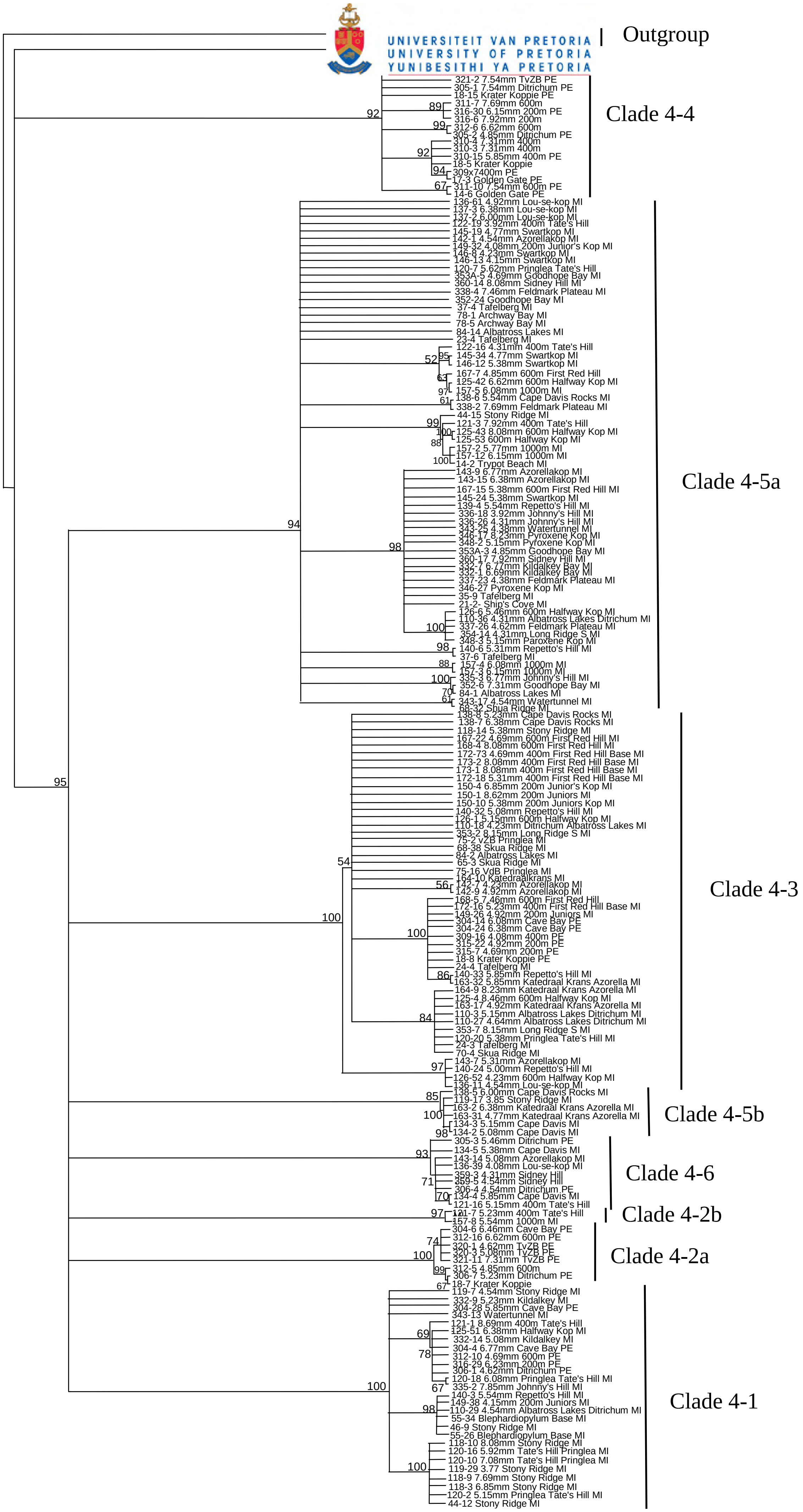
Table 3. jModelTest results obtained for the different datasets. In each case the outgroup was included. I = Proportion of invariable sites and G= Gamma distribution shape parameter

Dataset	Model selected	Base frequencies				Substitution model						I	G
		A	C	G	T	A-C	A-G	A-T	C-G	C-T	G-T		
Total Cladogram	TIM3+I+G	0.3111	0.1671	0.1296	0.3921	2.7910	46.0397	1.0000	2.7910	15.6917	1.0000	0.4090	0.2410
MI dataset	TIM3+I+G	0.3129	0.1668	0.1291	0.3912	2.5888	38.6352	1.0000	2.5888	13.5356	1.0000	0.4360	0.2480
PEI dataset	TrN+I	0.3098	0.1682	0.1309	0.3911	1.0000	37.0083	1.0000	1.0000	10.9496	1.0000	0.8220	Equal rates for all sites
Nested clade 4-1	TIM1+I	0.3027	0.1671	0.1390	0.3913	1.0000	92.6399	5.0722	5.0722	29.0701	1.0000	0.8470	Equal rates for all sites
Nested clade 4-2	TPM2uf+I	0.3016	0.1653	0.1405	0.3927	9.4493	47.3177	9.4493	1.0000	47.3177	1.0000	0.7550	Equal rates for all sites
Nested clade 4-3	TPM1uf+I +G	0.3110	0.1597	0.1409	0.3883	1.0000	885.2974	59.7997	59.7997	885.2974	1.0000	0.6660	0.2320
Nested clade 4-4	TPM2uf+G	0.3014	0.1663	0.1426	0.3897	172.1505	1175.5851	172.1505	1.0000	1175.5851	1.0000	-	0.1560
Nested clade 4-5	HKY+I+G	0.3095	0.1672	0.1462	0.3772	Transitions/ Transversions = 14.0814				8.9150	1.0000	0.8540	0.4590
Nested clade 4-6	TPM2uf+G	0.3040	0.1655	0.1427	0.3878	216.8281	1008.4432	216.8281	1.0000	1008.4432	1.0000	-	0.1210


125-4 8.46mm 600m Halfway Kop MI
110-27 4.64mm Albatross Lakes Ditrichum MI
70-4 Skua Ridge MI
353-7 8.15mm Long Ridge S MI
110-3 5.15mm Albatross Lakes Ditrichum MI
120-20 5.38mm Pringlea Tate's Hill MI
24-3 Tafelberg MI
163-17 4.92mm Katedraal Krans Azorella MI
164-9 8.23mm Katedraal Krans Azorella MI
167-22 4.69mm 600m First Red Hill MI
150-1 8.62mm 200m Juniors MI
150-10 5.38mm 200m Juniors Kop MI
173-1 8.08mm 400m First Red Hill Base MI
168-4 8.08mm 600m First Red Hill MI
140-32 5.08mm Repetto's Hill MI
118-14 5.38mm Stony Ridge MI
110-18 4.23mm Ditrichum Albatross Lakes MI
173-2 8.08mm 400m First Red Hill Base MI
84-2 Albatross Lakes MI
65-3 Skua Ridge MI
75-16 VdB Pringlea MI
126-1 5.15mm 600m Halfway Kop MI
172-18 5.31mm 400m First Red Hill Base MI
150-4 6.85mm 200m Junior's Kop MI
57
75-2 VdB Pringlea MI
353-2 8.15mm Long Ridge S MI
68-38 Skua Ridge MI
138-8 5.23mm Cape Davis Rocks MI
138-7 6.38mm Cape Davis Rocks MI
172-73 4.69mm 400m First Red Hill Base MI
164-10 Katedraalkrans MI
66
142-7 4.23mm Azorellakop MI
142-9 4.92mm Azorellakop MI
315-7 4.69mm 200m PE
79
309-16 4.08mm 400m PE
66
140-33 5.85mm Repetto's Hill MI
163-32 5.85mm Katedraal Krans Azorella MI
91
51
172-16 5.23mm 400m First Red Hill Base MI
168-5 7.46mm 600m First Red Hill MI
304-14 6.08mm Cave Bay PE
24-4 Tafelberg MI
149-26 4.92mm 200m Juniors MI
315-22 4.92mm 200m PE
304-24 6.38mm Cave Bay PE
18-8 Krater Koppie PE
86
126-52 4.23mm 600m Halfway Kop MI
143-7 5.31mm Azorellakop MI
140-24 5.00mm Repetto's Hill MI
136-11 4.54mm Lou-se-kop MI
Clade 4-3
81
121-7 5.23mm 400m Tate's Hill MI
157-8 5.54mm 1000m MI
Clade 4-2b
134-3 5.15mm Cape Davis MI
55
64
134-2 5.08mm Cape Davis MI
72
163-31 4.77mm Katedraal Krans Azorella MI
163-2 6.38mm Katedraal Krans Azorella MI
94
119-17 3.85 Stony Ridge MI
138-5 6.00mm Cape Davis Rocks MI
Clade 4-5b
121-1 8.69mm 400m Tate's Hill MI
332-9 5.23mm Kildalkey MI
118-9 7.69mm Stony Ridge MI
118-3 6.85mm Stony Ridge MI
118-10 8.08mm Stony Ridge MI
120-2 5.15mm Pringlea Tate's Hill MI
83
120-10 7.08mm Tate's Hill Pringlea MI
53
44-12 Stony Ridge MI
120-16 5.92mm Tate's Hill Pringlea MI
119-29 3.77 Stony Ridge MI
343-13 Watertunnel MI
140-3 5.54mm Repetto's Hill MI
55-26 Blephardiopylum Base MI
53
149-38 4.15mm 200m Juniors MI
55-34 Blephardiopylum Base MI
46-9 Stony Ridge MI
110-29 4.54mm Albatross Lakes Ditrichum MI
304-28 5.85mm Cave Bay PE
119-74.54mm Stony Ridge MI
332-14 5.08mm Kildalkey MI
125-51 6.38mm Halfway Kop MI
316-29 6.23mm 200m PE
304-4 6.77mm Cave Bay PE
312-10 4.69mm 600m PE
306-1 4.62mm Ditrichum PE
120-18 6.08mm Pringlea Tate's Hill MI
55
335-2 7.85mm Johnny's Hill MI
Clade 4-1
312-16 6.62mm 600m PE
320-1 4.62mm TvZB PE
67
321-11 7.31mm TvZB PE
320-3 5.08mm TvZB PE
79
304-6 6.46mm Cave Bay PE
80
312-5 4.85mm 600m PE
86
306-7 5.23mm Ditrichum PE
18-7 Krater Koppie PE
Clade 4-2a
305-3 5.46mm Ditrichum PE
134-4 5.85mm Cape Davis MI
359-3 4.31mm Sidney Hill MI
65
121-16 5.15mm 400m Tate's Hill MI
359-5 4.54mm Sidney Hill MI
143-14 5.08mm Azorellakop MI
136-39 4.08mm Lou-se-kop MI
134-5 5.38mm Cape Davis MI
58
306-4 4.54mm Ditrichum PE
Clade 4-6
143-15 6.38mm Azorellakop MI
145-24 5.38mm Swartkop MI
343-25 4.38mm Watertunnel MI
346-27 Pyroxene Kop MI
360-17 7.92mm Sidney Hill MI
21-2- Ship's Cove MI
35-9 Tafelberg MI
337-23 4.38mm Feldmark Plateau MI
346-17 8.23mm Pyroxene Kop MI
332-7 6.77mm Kildalkey Bay MI
348-2 5.15mm Pyroxene Kop MI
332-1 6.69mm Kildalkey Bay MI
353A-3 4.85mm Goodhope Bay MI
336-26 4.31mm Johnny's Hill MI
143-9 6.77mm Azorellakop MI
167-15 5.38mm 600m First Red Hill MI
139-4 5.54mm Repetto's Hill MI
336-18 3.92mm Johnny's Hill MI
85
348-3 5.15mm Paroxene Kop MI
337-26 4.62mm Feldmark Plateau MI
61
354-14 4.31mm Long Ridge S MI
126-6 5.46mm 600m Halfway Kop MI
110-36 4.31mm Albatross Lakes Ditrichum MI
137-3 6.38mm Lou-se-kop MI
335-3 6.77mm Johnny's Hill MI
93
352-6 7.31mm Goodhope Bay MI
87
84-1 Albatross Lakes MI
66
145-34 4.77mm Swartkop MI
146-12 5.38mm Swartkop MI
122-16 4.31mm 400m Tate's Hill MI
167-7 4.85mm 600m First Red Hill MI
65
125-42 6.62mm 600m Halfway Kop MI
60
157-5 6.08mm 1000m MI
75
157-4 6.08mm 1000m MI
157-3 6.15mm 1000m MI
343-17 4.54mm Watertunnel MI
68-32 Shua Ridge MI
78-5 Archway Bay MI
78-1 Archway Bay MI
145-19 4.77mm Swartkop MI
138-6 5.54mm Cape Davis Rocks MI
338-2 7.69mm Feldmark Plateau MI
353A-5 4.69mm Goodhope Bay MI
338-4 7.46mm Feldmark Plateau MI
146-13 4.15mm Swartkop MI
146-8 4.23mm Swartkop MI
352-24 Goodhope Bay MI
122-19 3.92mm 400m Tate's Hill MI
37-4 Tafelberg MI
23-4 Tafelberg MI
137-2 6.00mm Lou-se-kop MI
149-32 4.08mm 200m Junior's Kop MI
84-14 Albatross Lakes MI
142-1 4.54mm Azorellakop MI
360-14 8.08mm Sidney Hill MI
136-61 4.92mm Lou-se-kop MI
140-6 5.31mm Repetto's Hill MI
77
37-6 Tafelberg MI
120-7 5.62mm Pringlea Tate's Hill MI
44-15 Stony Ridge MI
125-43 8.08mm 600m Halfway Kop MI
83
125-53 600m Halfway Kop MI
121-3 7.92mm 400m Tate's Hill MI
86
157-12 6.15mm 1000m MI
69
157-2 5.77mm 1000m MI
14-2 Trypot Beach MI
Clade 4-5a
17-14 Golden Gate PE
78
312-6 6.62mm 600m PE
305-2 4.85mm Ditrichum PE
65
18-15 Krater Koppie PE
311-10 7.54mm 600m PE
71
14-6 Golden Gate PE
65
316-30 6.15mm 200m PE
316-6 7.92mm 200m PE
311-7 7.69mm 600m PE
305-1 7.54mm Ditrichum PE
304-13 7.08mm Cave Bay PE
316-15 8.15mm 200m PE
321-2 7.54mm TvZB PE
320-4 6.38mm TvZB PE
55
309x7400m PE
17-3 Golden Gate PE
310-4 7.31mm 400m PE
55
310-15 5.85mm 400m PE
310-3 7.31mm 400m PE
18-5 Krater Koppie PE
Clade 4-4
E.viridis 400-21 Heard Island
100
E.viridis 400-12 Heard Island
Outgroup

Fig. 15 Minimum Evolution (ME) tree inferred using the Tamura-Nei distance correction algorithm. In each case, the sample number is given followed by the body length measurement, vegetation type it was collected from, locality it was collected from, sex and island of origin. 'MI' denotes Marion Island samples whilst Prince Edward Island samples are indicated by 'PEI'. Nodal support obtained following 100 000 bootstrap replications above 50% is indicated. TvZB indicates samples collected at the top of Van Zinderen Bakker Peak at an elevation of 672 m above sea level. (On page 109)

Fig. 16 Bayesian phylogenetic analyses. For each taxon, the sample number is given followed by the body length measurement, vegetation type it was collected from, locality it was collected from, sex and island of origin. 'MI' denotes Marion Island samples whilst Prince Edward Island samples are indicated by 'PEI'. TvZB indicates samples collected at the top of Van Zinderen Bakker Peak at an elevation of 672 m above sea level. (On page 111)


Outgroup
Clade 4-4
321-2 7.54mm TvZB PE
305-1 7.54mm Ditrichum PE
18-15 Krater Koppie PE
92
89
311-7 7.69mm 600m
316-30 6.15mm 200m PE
316-6 7.92mm 200m
99
312-6 6.62mm 600m
305-2 4.85mm Ditrichum PE
92
310-4 7.31mm 400m
310-3 7.31mm 400m
310-15 5.85mm 400m PE
18-5 Krater Koppie
94
309x7400m PE
17-3 Golden Gate PE
67
311-10 7.54mm 600m PE
14-6 Golden Gate PE
Clade 4-5a
136-61 4.92mm Lou-se-kop MI
137-3 6.38mm Lou-se-kop MI
137-2 6.00mm Lou-se-kop MI
122-19 3.92mm 400m Tate's Hill
145-19 4.77mm Swartkop MI
142-1 4.54mm Azorellakop MI
149-32 4.08mm 200m Junior's Kop MI
146-8 4.23mm Swartkop MI
146-13 4.15mm Swartkop MI
120-7 5.62mm Pringlea Tate's Hill
353A-5 4.69mm Goodhope Bay MI
360-14 8.08mm Sidney Hill MI
338-4 7.46mm Feldmark Plateau MI
352-24 Goodhope Bay MI
37-4 Tafelberg MI
78-1 Archway Bay MI
78-5 Archway Bay MI
84-14 Albatross Lakes MI
23-4 Tafelberg MI
52
95
122-16 4.31mm 400m Tate's Hill
145-34 4.77mm Swartkop MI
146-12 5.38mm Swartkop MI
63
167-7 4.85mm 600m First Red Hill
125-42 6.62mm 600m Halfway Kop MI
97
157-5 6.08mm 1000m MI
61
138-6 5.54mm Cape Davis Rocks MI
338-2 7.69mm Feldmark Plateau MI
99
44-15 Stony Ridge MI
121-3 7.92mm 400m Tate's Hill
100
125-43 8.08mm 600m Halfway Kop MI
88
125-53 600m Halfway Kop MI
157-2 5.77mm 1000m MI
157-12 6.15mm 1000m MI
100
14-2 Trypot Beach MI
94
98
143-9 6.77mm Azorellakop MI
143-15 6.38mm Azorellakop MI
167-15 5.38mm 600m First Red Hill MI
145-24 5.38mm Swartkop MI
139-4 5.54mm Repetto's Hill MI
336-18 3.92mm Johnny's Hill MI
336-26 4.31mm Johnny's Hill MI
343-25 4.38mm Watertunnel MI
346-17 8.23mm Pyroxene Kop MI
348-2 5.15mm Pyroxene Kop MI
353A-3 4.85mm Goodhope Bay MI
360-17 7.92mm Sidney Hill MI
332-7 6.77mm Kildalkey Bay MI
332-1 6.69mm Kildalkey Bay MI
337-23 4.38mm Feldmark Plateau MI
346-27 Pyroxene Kop MI
35-9 Tafelberg MI
21-2- Ship's Cove MI
100
126-6 5.46mm 600m Halfway Kop MI
110-36 4.31mm Albatross Lakes Ditrichum MI
337-26 4.62mm Feldmark Plateau MI
354-14 4.31mm Long Ridge S MI
348-3 5.15mm Paroxene Kop MI
98
140-6 5.31mm Repetto's Hill MI
37-6 Tafelberg MI
88
157-4 6.08mm 1000m MI
157-3 6.15mm 1000m MI
100
335-3 6.77mm Johnny's Hill MI
352-6 7.31mm Goodhope Bay MI
70
84-1 Albatross Lakes MI
61
343-17 4.54mm Watertunnel MI
68-32 Shua Ridge MI
95
Clade 4-3
138-8 5.23mm Cape Davis Rocks MI
138-7 6.38mm Cape Davis Rocks MI
118-14 5.38mm Stony Ridge MI
167-22 4.69mm 600m First Red Hill MI
168-4 8.08mm 600m First Red Hill MI
172-73 4.69mm 400m First Red Hill Base MI
173-2 8.08mm 400m First Red Hill Base MI
173-1 8.08mm 400m First Red Hill Base MI
172-18 5.31mm 400m First Red Hill Base MI
150-4 6.85mm 200m Junior's Kop MI
150-1 8.62mm 200m Juniors MI
150-10 5.38mm 200m Juniors Kop MI
140-32 5.08mm Repetto's Hill MI
126-1 5.15mm 600m Halfway Kop MI
110-18 4.23mm Ditrichum Albatross Lakes MI
353-2 8.15mm Long Ridge S MI
75-2 vZB Pringlea MI
68-38 Skua Ridge MI
84-2 Albatross Lakes MI
54
65-3 Skua Ridge MI
75-16 VdB Pringlea MI
164-10 Katedraalkrans MI
56
142-7 4.23mm Azorellakop MI
142-9 4.92mm Azorellakop MI
100
168-5 7.46mm 600m First Red Hill
172-16 5.23mm 400m First Red Hill Base MI
149-26 4.92mm 200m Juniors MI
304-14 6.08mm Cave Bay PE
304-24 6.38mm Cave Bay PE
100
309-16 4.08mm 400m PE
315-22 4.92mm 200m PE
315-7 4.69mm 200m PE
18-8 Krater Koppie PE
24-4 Tafelberg MI
86
140-33 5.85mm Repetto's Hill MI
163-32 5.85mm Katedraal Krans Azorella MI
164-9 8.23mm Katedraal Krans Azorella MI
125-4 8.46mm 600m Halfway Kop MI
163-17 4.92mm Katedraal Krans Azorella MI
110-3 5.15mm Albatross Lakes Ditrichum MI
84
110-27 4.64mm Albatross Lakes Ditrichum MI
353-7 8.15mm Long Ridge S MI
120-20 5.38mm Pringlea Tate's Hill MI
24-3 Tafelberg MI
70-4 Skua Ridge MI
97
143-7 5.31mm Azorellakop MI
140-24 5.00mm Repetto's Hill MI
126-52 4.23mm 600m Halfway Kop MI
136-11 4.54mm Lou-se-kop MI
Clade 4-5b
85
138-5 6.00mm Cape Davis Rocks MI
119-17 3.85 Stony Ridge MI
163-2 6.38mm Katedraal Krans Azorella MI
100
163-31 4.77mm Katedraal Krans Azorella MI
134-3 5.15mm Cape Davis MI
98
134-2 5.08mm Cape Davis MI
Clade 4-6
305-3 5.46mm Ditrichum PE
93
134-5 5.38mm Cape Davis MI
143-14 5.08mm Azorellakop MI
136-39 4.08mm Lou-se-kop MI
359-3 4.31mm Sidney Hill
71
359-5 4.54mm Sidney Hill
306-4 4.54mm Ditrichum PE
70
134-4 5.85mm Cape Davis MI
121-16 5.15mm 400m Tate's Hill
Clade 4-2b
97
121-7 5.23mm 400m Tate's Hill
157-8 5.54mm 1000m MI
Clade 4-2a
304-6 6.46mm Cave Bay PE
74
312-16 6.62mm 600m PE
320-1 4.62mm TvZB PE
100
320-3 5.08mm TvZB PE
321-11 7.31mm TvZB PE
99
312-5 4.85mm 600m
306-7 5.23mm Ditrichum PE
67
18-7 Krater Koppie
Clade 4-1
119-7 4.54mm Stony Ridge MI
332-9 5.23mm Kildalkey MI
304-28 5.85mm Cave Bay PE
343-13 Watertunnel MI
121-1 8.69mm 400m Tate's Hill
69
125-51 6.38mm Halfway Kop MI
332-14 5.08mm Kildalkey MI
78
304-4 6.77mm Cave Bay PE
312-10 4.69mm 600m PE
316-29 6.23mm 200m PE
306-1 4.62mm Ditrichum PE
120-18 6.08mm Pringlea Tate's Hill MI
100
67
335-2 7.85mm Johnny's Hill MI
140-3 5.54mm Repetto's Hill MI
149-38 4.15mm 200m Juniors MI
98
110-29 4.54mm Albatross Lakes Ditrichum MI
55-34 Blephardiopylum Base MI
46-9 Stony Ridge MI
55-26 Blephardiopylum Base MI
118-10 8.08mm Stony Ridge MI
120-16 5.92mm Tate's Hill Pringlea MI
120-10 7.08mm Tate's Hill Pringlea MI
100
119-29 3.77 Stony Ridge MI
118-9 7.69mm Stony Ridge MI
118-3 6.85mm Stony Ridge MI
120-2 5.15mm Pringlea Tate's Hill MI
44-12 Stony Ridge MI

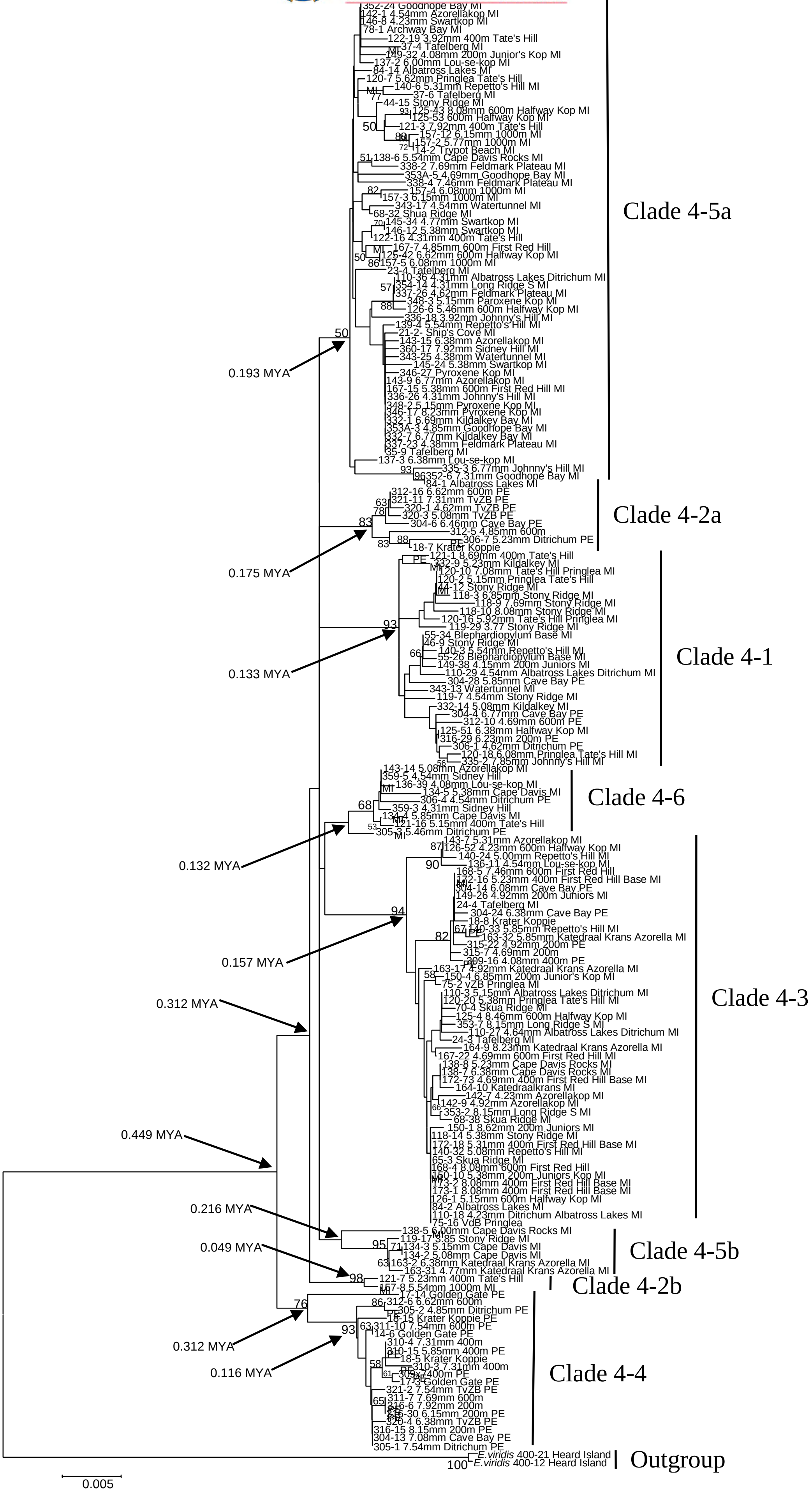
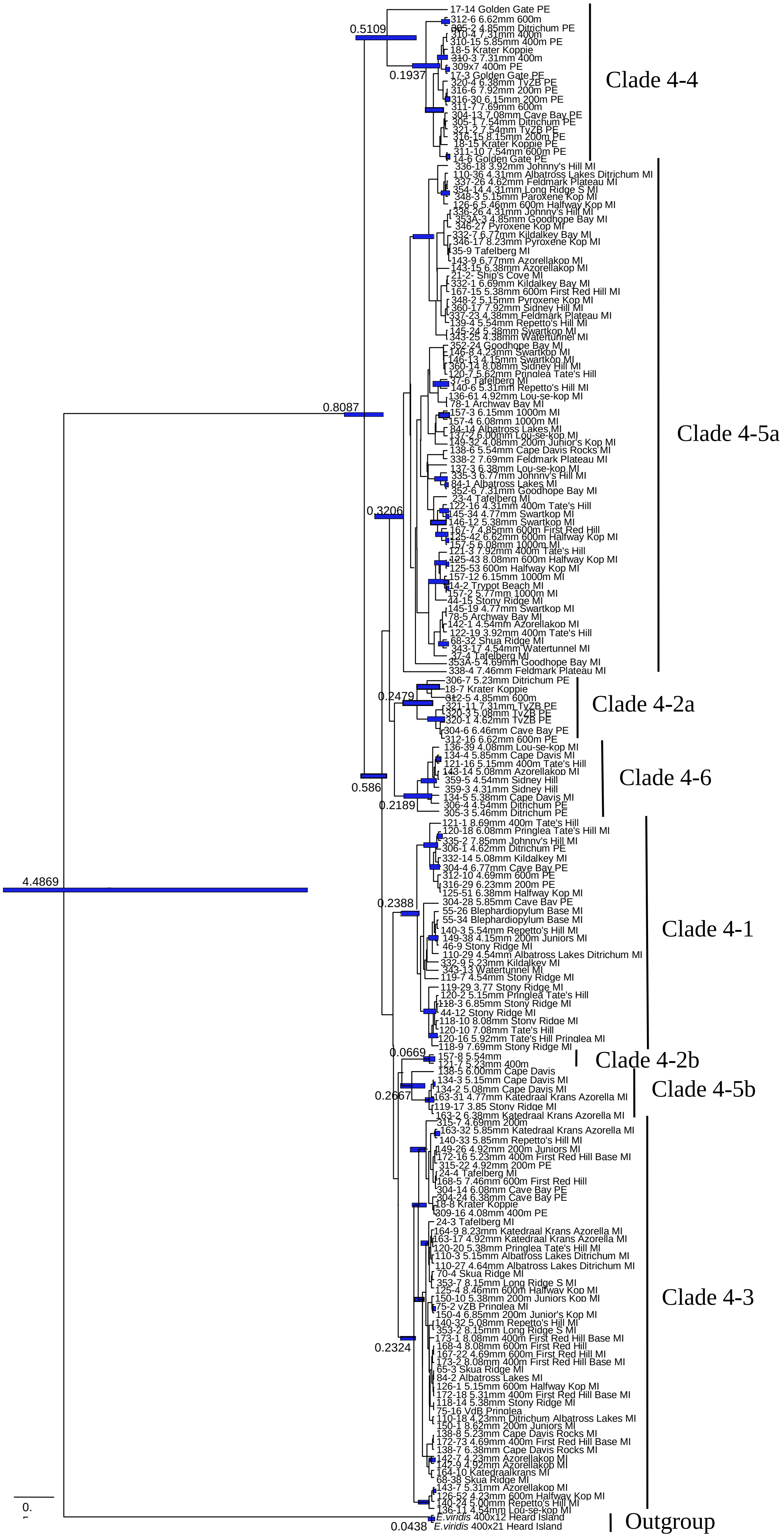

Clade 4-5a
Clade 4-2a
Clade 4-1
Clade 4-6
Clade 4-3
Clade 4-5b
Clade 4-2b
Clade 4-4
Outgroup
0.193 MYA
0.175 MYA
0.133 MYA
0.132 MYA
0.157 MYA
0.312 MYA
0.449 MYA
0.216 MYA
0.049 MYA
0.312 MYA
0.116 MYA
E.viridis 400-21 Heard Island
E.viridis 400-12 Heard Island
100
0.005

Fig. 17 Neighbour Joining (NJ) tree inferred using uncorrected p-distance values. For each taxon, the sample number is followed by the body length measurement, vegetation type it was collected from, locality it was collected from, sex, and its island of origin. 'MI' denotes Marion Island samples whilst Prince Edward Island samples are indicated by 'PEI'. Nodal support obtained following 100 000 bootstrap replications above 50% is indicated next to the relevant nodes. Time to lineage coalescence was estimated using a 2.3 % nucleotide sequence divergence per million years molecular clock calibration, based on the arthropod mtDNA survey of Brower (1994). Estimated time of coalescence is indicated by arrows. (On page 112)

Fig. 18 Ultrametric tree obtained with BEAST 1.6.1 (Drummond & Rambaut 2007) (On page 114). The numbers in the nodes correspond to the estimated age in MY. Blue bars correspond to the 95 % confidence interval. A clock rate of 2.3 % sequence divergence per million years (MY), based on the arthropod mtDNA survey of Brower (1994), was used. The BEAST 1.6.1 (Drummond & Rambaut, 2007) statistics as analyzed with Tracer v1.5 (Drummond & Rambaut, 2007) are summarised in Table 4.


17-14 Golden Gate PE
312-6 6.62mm 600m
305-2 4.85mm Ditrichum PE
310-4 7.31mm 400m
310-15 5.85mm 400m PE
18-5 Krater Koppie
310-3 7.31mm 400m
309x7 400m PE
17-3 Golden Gate PE
320-4 6.38mm TvZB PE
316-6 7.92mm 200m PE
316-30 6.15mm 200m PE
311-7 7.69mm 600m
304-13 7.08mm Cave Bay PE
305-1 7.54mm Ditrichum PE
321-2 7.54mm TvZB PE
316-15 8.15mm 200m PE
18-15 Krater Koppie PE
311-10 7.54mm 600m PE
14-6 Golden Gate PE
0.5109
0.1937
Clade 4-4
336-18 3.92mm Johnny's Hill MI
110-36 4.31mm Albatross Lakes Ditrichum MI
337-26 4.62mm Feldmark Plateau MI
354-14 4.31mm Long Ridge S MI
348-3 5.15mm Paroxene Kop MI
126-6 5.46mm 600m Halfway Kop MI
336-26 4.31mm Johnny's Hill MI
353A-3 4.85mm Goodhope Bay MI
346-27 Pyroxene Kop MI
332-7 6.77mm Kildalkey Bay MI
346-17 8.23mm Pyroxene Kop MI
35-9 Tafelberg MI
143-9 6.77mm Azorellakop MI
143-15 6.38mm Azorellakop MI
21-2- Ship's Cove MI
332-1 6.69mm Kildalkey Bay MI
167-15 5.38mm 600m First Red Hill MI
348-2 5.15mm Pyroxene Kop MI
360-17 7.92mm Sidney Hill MI
337-23 4.38mm Feldmark Plateau MI
139-4 5.54mm Repetto's Hill MI
145-24 5.38mm Swartkop MI
343-25 4.38mm Watertunnel MI
352-24 Goodhope Bay MI
146-8 4.23mm Swartkop MI
146-13 4.15mm Swartkop MI
360-14 8.08mm Sidney Hill MI
120-7 5.62mm Pringlea Tate's Hill
37-6 Tafelberg MI
140-6 5.31mm Repetto's Hill MI
136-61 4.92mm Lou-se-kop MI
78-1 Archway Bay MI
157-3 6.15mm 1000m MI
157-4 6.08mm 1000m MI
84-14 Albatross Lakes MI
137-2 6.00mm Lou-se-kop MI
149-32 4.08mm 200m Junior's Kop MI
138-6 5.54mm Cape Davis Rocks MI
338-2 7.69mm Feldmark Plateau MI
137-3 6.38mm Lou-se-kop MI
335-3 6.77mm Johnny's Hill MI
84-1 Albatross Lakes MI
352-6 7.31mm Goodhope Bay MI
23-4 Tafelberg MI
122-16 4.31mm 400m Tate's Hill
145-34 4.77mm Swartkop MI
146-12 5.38mm Swartkop MI
167-7 4.85mm 600m First Red Hill
125-42 6.62mm 600m Halfway Kop MI
157-5 6.08mm 1000m MI
121-3 7.92mm 400m Tate's Hill
125-43 8.08mm 600m Halfway Kop MI
125-53 600m Halfway Kop MI
157-12 6.15mm 1000m MI
14-2 Trypot Beach MI
157-2 5.77mm 1000m MI
44-15 Stony Ridge MI
145-19 4.77mm Swartkop MI
78-5 Archway Bay MI
142-1 4.54mm Azorellakop MI
122-19 3.92mm 400m Tate's Hill
68-32 Shua Ridge MI
343-17 4.54mm Watertunnel MI
37-4 Tafelberg MI
353A-5 4.69mm Goodhope Bay MI
338-4 7.46mm Feldmark Plateau MI
0.8087
0.3206
Clade 4-5a
306-7 5.23mm Ditrichum PE
18-7 Krater Koppie
312-5 4.85mm 600m
321-11 7.31mm TvZB PE
320-3 5.08mm TvZB PE
320-1 4.62mm TvZB PE
304-6 6.46mm Cave Bay PE
312-16 6.62mm 600m PE
0.2479
Clade 4-2a
136-39 4.08mm Lou-se-kop MI
134-4 5.85mm Cape Davis MI
121-16 5.15mm 400m Tate's Hill
143-14 5.08mm Azorellakop MI
359-5 4.54mm Sidney Hill
359-3 4.31mm Sidney Hill
134-5 5.38mm Cape Davis MI
306-4 4.54mm Ditrichum PE
305-3 5.46mm Ditrichum PE
0.586
0.2189
Clade 4-6
121-1 8.69mm 400m Tate's Hill
120-18 6.08mm Pringlea Tate's Hill MI
335-2 7.85mm Johnny's Hill MI
306-1 4.62mm Ditrichum PE
332-14 5.08mm Kildalkey MI
304-4 6.77mm Cave Bay PE
312-10 4.69mm 600m PE
316-29 6.23mm 200m PE
125-51 6.38mm Halfway Kop MI
304-28 5.85mm Cave Bay PE
55-26 Blephardiopylum Base MI
55-34 Blephardiopylum Base MI
140-3 5.54mm Repetto's Hill MI
149-38 4.15mm 200m Juniors MI
46-9 Stony Ridge MI
110-29 4.54mm Albatross Lakes Ditrichum MI
332-9 5.23mm Kildalkey MI
343-13 Watertunnel MI
119-7 4.54mm Stony Ridge MI
119-29 3.77 Stony Ridge MI
120-2 5.15mm Pringlea Tate's Hill
118-3 6.85mm Stony Ridge MI
44-12 Stony Ridge MI
118-10 8.08mm Stony Ridge MI
120-10 7.08mm Tate's Hill
120-16 5.92mm Tate's Hill Pringlea MI
118-9 7.69mm Stony Ridge MI
4.4869
0.2388
Clade 4-1
157-8 5.54mm
121-7 5.23mm 400m
138-5 6.00mm Cape Davis
0.0669
Clade 4-2b
134-3 5.15mm Cape Davis MI
134-2 5.08mm Cape Davis MI
163-31 4.77mm Katedraal Krans Azorella MI
119-17 3.85 Stony Ridge MI
163-2 6.38mm Katedraal Krans Azorella MI
0.2667
Clade 4-5b
315-7 4.69mm 200m
163-32 5.85mm Katedraal Krans Azorella MI
140-33 5.85mm Repetto's Hill MI
149-26 4.92mm 200m Juniors MI
172-16 5.23mm 400m First Red Hill Base MI
315-22 4.92mm 200m PE
24-4 Tafelberg MI
168-5 7.46mm 600m First Red Hill
304-14 6.08mm Cave Bay PE
304-24 6.38mm Cave Bay PE
18-8 Krater Koppie
309-16 4.08mm 400m PE
24-3 Tafelberg MI
164-9 8.23mm Katedraal Krans Azorella MI
163-17 4.92mm Katedraal Krans Azorella MI
120-20 5.38mm Pringlea Tate's Hill MI
110-3 5.15mm Albatross Lakes Ditrichum MI
110-27 4.64mm Albatross Lakes Ditrichum MI
70-4 Skua Ridge MI
353-7 8.15mm Long Ridge S MI
125-4 8.46mm 600m Halfway Kop MI
150-10 5.38mm 200m Juniors Kop MI
75-2 vZB Pringlea MI
150-4 6.85mm 200m Junior's Kop MI
140-32 5.08mm Repetto's Hill MI
353-2 8.15mm Long Ridge S MI
173-1 8.08mm 400m First Red Hill Base MI
168-4 8.08mm 600m First Red Hill
167-22 4.69mm 600m First Red Hill MI
173-2 8.08mm 400m First Red Hill Base MI
65-3 Skua Ridge MI
84-2 Albatross Lakes MI
126-1 5.15mm 600m Halfway Kop MI
172-18 5.31mm 400m First Red Hill Base MI
118-14 5.38mm Stony Ridge MI
75-16 VdB Pringlea
110-18 4.23mm Ditrichum Albatross Lakes MI
150-1 8.62mm 200m Juniors MI
138-8 5.23mm Cape Davis Rocks MI
172-73 4.69mm 400m First Red Hill Base MI
138-7 6.38mm Cape Davis Rocks MI
142-7 4.23mm Azorellakop MI
142-9 4.92mm Azorellakop MI
164-10 Katedraalkrans MI
68-38 Skua Ridge MI
143-7 5.31mm Azorellakop MI
126-52 4.23mm 600m Halfway Kop MI
140-24 5.00mm Repetto's Hill MI
136-11 4.54mm Lou-se-kop MI
0.2324
Clade 4-3
E.viridis 400x12 Heard Island
E.viridis 400x21 Heard Island
0.0438
Outgroup
0.

A neighbour joining p-distance tree with *E. viridis* as outgroup is presented in Fig. 17. The molecular clock, with a clock rate of 2.3 % sequence divergence per million years (MY) based on the arthropod mtDNA survey of Brower (1994), was utilised to determine the time when the individuals in each 4-step clade last shared a common ancestor so as to give a rough indication of when each of the 4-step clades originated on the PEIA. A Neighbour-Joining p-distance tree (Fig. 17) as well as an ultrametric tree obtained with BEAST (Fig. 18) to estimate times of coalescence were utilised. The results obtained are presented in Table 5. All BEAST estimates are older than those estimated by Neighbour-Joining uncorrected p-distance values. In each case, clade 4-4, representing *E. kucheli* (Grobler *et al.*, 2006), exhibits to oldest coalescence times with nested clade 4-5, consisting of clades 4-5a and 4-5b, exhibiting the next oldest coalescence times. This supports the theory that nested clade 4-5 was the first to colonize Marion Island.

Table 4 BEAST 1.6.1 (Drummond & Rambaut, 2007) statistics as analyzed with Tracer v1.5 (Drummond & Rambaut, 2007).

Statistic	Mean	ESS
posterior	-3768.93	961.232
prior	-401.868	288.1
likelihood	-3367.062	1592.394
treeModel.rootHeight	4.593	13816.543
tmrca(4-1)	0.225	2918.564
tmrca(4-2a)	0.235	6186.949
tmrca(4-2b)	5.668E-2	11594.391
tmrca(4-3)	0.218	3832.055
tmrca(4-5a)	0.309	2837.015
tmrca(4-5b)	0.268	2842.287
tmrca(4-6)	0.21	4599.945
tmrca(Outgroup)	3.245E-2	4334.886
tmrca(4-4)	0.514	8447.389
constant.popSize	3.057	5423.428
ac	0.163	3522.169
ag	2.888	1715.709
at	8.15E-2	3099.201
cg	0.195	1447.834
gt	1.82E-2	2102.082
alpha	1.01	916.967
pInv	0.681	494.606
clock.rate	2.3E-2	-
treeLikelihood	-3367.062	1592.394
coalescent	-396.494	5675.378

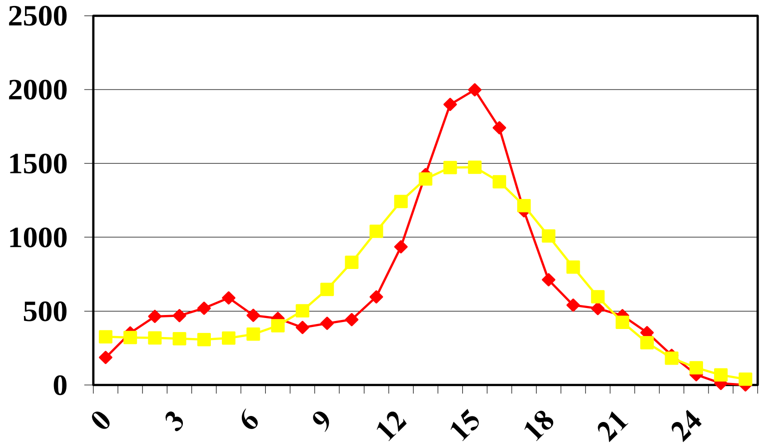
Table 5 Estimates of lineage coalescence for the major clades as determined by Neighbour-Joining (NJ) uncorrected p-distance values (Fig. 17) and BEAST (Fig. 18) using a clock rate of 2.3 % sequence divergence per million years (MY) based on the arthropod mtDNA survey of Brower (1994).

Clade	**NJ estimates**	**BEAST estimates**
Clade 4-1	0.133 MYA	0.2388 MYA
Clade 4-2a	0.175 MYA	0.2479 MYA
Clade 4-2b	0.049 MYA	0.0669 MYA
Clade 4-3	0.157 MYA	0.2324 MYA
Clade 4-4 (*E. kucheli*)	0.312 MYA	0.5109 MYA
Clade 4-5a	0.193 MYA	0.3206 MYA
Clade 4-5b	0.216 MYA	0.2667 MYA
Clade 4-6	0.132 MYA	0.2189 MYA

Mismatch analysis and population expansion

Fig. 19 a-j comprises of mismatch distributions under the sudden expansion model for the archipelago as a whole, each island on its own as well as the mismatch distributions of each of the eight discrete clades as identified in the phylogenetic trees (Figs. 15 & 16). Fig. 20 a-j, on the other hand, comprises the mismatch distributions under the spatial expansion model, of the archipelago as a whole, each island on its own as well as the mismatch distributions of each of the eight discrete clades as identified in the phylogenetic trees (Figs. 15 & 16). Both SSD and raggedness index values are shown in Table 6 under the sudden expansion model and in Table 7 under the spatial expansion model. None of these values shows any significant deviation from either the sudden expansion model or the spatial expansion model ($P > 0.05$), indicating a recent population expansion for each island as well as for each group on its own. In each case, demographic expansions predate range expansions, except in the cases of clades 4-2b and 4-6. The earliest demographic expansion for the different clade populations is estimated to have occurred more than 100 000 years ago (clades 4-1, 4-3 & 4-5a) with the most recent demographic expansion occurring more than 40 000 years ago (clades 4-b & 4-6). The earliest range expansions occurred approximately 170 000 years ago in clade 4-2b and the most recent approximately 40 000 years ago in clade 4-5b. Under the assumption of a purely demographic expansion, the populations represented by each clade were inferred to have expanded from small effective female population sizes to large effective female population sizes. Clades 4-5a & 4-6 needed larger initial effective female population sizes in order to explain demographic expansion. Under the assumption of a spatial expansion, populations represented in clades 4-5a, 4-3 & 4-2a required large effective female population sizes and no genetic exchange with neighboring populations to explain the inferred spatial expansion, while the population that is represented by clade 4-6 required a large effective female population size and very little genetic exchange with neighboring populations. The population represented by clade 4-5b required a small effective female population size and extensive genetic exchange with neighboring populations to explain the inferred spatial expansion. This is presumably due to individual 138-5 that may be from another population that was poorly sampled. Clade 4-5b also nested with clade 4-5a. Clade 4-4 also required a degree of genetic exchange with neighboring populations to explain the inferred spatial expansion, and this may possibly also be explained by individual 17-14 that is from another poorly sampled population.

(a)


2500
2000
1500
1000
500
0
0
3
6
9
12
15
18
21
24

(b)


1600
1400
1200
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800
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400
200
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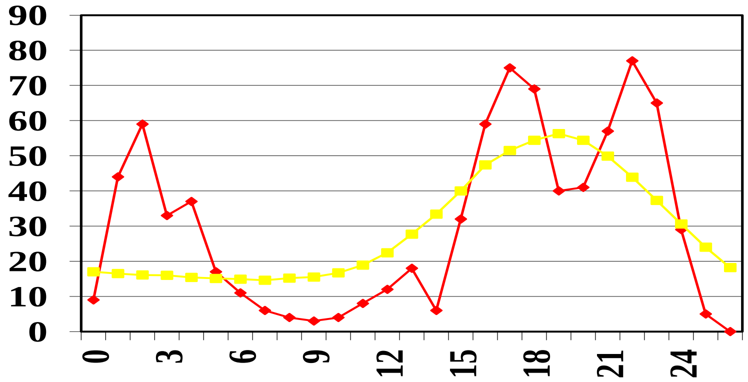
24

(c)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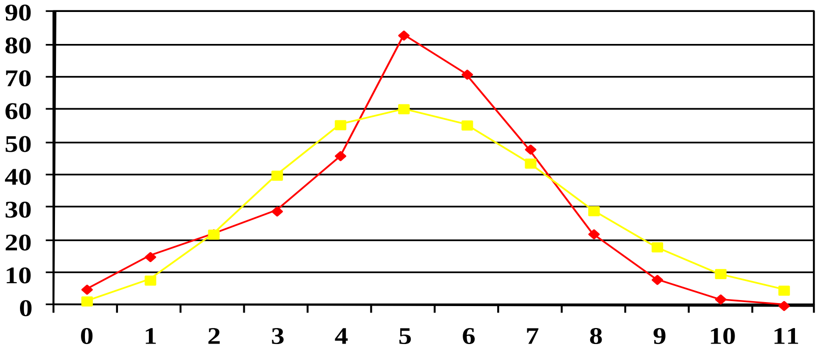
24

(d)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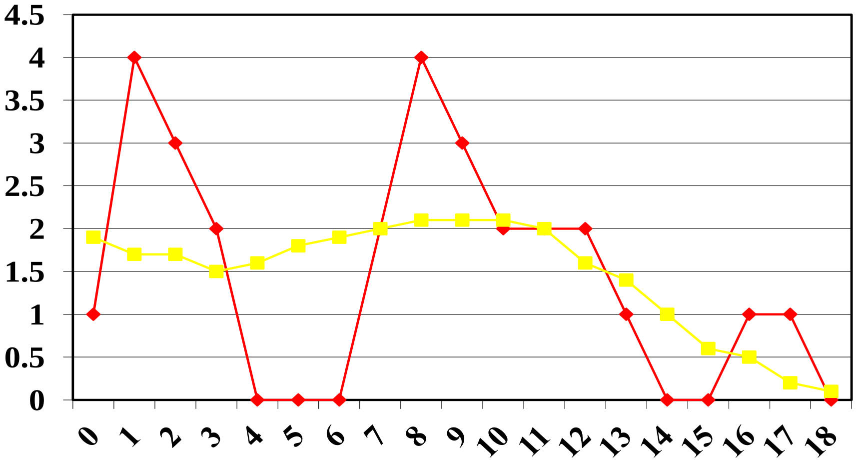
10
11

(e)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4
3.5
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2.5
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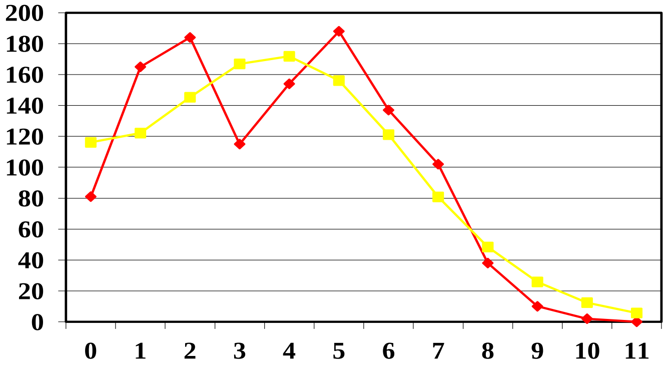
1.5
1
0.5
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

(f)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120
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80
60
40
20
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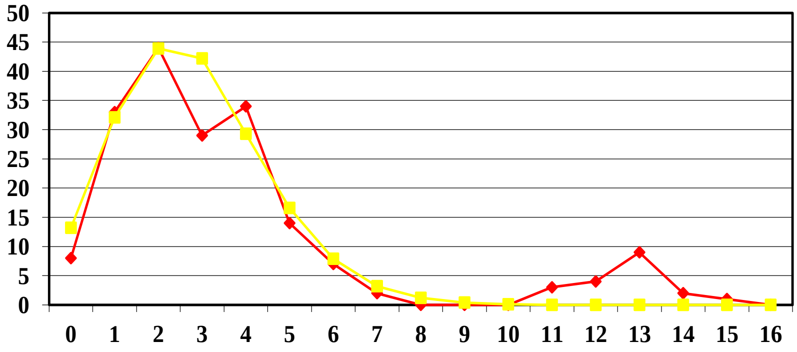
(g)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45
40
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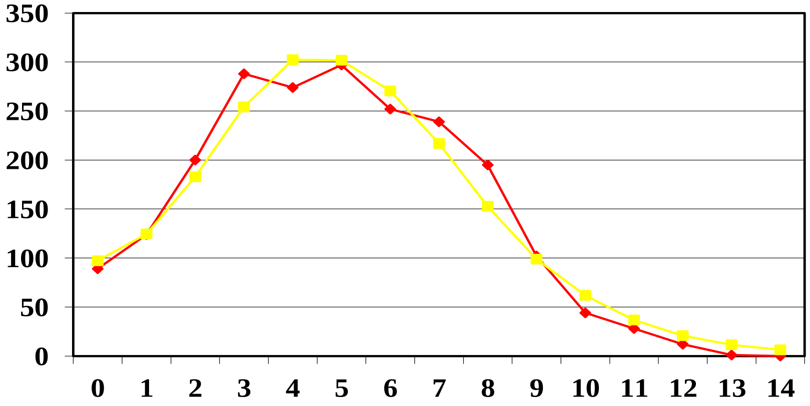
30
25
20
15
10
5
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16

(h)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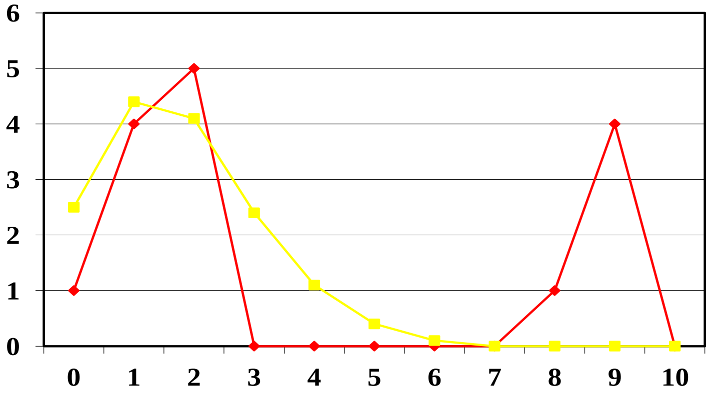
300
250
200
150
100
50
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14

(i)



(j)

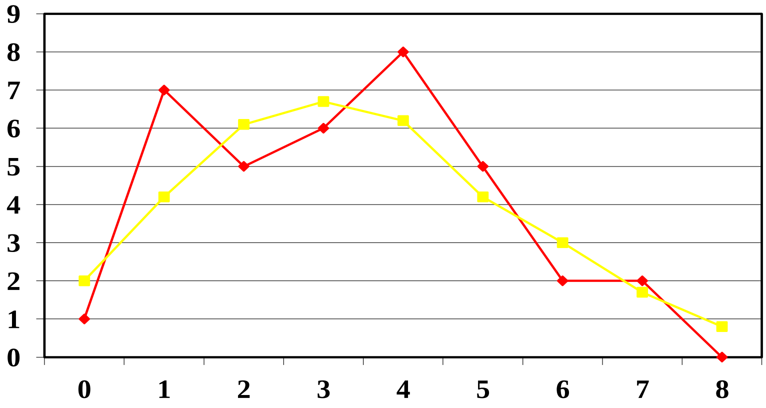
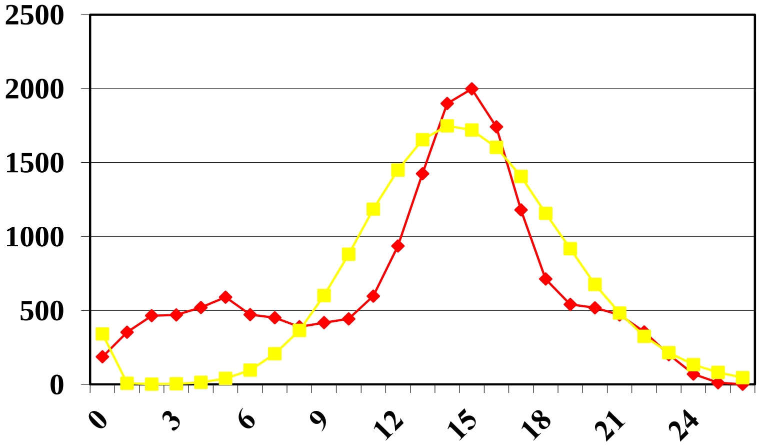


Fig. 19 Mismatch distribution estimated under the sudden expansion model for the different data sets: a) Prince Edward Islands Archipelago (PEIA), b) Marion Island (MI), c) Prince Edward Island (PEI), d) nested clade 4-1, e) clade 4-2a, f) nested clade 4-3, g) nested clade 4-4, h) clade 4-5a and i) clade 4-5b j) nested clade 4-6. The yellow line represents the simulated stepwise expansion model and the red line represents the observed data. No mismatch analyses were possible for clade 4-2b because of a small sample size.

Table 6 Mismatch parameters estimated under the sudden expansion model: τ is the expansion parameter or date of the Growth or Decline measured in units of mutational time with $\tau = 2ut$ where u is the mutation rate and t is the time in generations. The timing of the most important expansion in each group ($t_{divergence}$) was calculated based on the equation $\tau = 2\mu t$. θ_0 and θ_1 are the substitution rates before and after expansion. SSD is the test of the validity of a stepwise expansion model based on the sum of the square deviations between the observed and the expected mismatch. The raggedness index quantifies the smoothness of the observed pairwise differences distribution. PEIA = Prince Edward Islands Archipelago; PEI = Prince Edward Island; MI = Marion Island. The significance of both SSD and the raggedness index are estimated with a parametric bootstrap approach (probability values: * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$).

Population	Mean number of differences	Mismatch observed variance	τ (alpha = 0.100 confidence values)	$t_{divergence}$ (years)	θ_0/ $N_{ft = 0}$	θ_1/ $N_{ft = 0}$	SSD	P(Sim. SSD ≥ Obs. SSD)	Raggedness index	P(Sim. Rag. ≥ Obs. Rag.)
PEIA	12.838	30.069	15.448 (10.840-18.299)	379464 (266273-449496)	0.004/ 98	52.266/ 1283861	0.0049468	0.179	0.00453067	0.367
PEI	14.609	59.701	20.406 (13.926-24.506)	501252 (342078-601965)	0.002/ 49	48.091/ 1181306	0.0127341	0.095	0.01198245	0.297
MI	11.087	25.953	14.458 (9.697-17.828)	355146 (238197-437926)	0.002/ 49	38.125/ 936502	0.0088584	0.131	0.00598689	0.414
4-1	5.057	3.894	5.494 (4.232-6.676)	134954 (103954-163989)	0.000/ 0	>99999.0/ $>2\times10^9$	0.0103789	0.112	0.02792997	0.177
4-2a	7.179	23.411	10.586 (4.113-15.930)	260034 (101031-391304)	0.000/ 0	13.398/ 329108	0.0290171	0.781	0.03698980	0.941
4-2b	2.000	0.0000	-	-	-	-	-	-	-	-
4-3	3.728	5.216	4.984 (2.090-7.809)	122426 (51338-191820)	0.032/ 786	9.736/ 239154	0.0071099	0.599	0.01708562	0.822
4-4	3.742	11.272	2.867 (1.539-3.842)	70424 (37803-94374)	0.002/ 49	69.531/ 1707958	0.0090510	0.313	0.04321330	0.465
4-5a	4.912	6.891	4.570 (2.711-8.467)	112257 (66592-207983)	1.106/ 27167	23.008/ 565168	0.0012460	0.865	0.00700866	0.950
4-5b	3.867	13.410	1.771(0.293-3.455)	43502 (7197-84868)	0.000/ 0	>99999.0/ $>2\times10^9$	0.1221409	0.119	0.27111111	0.252
4-6	3.278	3.349	3.033 (1.330-6.082)	47502 (32670-149398)	0.643/ 15794	31.055/ 762834	0.0126028	0.643	0.05169753	0.721

(a)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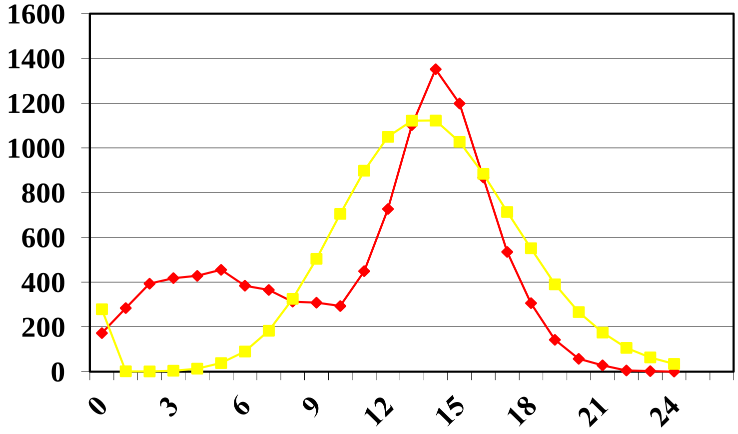
(b)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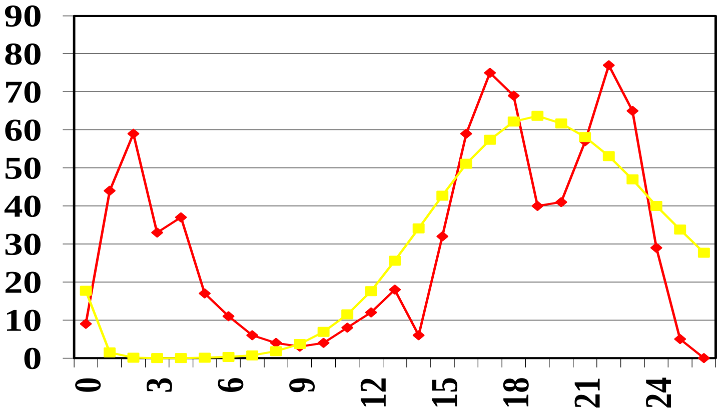
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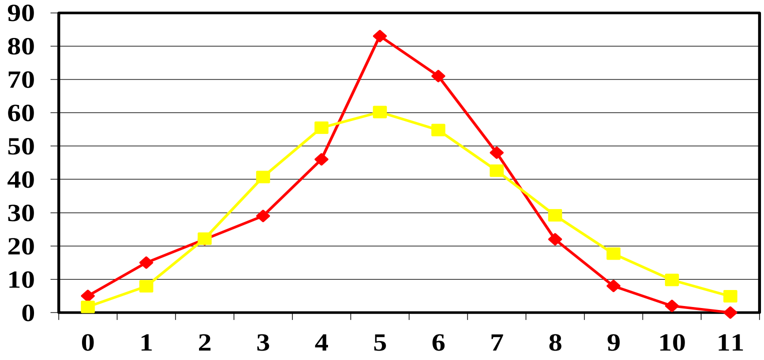
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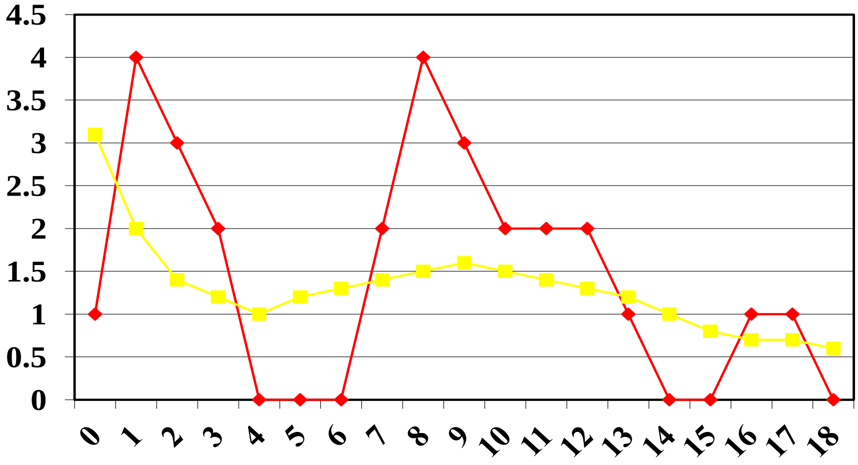
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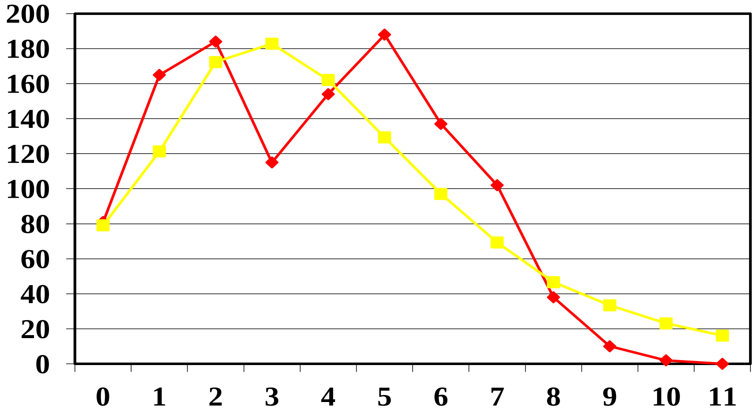
(f)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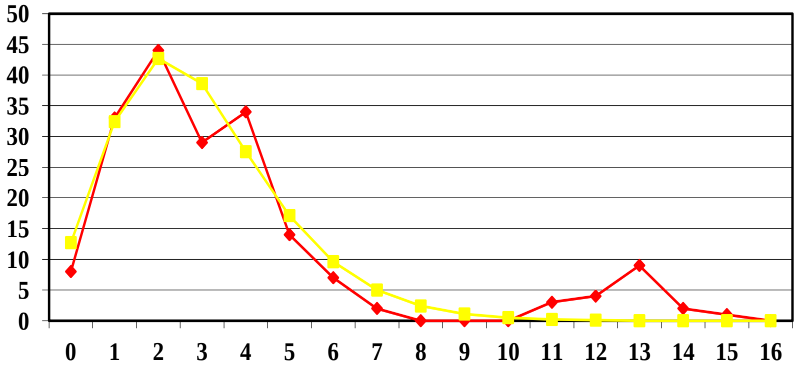
(g)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(h)


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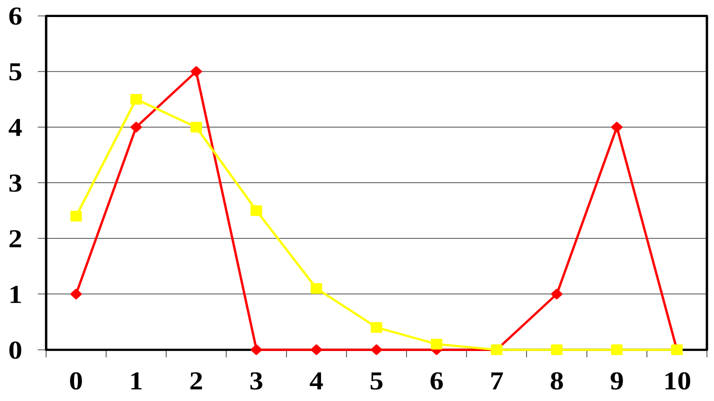

(j)

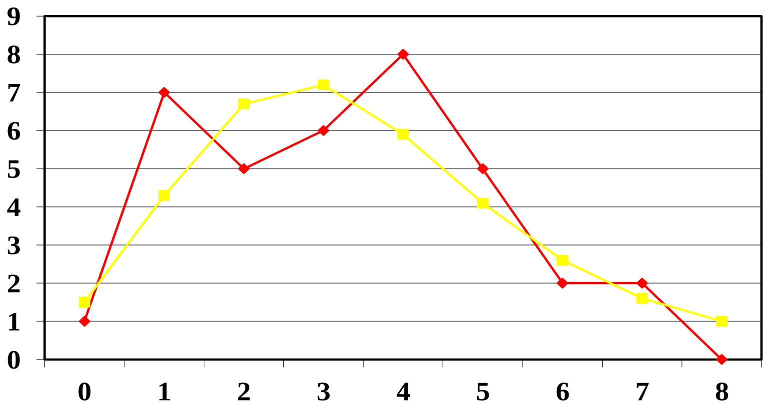

Fig. 20 Mismatch distribution estimated under the spatial expansion model for the different data sets: a) Prince Edward Islands Archipelago (PEIA), b) Marion Island (MI), c) Prince Edward Island (PEI), d) nested clade 4-1, e) clade 4-2a, f) nested clade 4-3, g) nested clade 4-4, h) clade 4-5a and i) clade 4-5b j) nested clade 4-6. The yellow line represents the simulated stepwise expansion model and the red line represents the observed data. No mismatch analyses were possible for clade 4-2b because of a small sample size.

Table 7 Mismatch parameters estimated under the spatial expansion model: τ is the expansion parameter or date of the Growth or Decline measured in units of mutational time with $\tau = 2ut$ where u is the mutation rate, and t is the time in generations. The timing of the most important expansion in each group ($t_{divergence}$) was calculated based on the equation $\tau = 2\mu t$. θ is ancestral population size and $M = 2Nm$ is an indication of migration. m is the rate at which the sampled deme would exchange migrants with a unique population of infinite size. The effective female population size $N_f = \theta/2u$. SSD is the test of the validity of a stepwise expansion model based on the sum of the square deviations between the observed and the expected mismatch. The raggedness index quantifies the smoothness of the observed pairwise differences distribution. PEIA = Prince Edward Islands Archipelago; PEI = Prince Edward Island; MI = Marion Island. The significance of both SSD and the raggedness index are estimated with a parametric bootstrap approach (probability values: * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$).

Population	Mean number of differences	Mismatch observed variance	τ (alpha = 0.100 confidence values)	$t_{divergence}$ (years)	θ / N_f	M / m	SSD	P(Sim. SSD ≥ Obs. SSD)	Raggedness index	P(Sim. Rag. ≥ Obs. Rag.)
PEIA	12.838	30.069	14.238 (11.912-16.261)	349742 (292606-399435)	0.884/ 21714.566	49.775/ 0.0011	0.009	0.007**	0.00453067	0.610
PEI	14.609	59.701	17.413 (14.268-21.705)	427732 (350478-533161)	3.507/ 86145.910	40.687/ 0.0002	0.019	0.000***	0.01198245	0.475
MI	11.087	25.953	13.889 (11.028-15.340)	341169 (270891-376811)	0.157/ 3856.546	37.661/ 0.0049	0.015	0.004**	0.00598689	0.685
4-1	5.057	3.894	5.494 (3.301-6.565)	134954 (81085-161262)	0.001/ 24.564	1003.383/ 20.4238	0.010	0.095	0.02792997	0.200
4-2a	7.179	23.411	6.946 (0.741-20.289)	170621 (18201-498378)	6.053/ 148685.83	2.053/ 0.000006	0.034	0.718	0.03698990	0.980
4-2b	2.000	0.0000	-	-	-	-	-	-	-	-
4-3	3.728	5.216	1.964 (0.810-5.255)	48243 (19896-129083)	2.608/ 64062.884	28.924/ 0.0002	0.011	0.271	0.01708562	0.740
4-4	3.742	11.272	2.025 (1.284-4.047)	49742 (31540-99410)	0.034/ 835.176	99999/ 59.867	0.008	0.339	0.04321330	0.473
4-5a	4.912	6.891	3.562 (2.332-6.298)	87496 (57283-154704)	1.923/ 47236.551	28.069/ 0.0003	0.002	0.747	0.00700866	0.966
4-5b	3.867	13.410	1.770 (0.732-3.267)	43478 (17980-80250)	0.001/ 24.564	99999/ 2035.479	0.122	0.057	0.27111111	0.222
4-6	3.278	3.349	2.414 (1.214-5.125)	59297 (29820-125890)	1.215/ 29845.247	99999/ 1.675	0.013	0.590	0.05169753	0.732

Table 8 Population expansion statistics showing Fu's Fs values (probability values: * *P* < 0.05, ** *P* < 0.01, *** *P* < 0.001), Tajima's D as well as Tajima's estimations for θ. PEIA = Prince Edward Islands Archipelago; PEI = Prince Edward Island; MI = Marion Island.

Population	Fu's F_s test	P(sim_Fs ≤obs_Fs)	Fu's estimations for θ	Tajima's D	P(sim_D ≤obs_D)	Tajima's estimations for θ
Ectemnorhinus						
PEIA	-23.98497***	0.00100	12.83831	-1.38277	0.04600	12.83831
PE	-13.56464***	0.00100	14.60854	-0.33924	0.44300	14.60854
Marion	-24.22080***	0.00100	11.08654	-1.40322	0.04300	11.08654
4-1	-17.73110***	0.00000	5.05698	-1.37102	0.06600	5.05698
4-2a	-1.11105	0.21200	7.17857	-1.49761	0.05900	7.17857
4-2b	0.69315	0.36800	2	0	1	2
4-3	-24.46672***	0.00000	3.72789	-1.55217	0.04200	3.72789
4-4	-6.90308***	0.00100	3.74211	-1.62575	0.04000	3.74211
4-5a	-25.57643***	0.00000	4.91235	-2.10023	0.00200	4.91235
4-5b	-0.80758	0.22100	3.86667	-1.19369	0.13500	3.86667
4-6	-4.03444**	0.01000	3.27778	-1.74560	0.02700	3.27778

Fu’s Fs statistic (Table 8) showed significant large negative values for most groups. Only clades 4-2a, 4-2b and 4-5b have no significant large negative values. A significant large negative Fs value is an indication of population expansion. The Fs values for clades 4-2a and 4-5b are still negative and thus show a tendency for population growth (Fu, 1997). The fact that clades 4-2a and 4-5b do not show significant Fs values may be due to some individuals in these clades being separated by up to seven missing haplotypes (Fig. 6). Clade 4-2b is the only clade with a positive Fs value, however as it comprises of only two individuals, it is not possible to compute any reliable statistics. Tajima’s (1983) estimate for θ (Table 8) is based on the calculation of the mean number of pairwise differences of the sequences. Tajima’s estimate of θ puts more weight on ancient mutations, therefore reflecting ancient population events (Fu, 1997).

Statistical analyses

Haplotype diversity (h) and nucleotide diversity (π) values for the PEIA as a whole, each island, and the different discrete clades as identified in the phylogenetic trees (Fig. 15 and Fig. 16) are summarised in Table 9. In every case, h is very close to 1. The number of haplotypes and parsimony informative sites are also summarised in Table 9. The number of haplotypes in the different clades as identified in the phylogenetic trees (Figs. 15 & 16) varied between 2 and 42, while the number of parsimony informative sites varied between 1 and 31.

Table 10 summarizes the population pairwise distance F_{ST} values as computed in Arlequin version 3.5.1.2 (Excoffier & Lischer, 2010) as well as the absolute number of migrants exchanged between two populations. This was computed between each of the eight discrete clades as identified in the phylogenetic trees (Figs. 15 & 16). F_{ST} assesses the variation in the subpopulations relative to that in the total population and has values between 0 and 1.0. An F_{ST} of zero means that all the subpopulations have the same gene frequencies while an F_{ST} of 1.0 means that the subpopulations have completely non-overlapping sets of alleles. Natural panmictic populations tend to have F_{ST} values that range between near zero up to just greater than 0.5. Values of F_{ST} above approximately 0.2 are considered "high". Consequently, all the Fst values in Table 10 can be considered "high" with the lowest value being 0.578 between genetically distinct clades 4-5a and 4-6. The only other F_{ST} values below 0.6 were those between genetically distinct clades 4-5a and 4-5b (F_{ST} = 0.580) and between genetically distinct clades 4-2a and 4-5a (F_{ST} = 0.583). In each case, the number of migrants exchanged between the distinct clades was less than one migrant per generation with the estimate of 0.366 migrants per generation, between clades 4-5a and 4-6, being the highest estimate obtained. Thus, the higher the F_{ST} value the lower the migration rate. The Hudson *et al.*'s *(*1992) F_{ST} values as estimated in DNASP 5.1 (Librado & Rozas, 2009) and presented in Table 11 show a similar trend to the F_{ST} values presented in Table 10. All Hudson *et al*.'s (1992) F_{ST} values can again be considered high with the lowest F_{ST} values observed between clades 4-2a and 4-5a ($F_{ST} = 0.56502$) and between clades 4-5a and 4-5b ($F_{ST} = 0.59530$). The N_{ST} values in Table 12 (F_{ST} to which the correction of Jukes & Cantor (1969) has been applied) almost mirror the F_{ST} values in Table 11, with the differences being negligible. The number of pairwise differences between populations as presented in Table 13 reveal that the number of pairwise differences between populations correlates with the F_{ST} values found in the previous tables: The lower the F_{ST} values between two genetically distinct clades, the lower the number of pairwise differences between them. This is to be expected as fewer differences show a closer resemblance between populations whereas high F_{ST} values are an indication of differentiation between populations. Table 14 shows that the variation between the genetically distinct clades is more than double the variation within the clades. The overall fixation index of 0.73 is also very high. All F_{ST} values suggest that there are a low number of overlapping alleles between clades with less than one migrant between clades per generation. Given that these distinct clades overlap in geographical range, it may be possible that there is either some barrier that prevents interbreeding between individuals from different genetically identified clades, or that insufficient time has passed to eradicate genetic signatures of past isolation coupled with differentiation. Table 15 summarizes the tau values as well as their *P* values as calculated by Arlequin version 3.5.1.2 (Excoffier & Lischer, 2010) for divergence times between the different genetically identified clades. None of the tau values have *P* values under the 0.05 confidence level. Divergence times between clade 4-4, representing *E. kucheli* (Grobler *et al*., 2006), and the other clades are in each instance the oldest.

Table 9 Summary of mitochondrial DNA diversity. NH = number of unique haplotypes, h = haplotype diversity and π = nucleotide diversity. PEIA = Prince Edward Islands Archipelago; PEI = Prince Edward Island; MI = Marion Island.

Dataset (N)	NH	h	π	Parsimony informative sites
PEIA (*n* = 187)	131	0.9893	0.01451	84
MI (*n* = 146)	99	0.984	0.01253	69
PEI (*n* = 41)	34	0.989	0.01651	43
Clade 4-1 (*n* = 27)	23	0.986	0.00571	11
Clade 4-2a (*n* = 8)	7	0.964	0.00577	4
Clade 4-2b (*n* = 2)	2	1	0.00226	0
Clade 4-3 (*n* = 49)	30	0.931	0.00421	14
Clade 4-4 (*n* = 20)	14	0.958	0.00423	9
Clade 4-5a (*n* = 66)	42	0.959	0.00552	31
Clade 4-5b (*n* = 6)	5	0.933	0.00437	1
Clade 4-6 (*n* = 9)	8	0.972	0.00370	1

Table 10 Population pairwise distance F_{ST} values as computed in Arlequin version 3.5.1.2 (Excoffier & Lischer, 2010) using Tamura Nei (1993) distances and gamma as estimated by jModelTest 0.1.1 (Posada, 2008; Guindon & Gascuel, 2003). Pairwise F_{ST} values can be used as short-term genetic distances between populations (Reynolds, *et al*.; 1983; Slatkin, 1995). All *P* values estimated for F_{ST} values are significant at the 0.05 level. The value after the "/" is the *M* value (Slatkin, 1991) obtained in Arlequin version 3.5.1.2 (Excoffier & Lischer, 2010) where *M* is the absolute number of migrants exchanged between two populations.

	4-2a	4-2b	4-3	4-4	4-5a	4-5b	4-6
4-1	0.70819 / 0.20602	0.71085 / 0.20339	0.76985 / 0.14948	0.79697 / 0.12737	0.67993 / 0.23537	0.70290 / 0.21134	0.70031 / 0.21397
4-2a		0.62887 / 0.29508	0.78374 / 0.13797	0.78003 / 0.14100	0.58263 / 0.35818	0.67785 / 0.23763	0.64613 / 0.27384
4-2b			0.74562 / 0.17058	0.78705 / 0.13529	0.60757 / 0.32295	0.70664 / 0.20757	0.72504 / 0.18962
4-3				0.84003 / 0.09522	0.71118 / 0.20305	0.76549 / 0.15317	0.75907 / 0.15870
4-4					0.71450 / 0.19979	0.79462 / 0.12923	0.80109 / 0.12415
4-5a						0.57977 / 0.36241	0.57758 / 0.36567
4-5b							0.68816 / 0.22657

Table 11 Hudson *et al*.'s (1992) F_{ST} values as estimated in DNASP 5.1 (Librado & Rozas, 2009). An average F_{ST} value of 0.72745 was estimated as well as an average Nm (Number of migrants) of 0.09. Nm is based on the island model of population structure: Fst = 1 / (1 + 2Nm) (Wright, 1951).

	4-2a	4-2b	4-3	4-4	4-5a	4-5b	4-6
4-1	0.68663	0.77317	0.74400	0.78477	0.65725	0.70255	0.70519
4-2a		0.70232	0.74327	0.75402	0.56502	0.67169	0.63053
4-2b			0.78770	0.82056	0.69697	0.74857	0.75515
4-3				0.82590	0.70037	0.74500	0.75371
4-4					0.71837	0.78261	0.79474
4-5a						0.59430	0.60340
4-5b							0.66741

Table 12 Lynch and Crease's (1990) N_{ST} / Number of migrants (Nm) as estimated in DNASP 5.1 (Librado & Rozas, 2009). An average N_{ST} value of 0.72941 was estimated as well as an average Nm of 0.09. Nm is based on the island model of population structure: Nst = 1 / (1 + 2Nm) (Wright, 1951).

	4-2a	4-2b	4-3	4-4	4-5a	4-5b	4-6
4-1	0.68902	0.77505	0.74630	0.78712	0.65951	0.70452	0.70724
4-2a		0.70382	0.74548	0.75615	0.56682	0.67339	0.63219
4-2b			0.78924	0.82205	0.69848	0.74978	0.75654
4-3				0.82797	0.70238	0.74672	0.75553
4-4					0.72031	0.78437	0.79656
4-5a						0.59564	0.60496
4-5b							0.66869

Table 13 Above diagonal: Average number of pairwise differences between genetically distinct clades (PiXY). Diagonal elements (indicated with grey shading): Average number of pairwise differences within genetically distinct clades (PiX). Below diagonal: Corrected average pairwise difference (PiXY-(PiX+PiY)/2). All values were calculated in Arlequin version 3.5.1.2 (Excoffier & Lischer, 2010) according to Nei & Li (1979) using Tamura Nei (1993) distances and gamma as estimated by jModelTest 0.1.1 (Posada ,2008; Guindon & Gascuel, 2003).

	4-1	4-2a	4-2b	4-3	4-4	4-5a	4-5b	4-6
4-1	5.270	18.179	17.098	19.121	23.111	16.19	16.816	15.675
4-2a	12.847	5.393	12.863	19.240	19.992	12.461	15.043	12.263
4-2b	13.433	9.136	2.061	14.606	17.689	12.242	12.640	11.541
4-3	14.556	14.613	11.646	3.860	24.300	15.819	16.663	15.589
4-4	18.503	15.321	14.685	20.397	3.947	16.751	19.457	18.907
4-5a	10.995	7.195	8.642	11.320	12.208	5.139	11.708	11.111
4-5b	12.112	10.277	9.540	12.664	15.415	7.069	4.139	11.846
4-6	11.348	7.875	8.819	11.968	15.242	6.849	8.085	3.383

Table 14 AMOVA analyses using Tamura Nei (1993) distances and gamma as estimated by jModelTest 0.1.1 (Posada ,2008; Guindon & Gascuel, 2003) as calculated by Arlequin version 3.5.1.2 (Excoffier & Lischer, 2010). The eight genetically distinct clades were used as different populations. Va and F_{ST}: *P*(random value > observed value) = 0.00000, *P*(random value = observed value) = 0.00000 and *P*(random value ≥ observed Value) = 0.00000+-0.00000.

Source of variation	**Degrees of freedom**	**Sum of squares**	**Variance components**	**Percentage of variation**
Among clades	7	907.362	6.19684 Va	73.04
Within clades	179	409.447	2.28742 Vb	26.96
Total	186	1316.810	8.48425	
Fixation Index F_{ST}: 0.73039				

Table 15 Divergence times allowing for unequal population sizes (tau) / tau *P* values. All values were calculated in Arlequin, version 3.5.1.2 (Excoffier & Lischer 2010) using Tamura Nei (1993) distances and gamma as estimated by jModelTest 0.1.1 (Posada, 2008, Guindon & Gascuel, 2003). Time in years (t) was determined using the equation $\tau = 2ut$, where $u = m_T\mu$ (m_T is the number of nucleotides used and μ is the mutation rate per generation), and is shown under the grey-shaded diagonal.

	4-1	4-2a	4-2b	4-3	4-4	4-5a	4-5b	4-6
4-1		8.887 / 0.478	10.073 / 0.414	10.649 / 0.482	14.243 / 0.535	7.414 / 0.541	8.471 / 0.312	7.931 / 0.397
4-2a	218300		6.126 / 0.654	10.666 / 0.387	11.279 / 0.420	4.487 / 0.437	6.928 / 0.570	5.056 / 0.541
4-2b	247433	150478		8.909 / 0.336	11.789 / 0.212	5.777 / 0.424	6.974 / 0.470	6.459 / 0.368
4-3	261581	261999	218840		16.597 / 0.457	7.872 / 0.6115	9.267 / 0.596	8.835 / 0.481
4-4	349864	277057	289584	407688		8.612 / 0.536	11.740 / 0.601	11.826 / 0.468
4-5a	182117	110218	141906	193367	211545		4.472 / 0.453	4.312 / 0.483
4-5b	208081	170179	171309	227634	288381	109850		5.456 / 0.487
4-6	194816	124195	158658	217022	290493	105919	134012	