OP-061 [Bee Biology]
Mitochondrial DNA Variability in the Honey bee Apis mellifera L., Implications for Conservation

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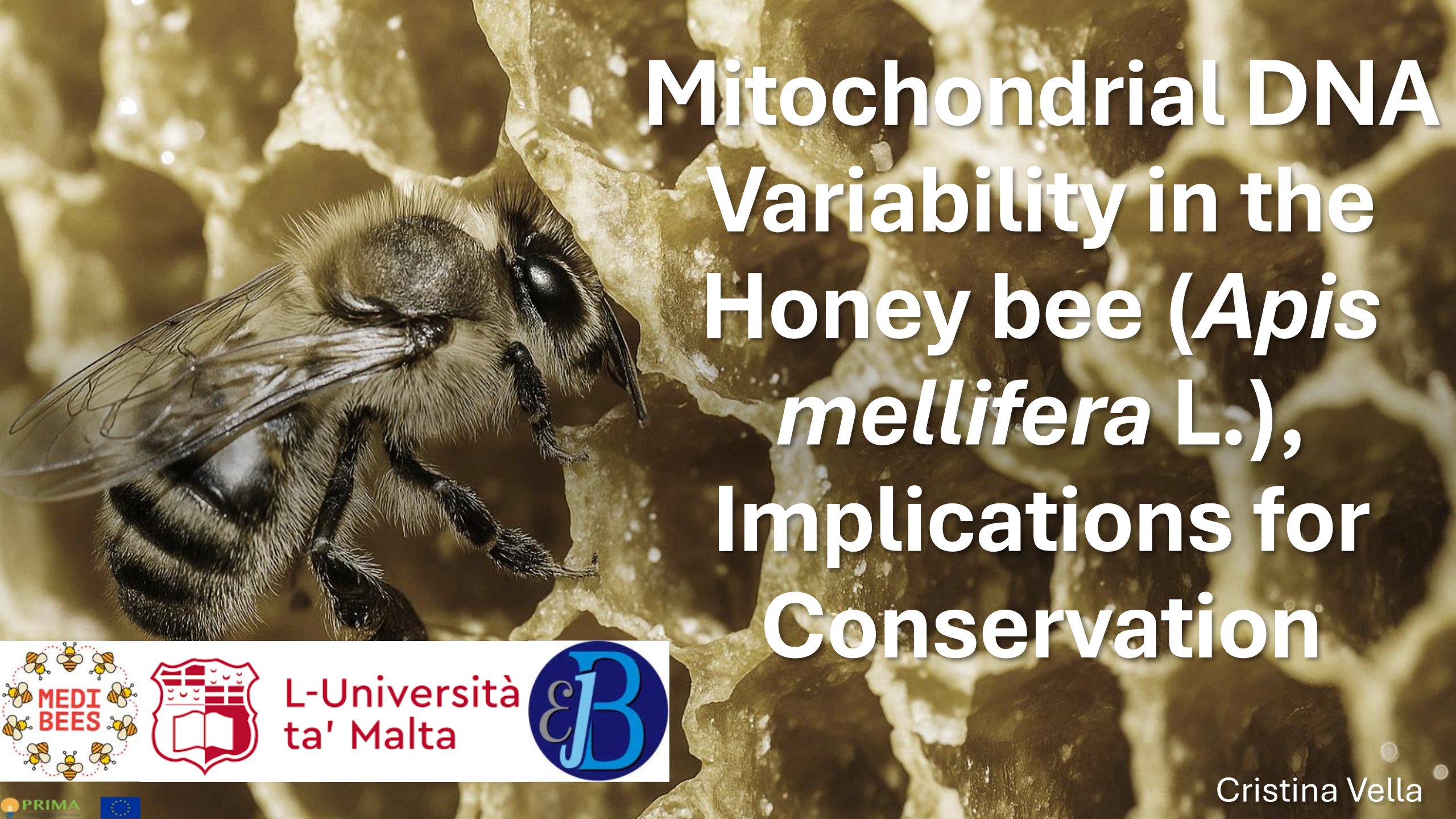
The Western honey bee (Apis mellifera L.) is a keystone species that plays a vital role in maintaining environmental health and agricultural productivity. However, it faces significant threats, including indiscriminate pesticide use, parasite ecosystem expansion, climate change, and the uncontrolled importation of non-native subspecies. The PRIMA project MEDIBEES (Monitoring the Mediterranean Honey Bee Subspecies and Their Resilience to Climate Change for Sustainable Agro-Ecosystems) aims to identify the current genetic structure of native honey bee populations across the Mediterranean and neighbouring regions to help support breeding programmes and conservation efforts.

A. mellifera subspecies may be classified into four major mitochondrial DNA lineages: A (Africa), M (Western and Northern Europe), C (Eastern and Central Europe) and O (Western and Central Asia), each of which is sub-divided into a number of haplotypes. The occurrence of non-native lineages is a strong indicator of introduction of foreign subspecies.

In this study, the mtDNA tRNA-COII region of over 1,344 DNA samples was amplified using standard PCR methods, sequenced and then analysed using Geneious Prime 2024 software. These samples were collected from the Mediterranean and neighbouring regions including A.m. ligustica (Italy), A.m. siciliana (Italy, Sicily), A.m. cypria (Cyprus), A.m. syriaca (Jordan and Lebanon), A.m. ruttneri (Malta), A.m. meda (Iran), A.m. anatoliaca and A.m. caucasica (Turkey), A.m. jemenitica (UAE and Oman), A.m. sahariensis (Morocco and Algeria), A.m. macedonica (Greece) and A.m. intermissa (Algeria).

Results indicate that lineage C, typical of A.m. ligustica and A.m. carnica, was present in a number of studied samples, suggesting the introduction of non-native C lineage subspecies through the importation of commercially managed colonies. This presentation will focus on describing the current distribution of mtDNA haplotypes within these subspecies as well as evidence of non-native lineages, indicating the possible introduction of other subspecies into these regions. The implications of the data including insights into the movement and transfer of subspecies in these areas and potential impact on local beekeeping practices will be discussed.



Mitochondrial DNA Variability in the Honey bee (*Apis mellifera* L.), Implications for Conservation

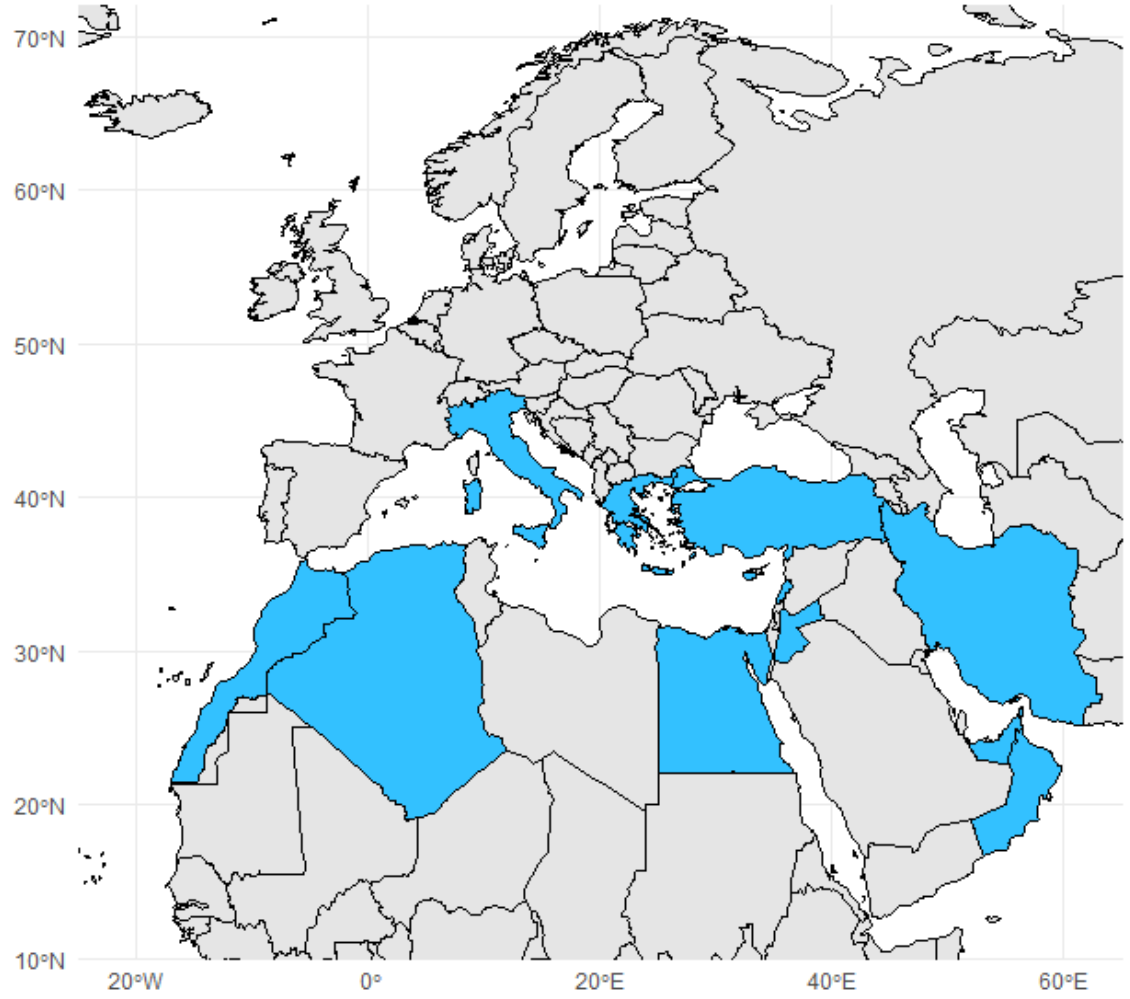
MEDI BEES

L-Università ta' Malta

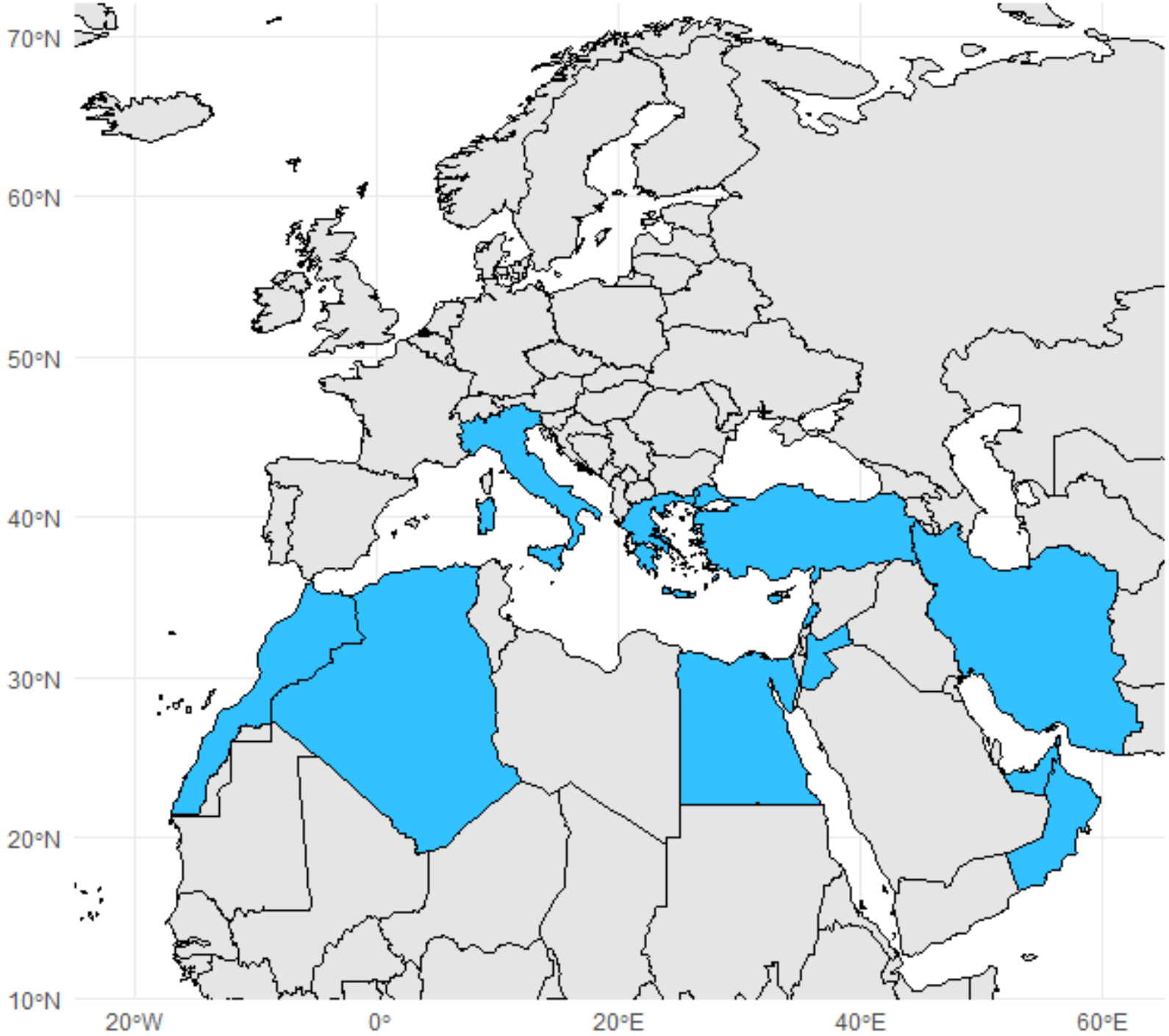
PRIMA

Cristina Vella

Aim



Identify mitochondrial DNA haplotypes of native honey bee subspecies from the Mediterranean and neighbouring regions


70°N
60°N
50°N
40°N
30°N
20°N
10°N
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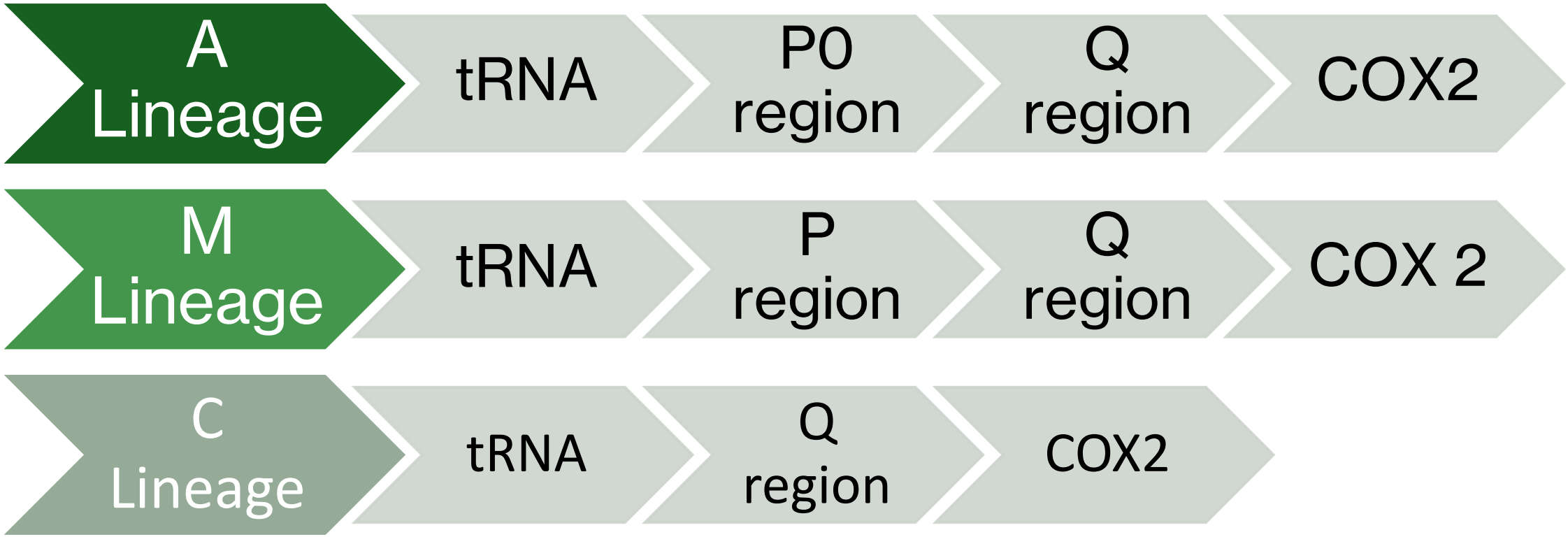
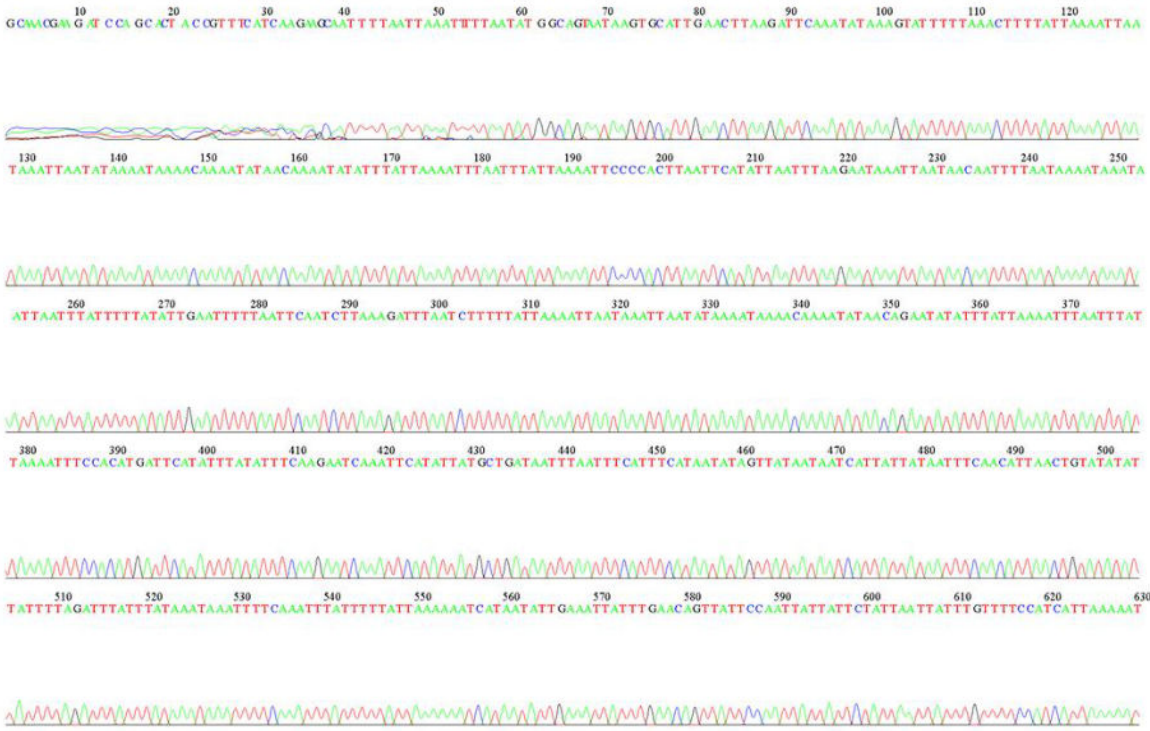
0°
20°E
40°E
60°E

tRNA-COX2 region in different mitochondrial DNA lineages



Results Strategy

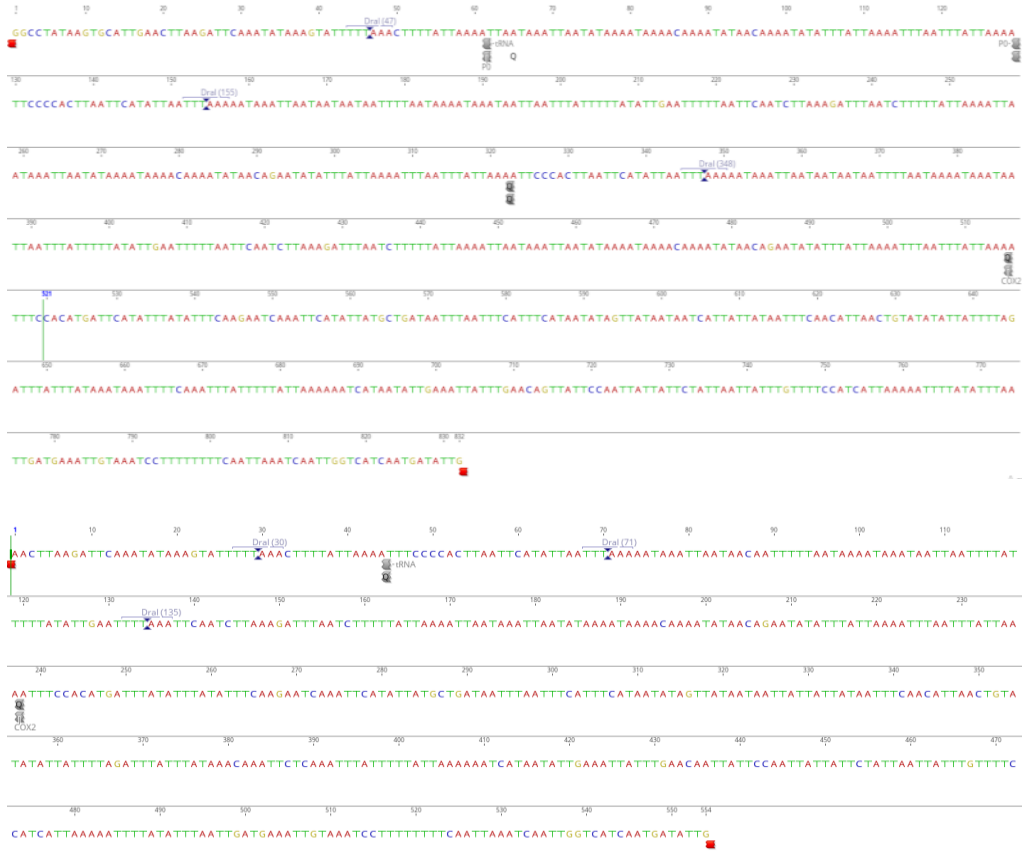
Amplification method - Madella et al.,(2021)



Results Strategy

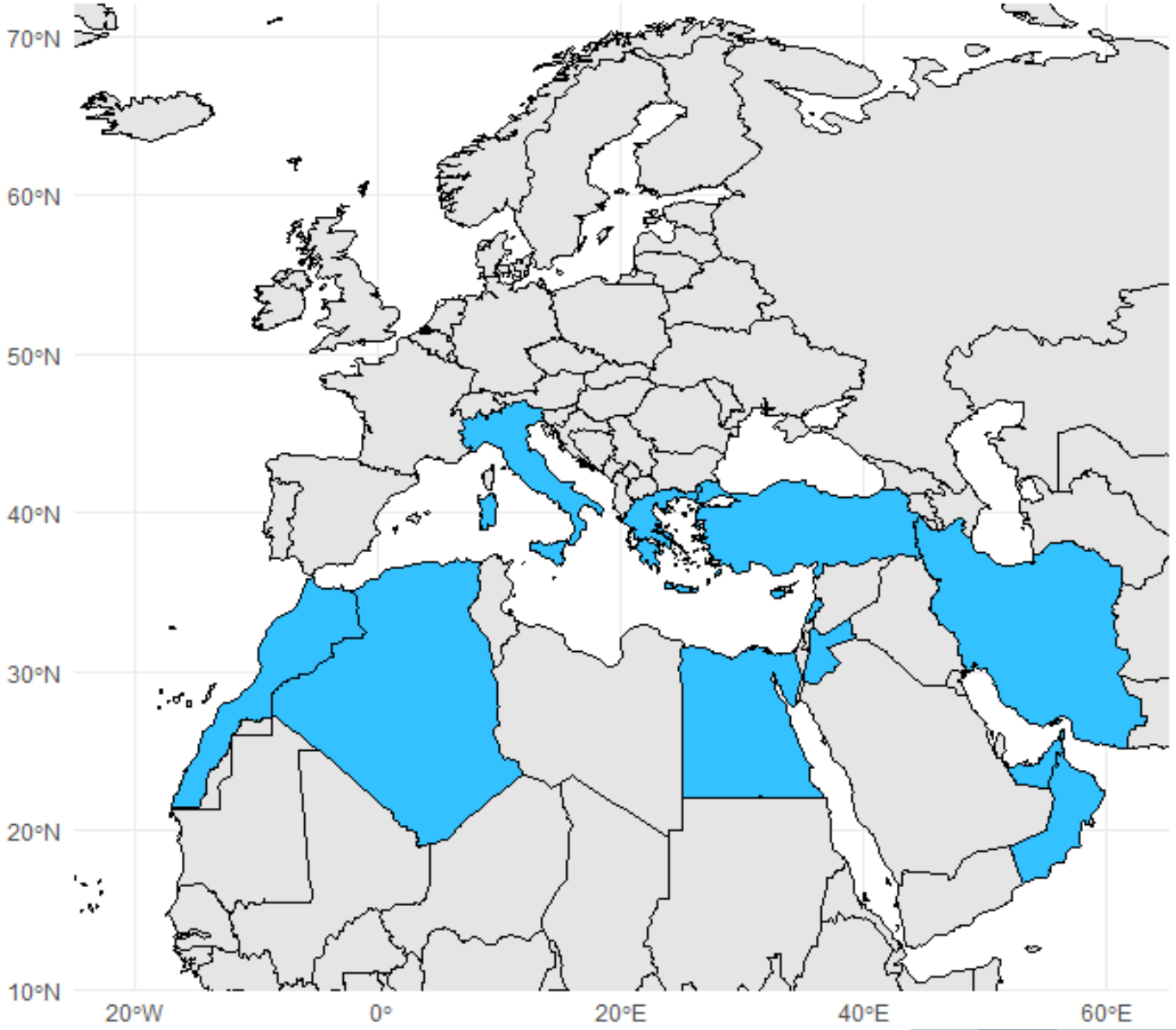
Sequence Analysis

- Presence/absence of the P element
- Number of repeats of Q region
- DraI sites



Haplotype assignment – Restriction maps and verified through Geneious prime

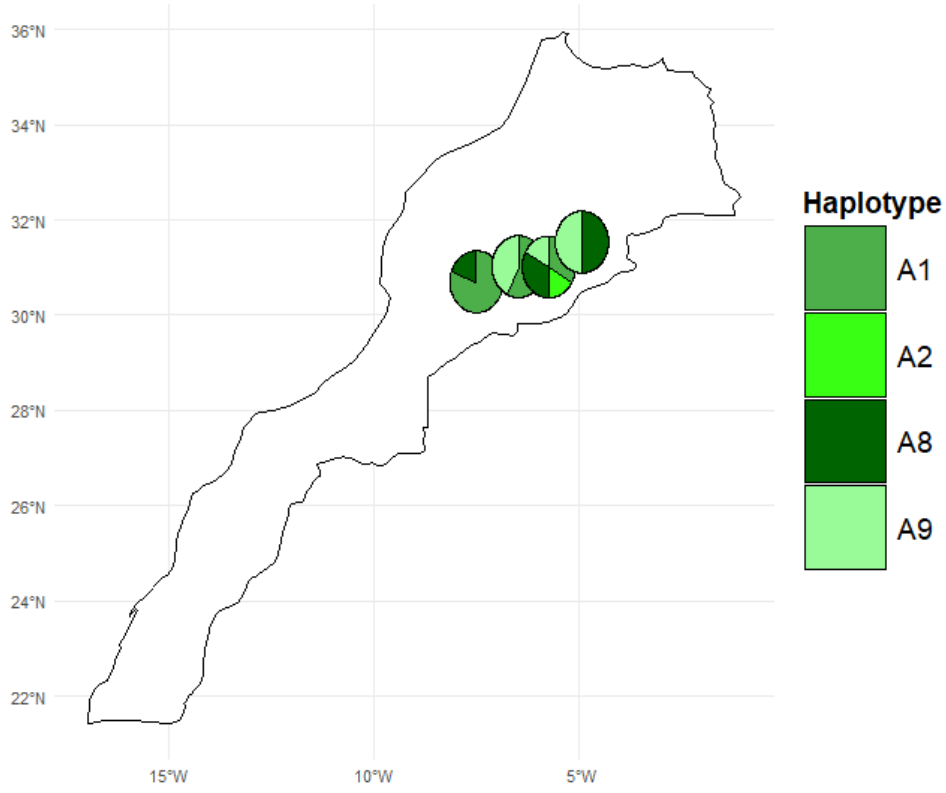
Results



70°N
60°N
50°N
40°N
30°N
20°N
10°N
20°W
0°
20°E
40°E
60°E

Morocco

- Sample No. 20
- Overall Haplotype Diversity Index: 0.68



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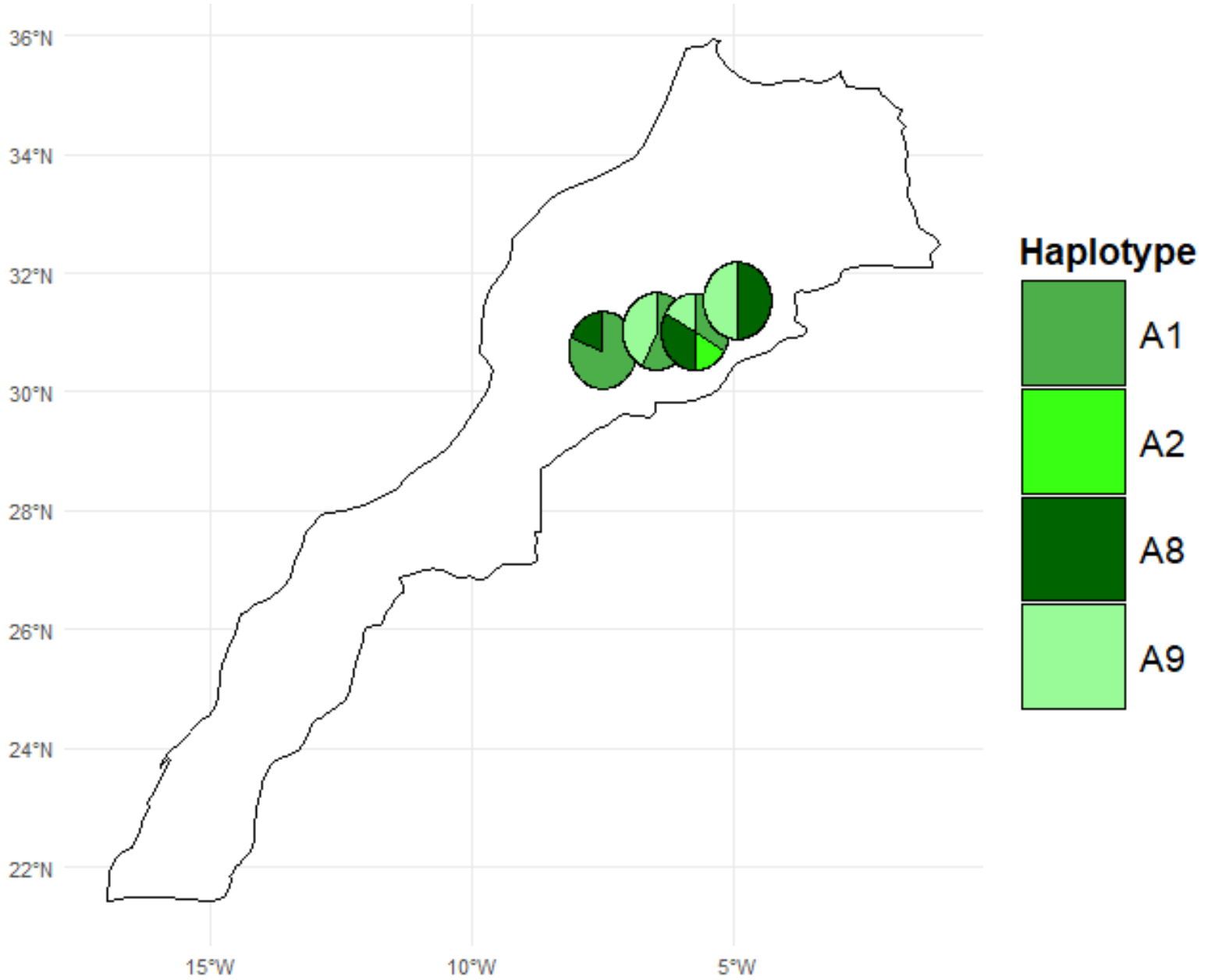
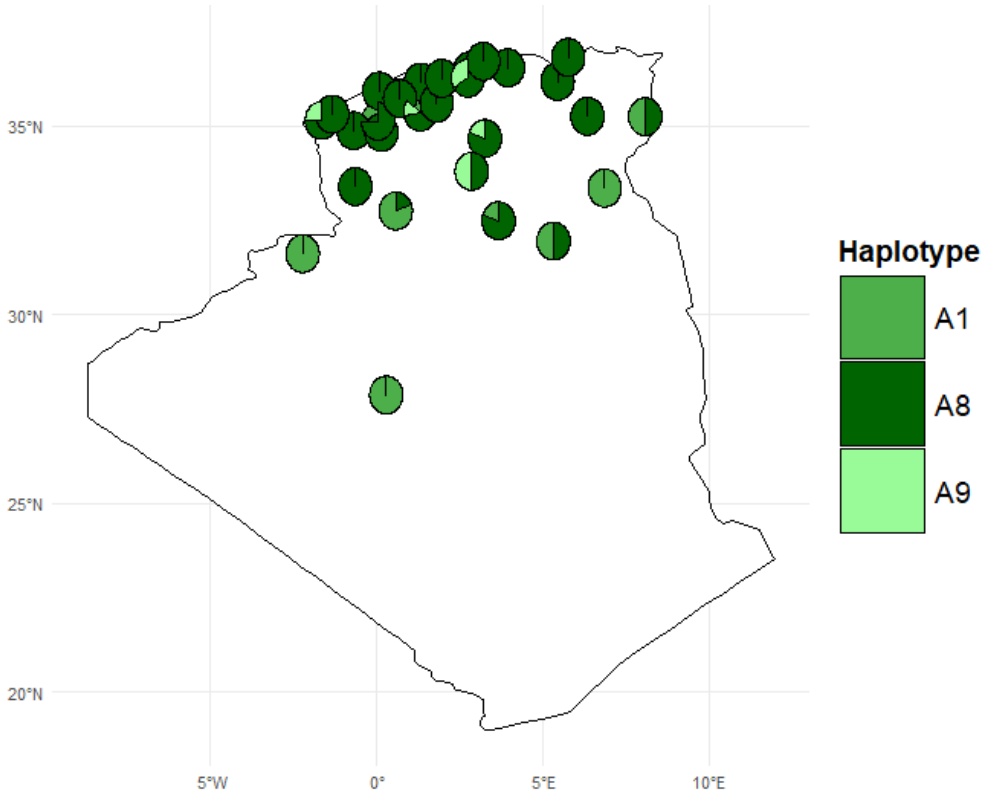


Dominant Haplotype: A1

70°N
60°N
50°N
40°N
30°N
20°N
10°N
20°W
0°
20°E
40°E
60°E

Algeria

- Sample No. 66
- Overall Haplotype Diversity Index: 0.45



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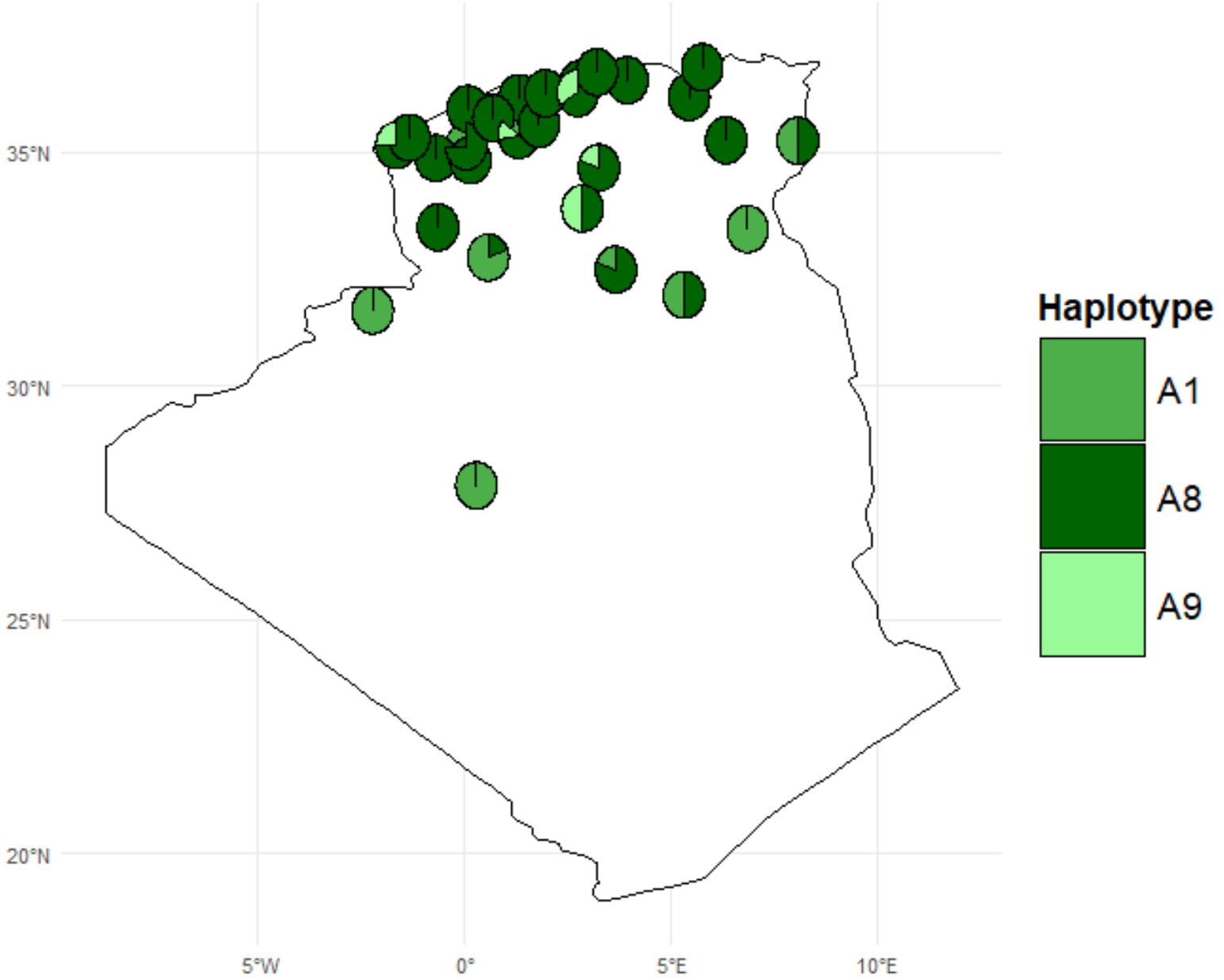
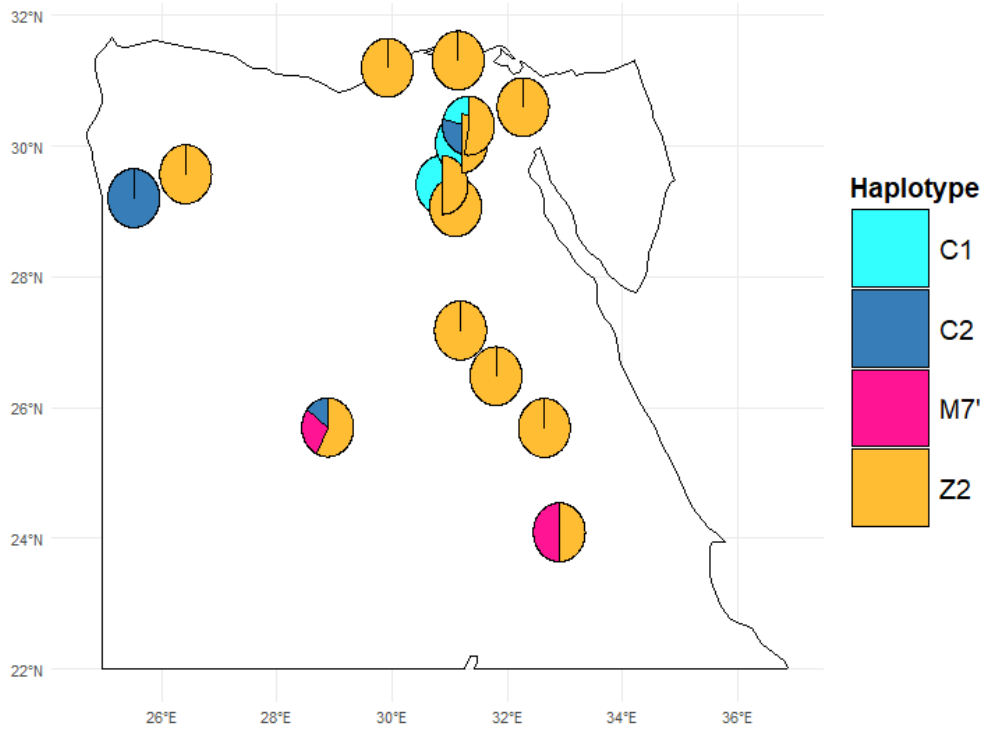


Dominant Haplotype: A8

70°N
60°N
50°N
40°N
30°N
20°N
10°N
20°W
0°
20°E
40°E
60°E

Egypt

- Sample No. 61
- Overall Haplotype Diversity Index: 0.50



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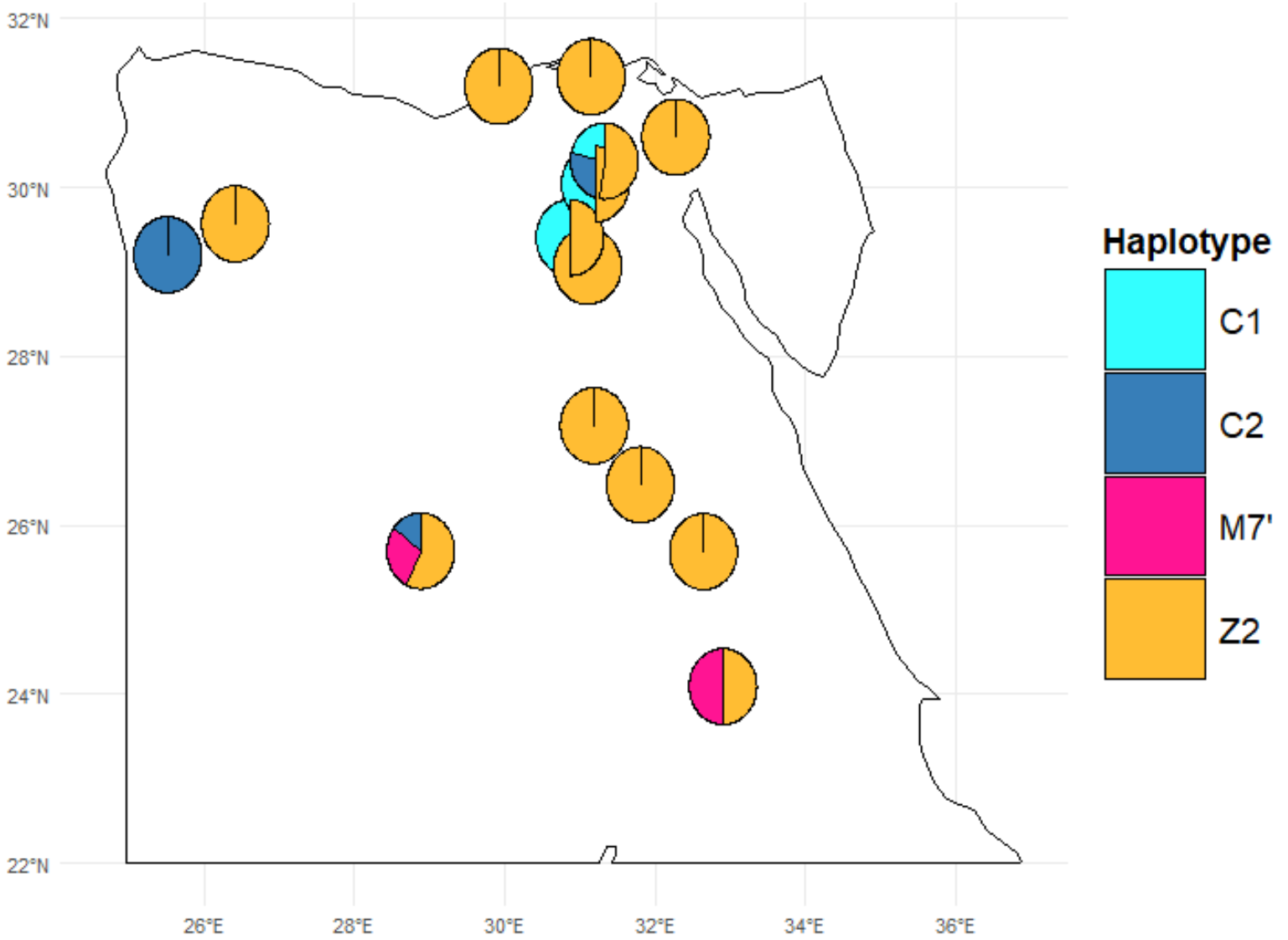
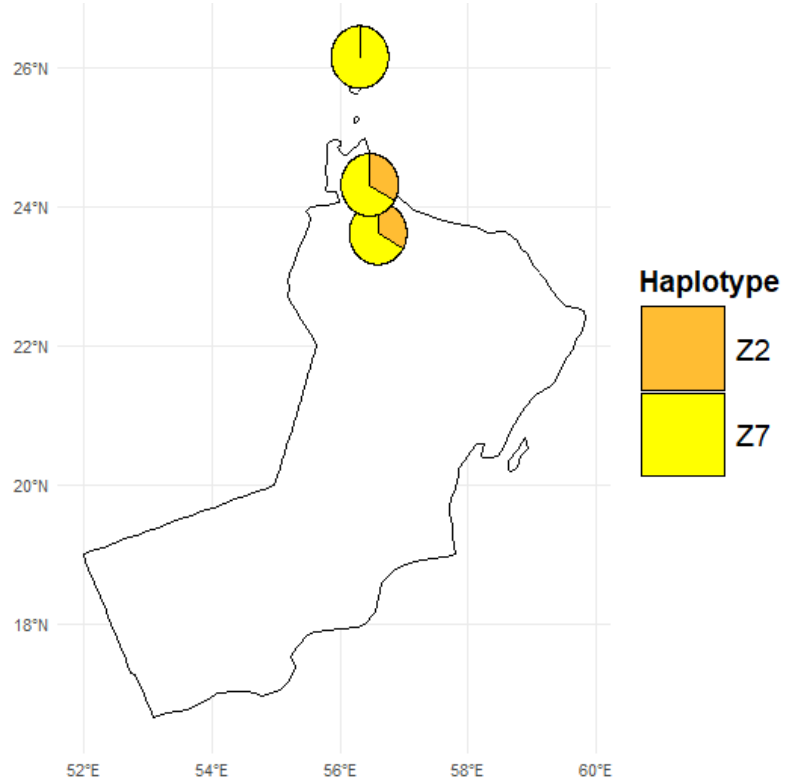


Dominant Haplotype: Z2

70°N
60°N
50°N
40°N
30°N
20°N
10°N
20°W
0°
20°E
40°E
60°E

Oman

- Sample No. 11
- Overall Haplotype Diversity Index: 0.69



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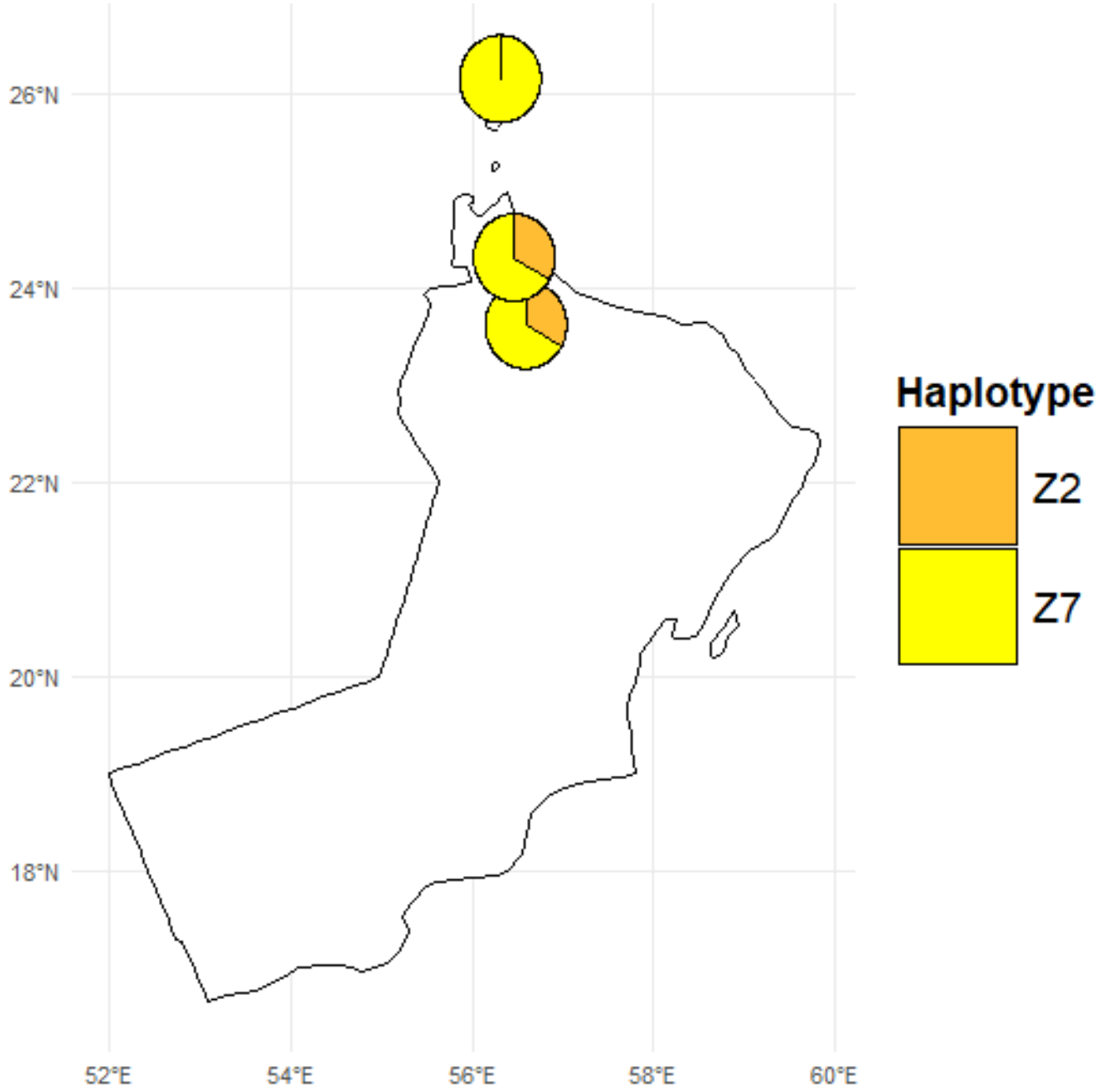
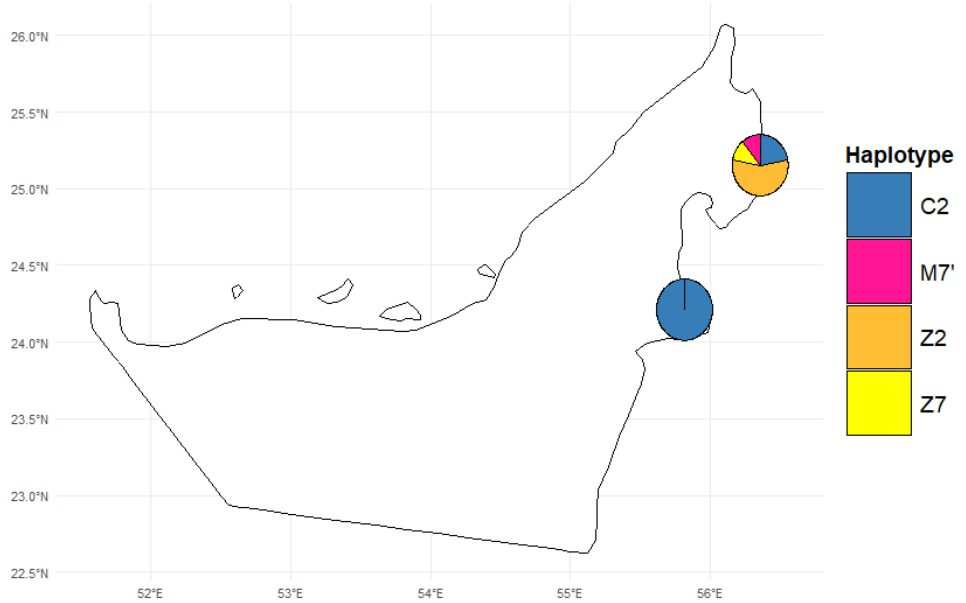


Dominant Haplotype: Z7

70°N
60°N
50°N
40°N
30°N
20°N
10°N
20°W
0°
20°E
40°E
60°E

United Arab Emirates

- Sample No. 12
- Overall Haplotype Diversity Index: 0.76
- Native Haplotype Diversity Index: 0.54



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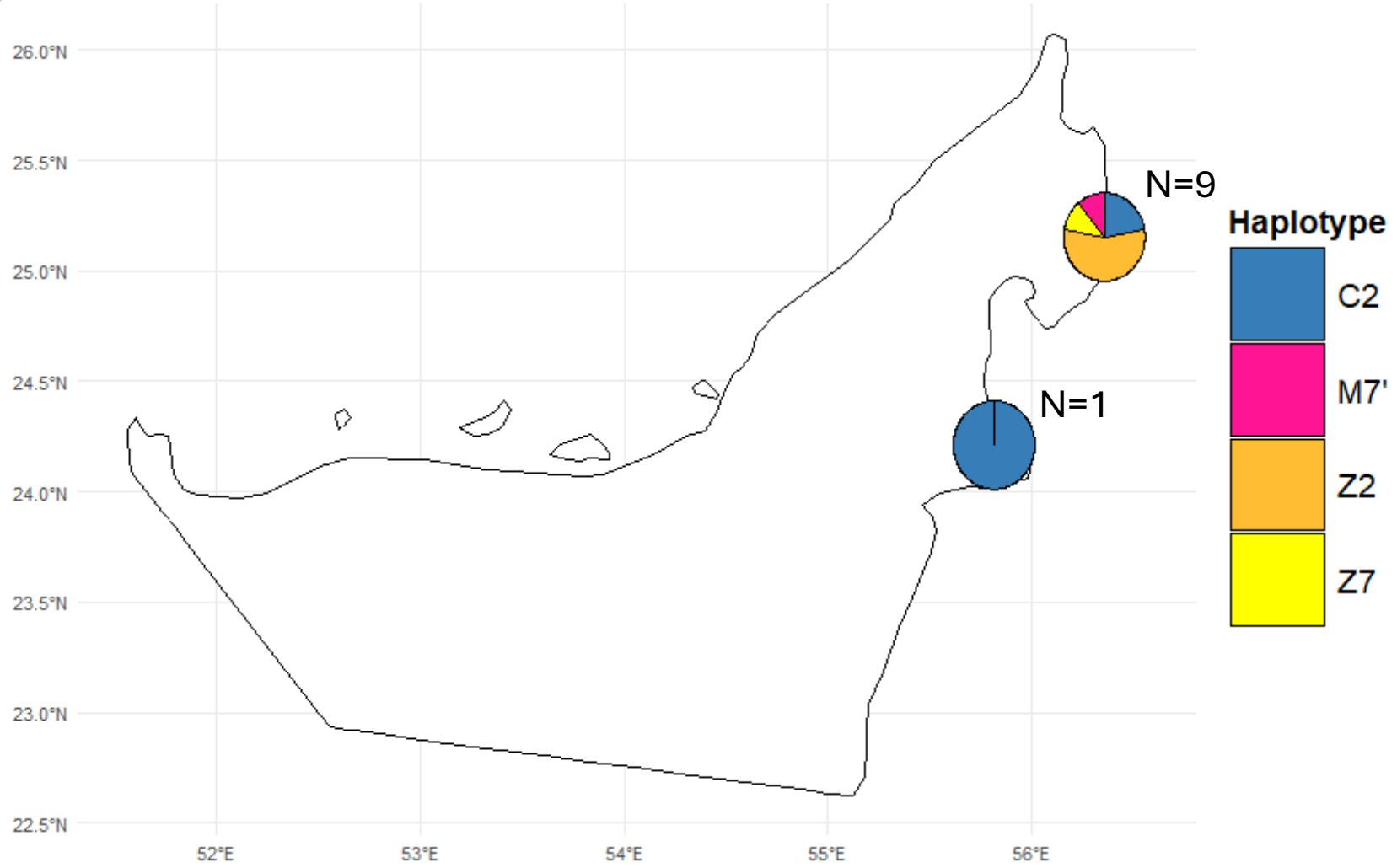
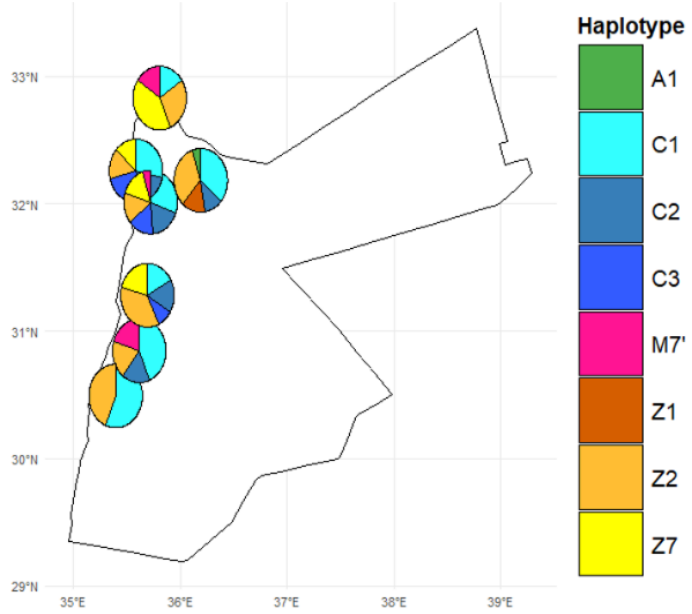


Dominant Haplotype: Z2

70°N
60°N
50°N
40°N
30°N
20°N
10°N
20°W
0°
20°E
40°E
60°E

Jordan

- Sample No. 220
- Overall Haplotype Diversity Index: 0.81
- Native Haplotype Diversity Index: 0.66



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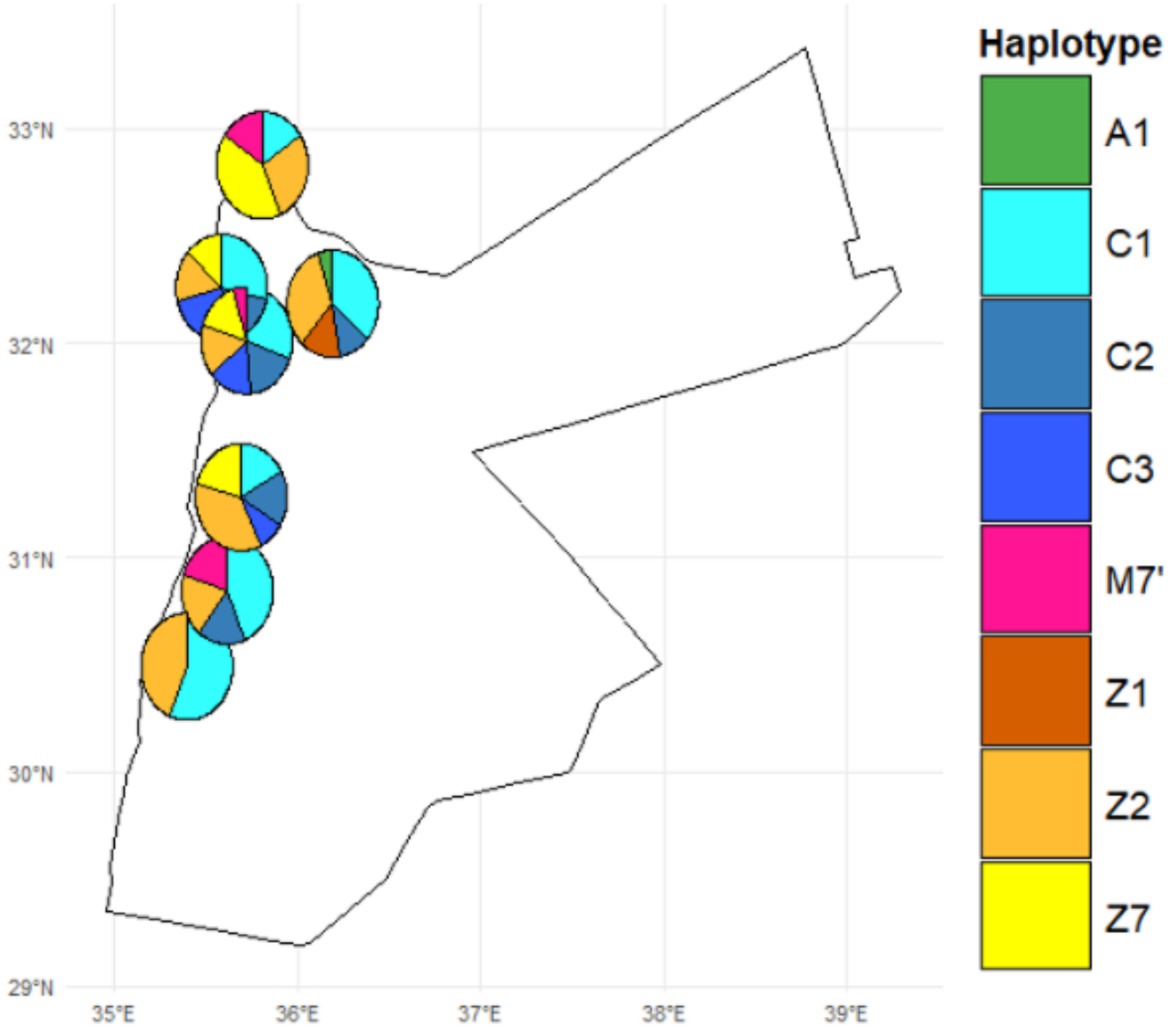

Dominant Haplotype: C1

70°N
60°N
50°N
40°N
30°N
20°N
10°N
20°W
0°
20°E
40°E
60°E

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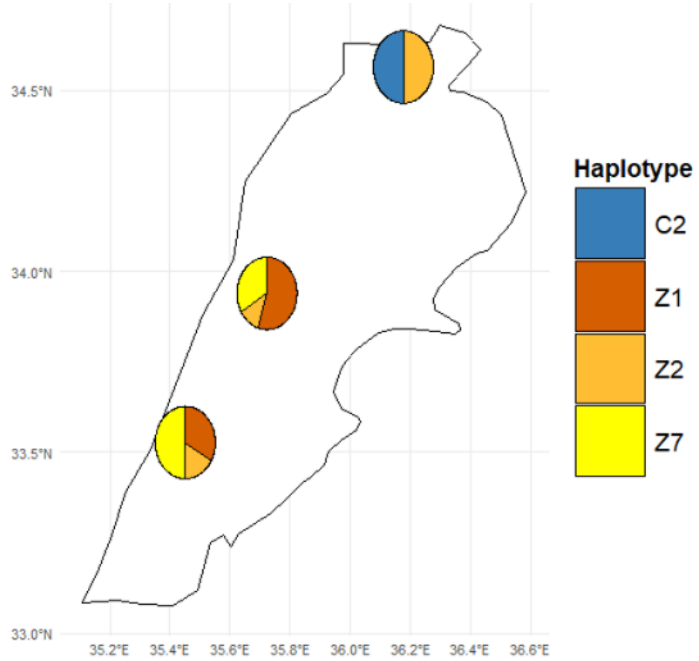
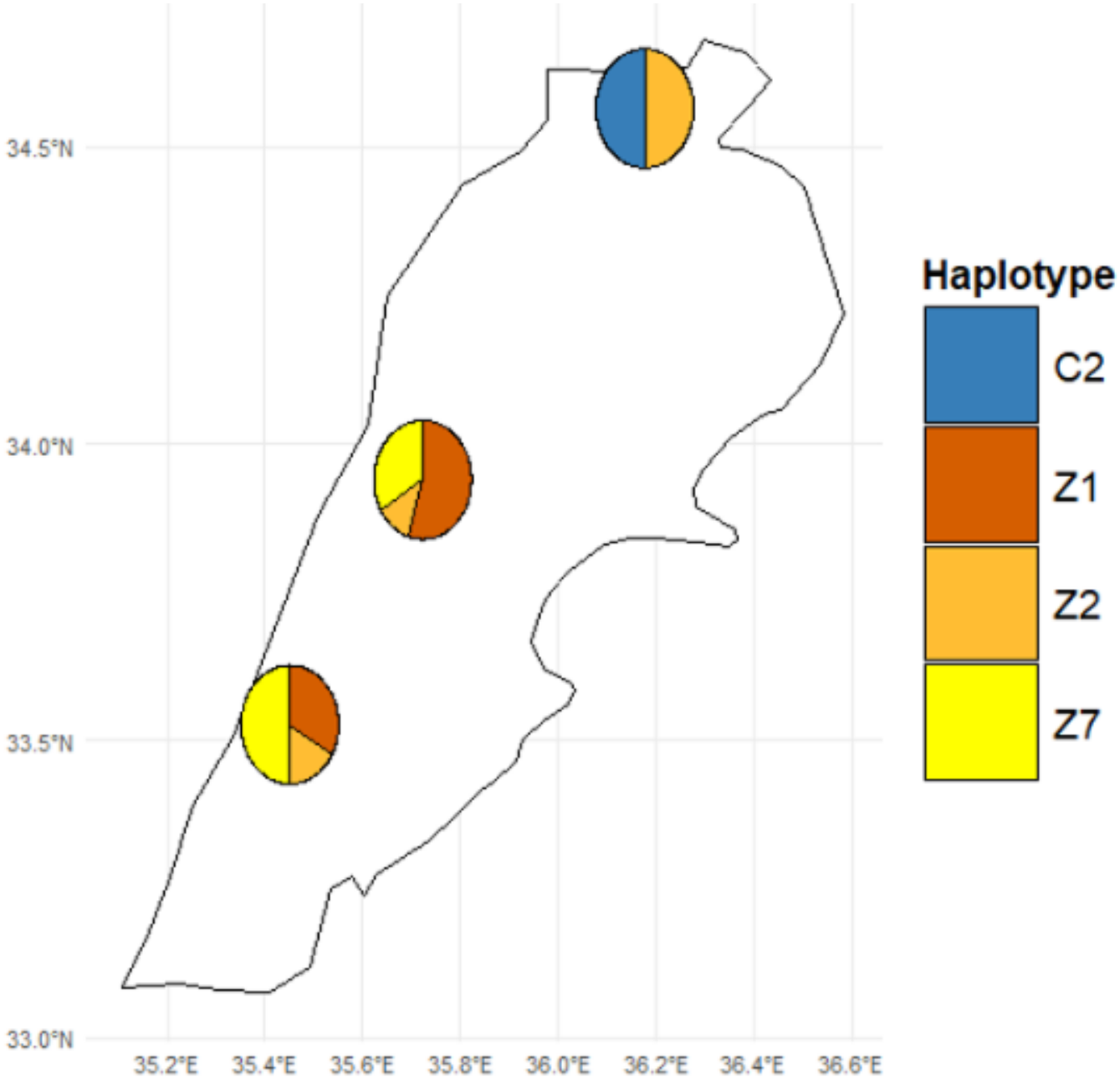
Lebanon

- Sample No. 27
- Overall Haplotype Diversity Index: 0.66
- Native Haplotype Diversity Index: 0.63



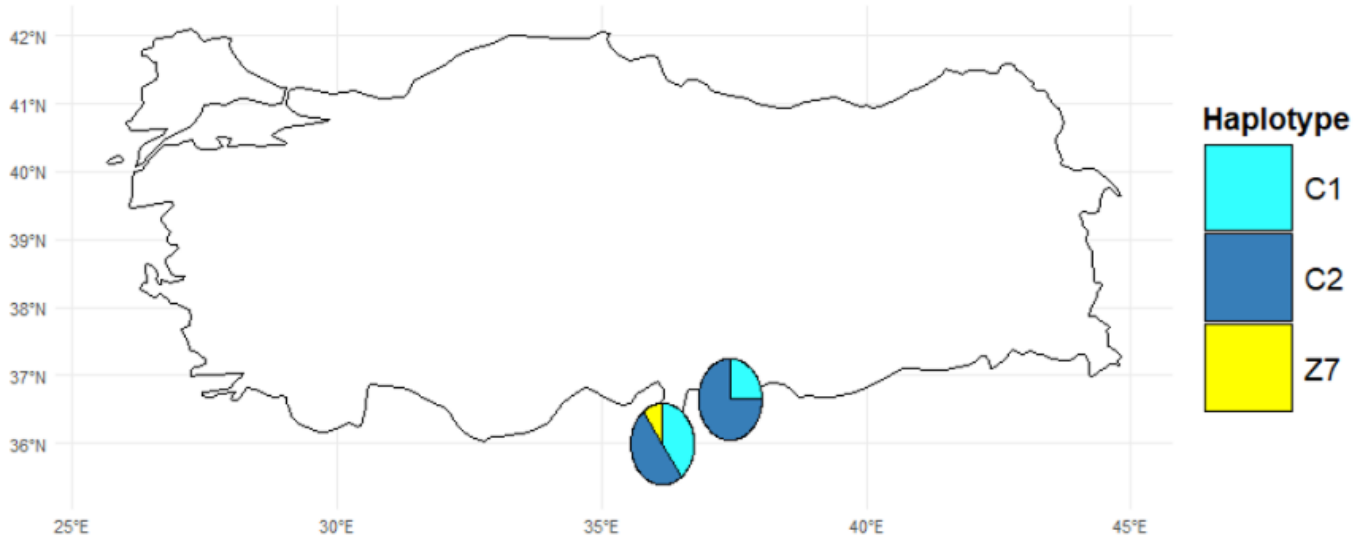


Dominant Haplotype: Z1

70°N
60°N
50°N
40°N
30°N
20°N
10°N
20°W
0°
20°E
40°E
60°E

Turkey

- Sample No. 14
- Overall Haplotype Diversity Index: 0.58



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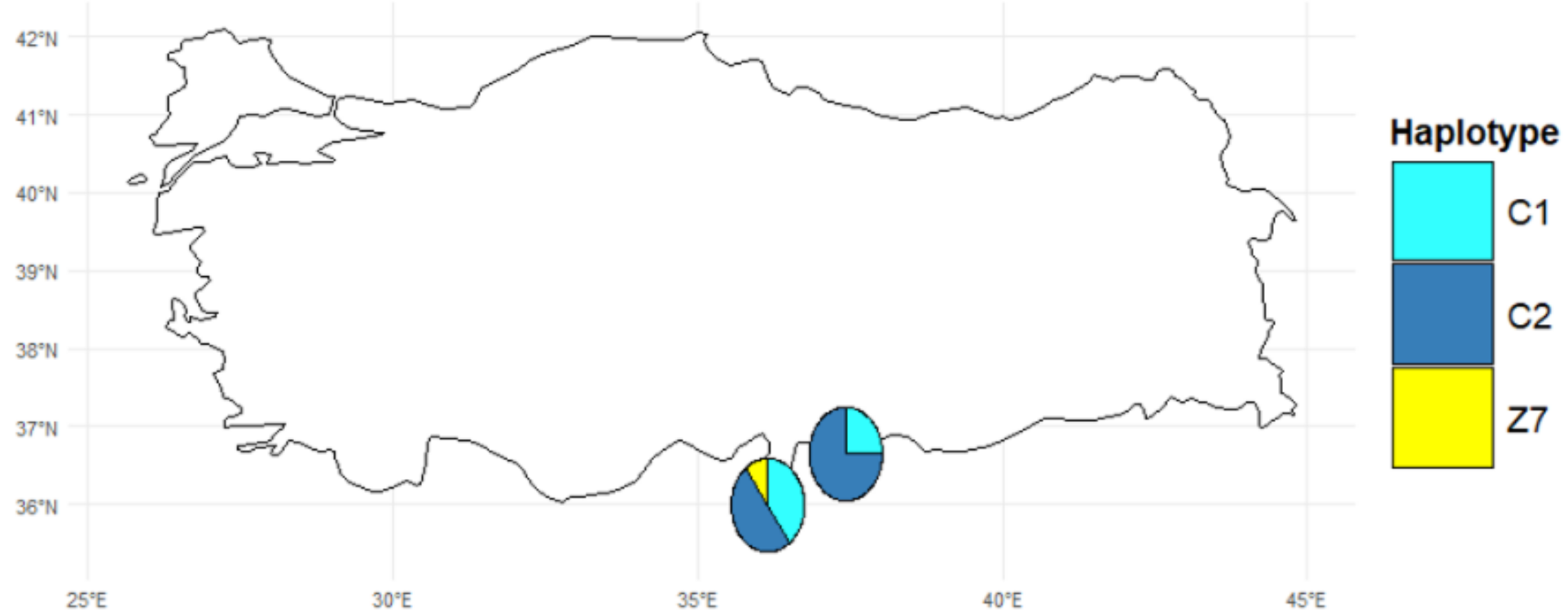

Dominant Haplotype: C2

70°N
60°N
50°N
40°N
30°N
20°N
10°N
20°W
0°
20°E
40°E
60°E

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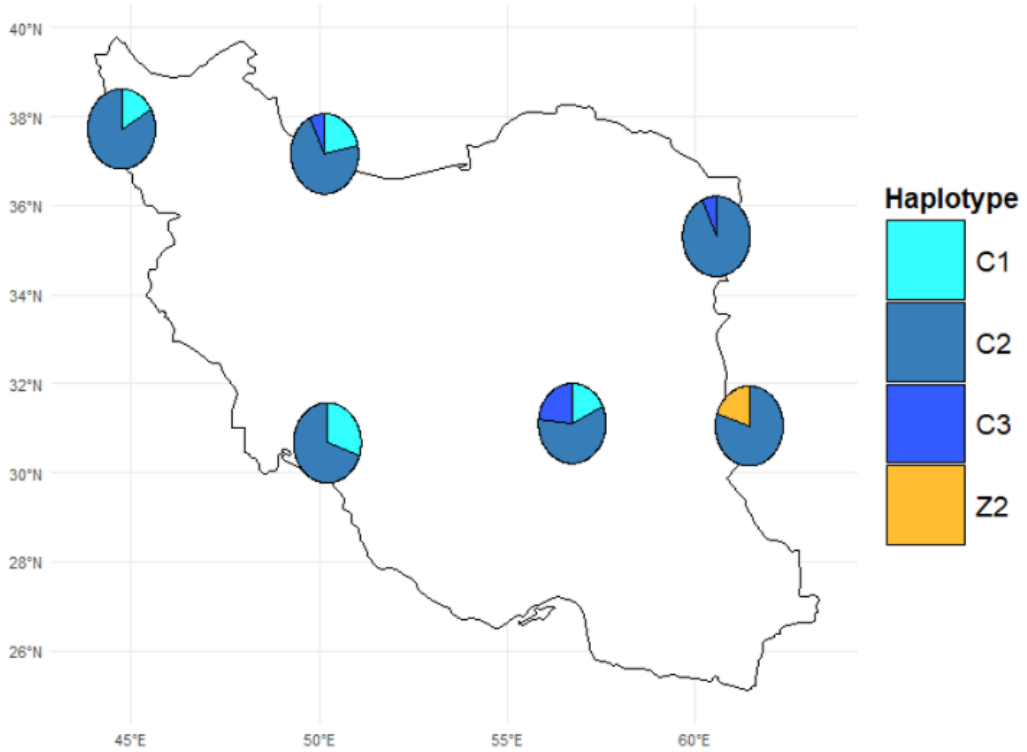
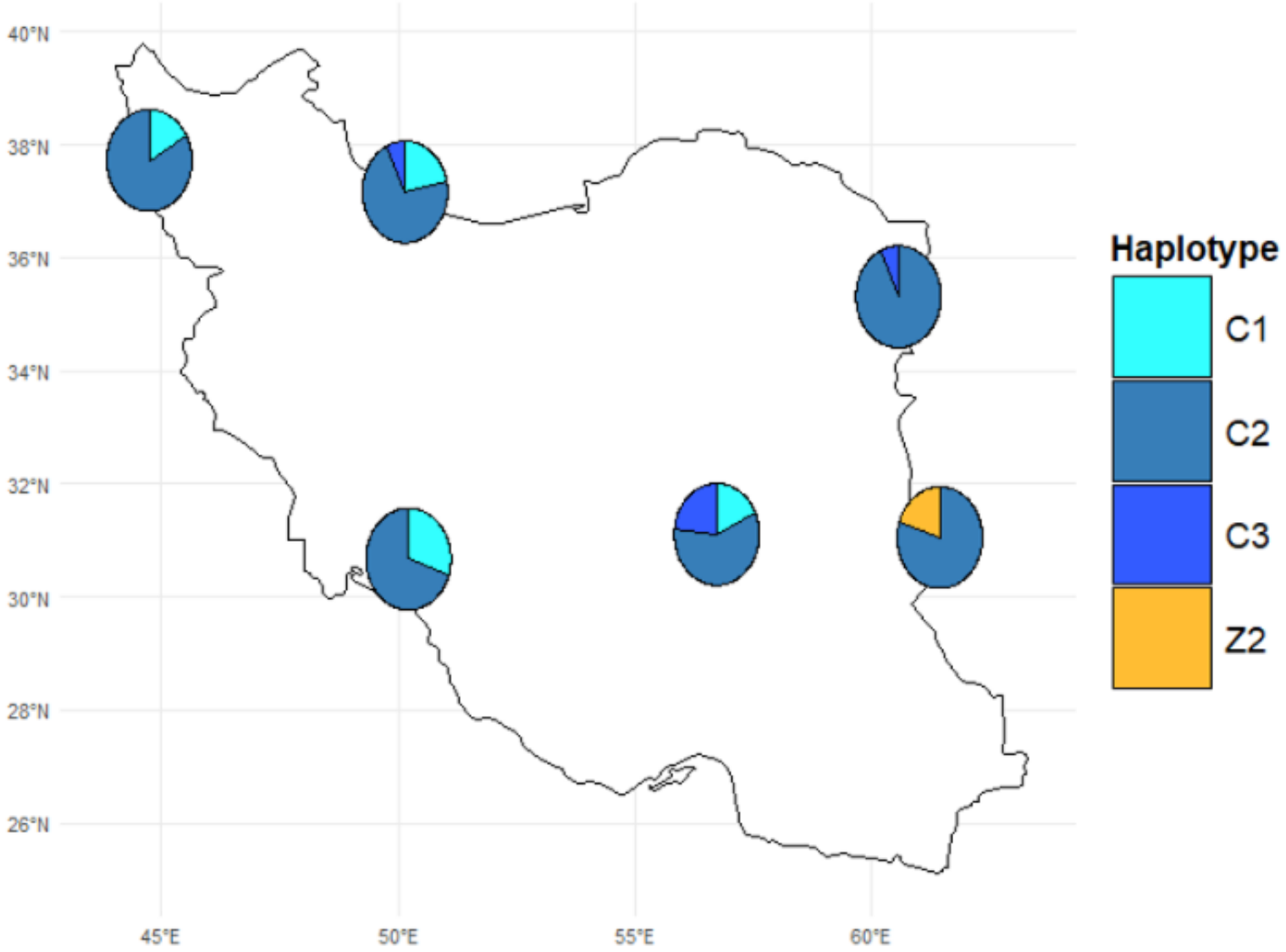
Iran

- Sample No. 67
- Overall Haplotype Diversity Index: 0.42





Dominant Haplotype: C2

70°N
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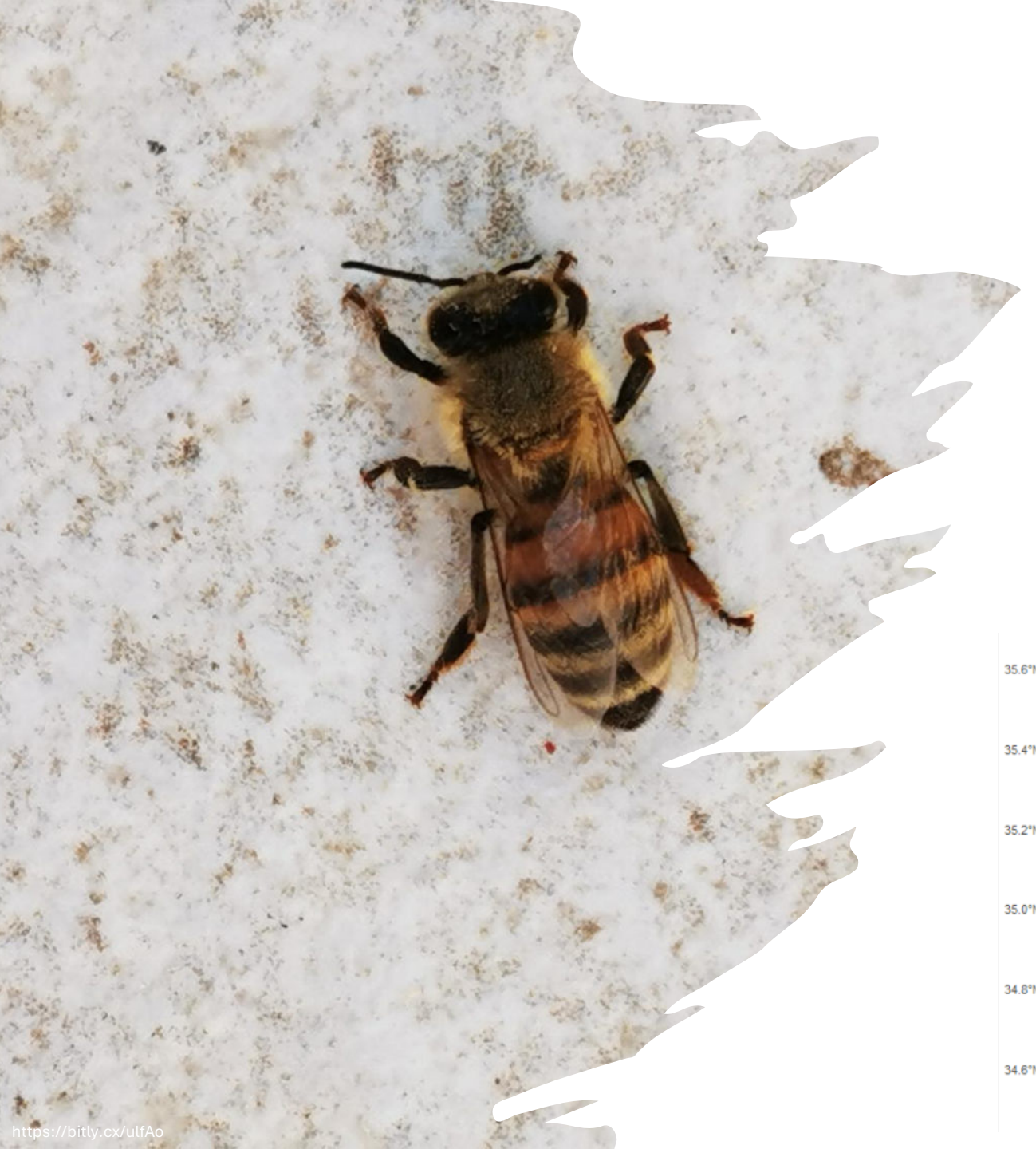
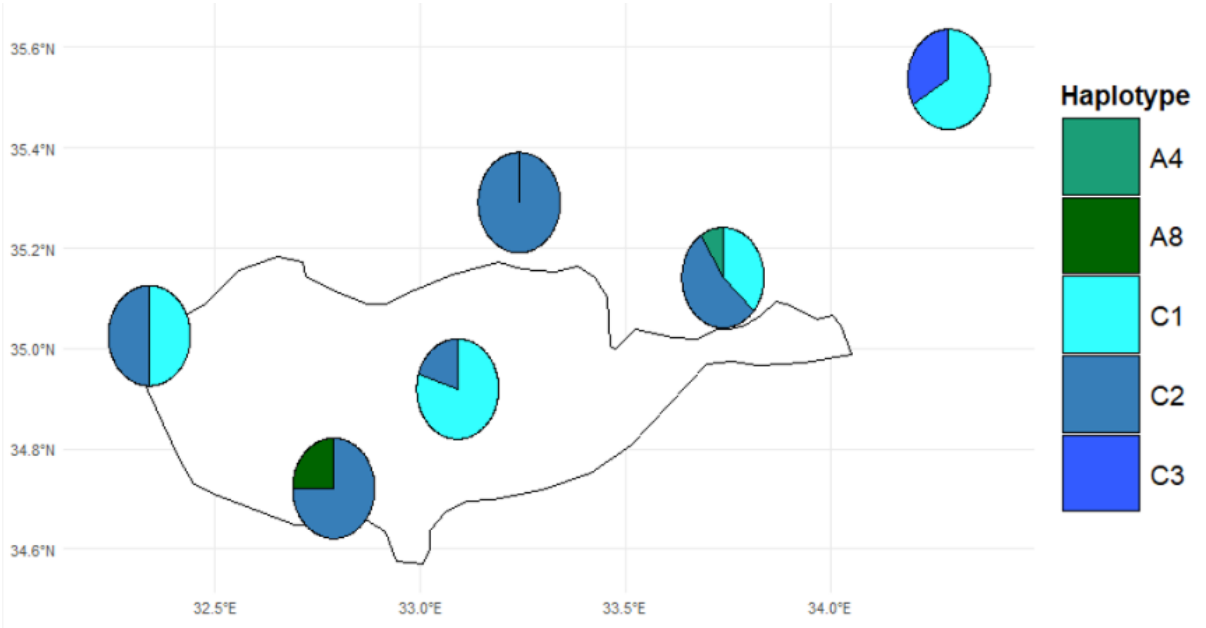
40°E
60°E



Cyprus

- Sample No. 31
- Overall Haplotype Diversity Index: 0.61
- Native Haplotype Diversity Index: 0.55



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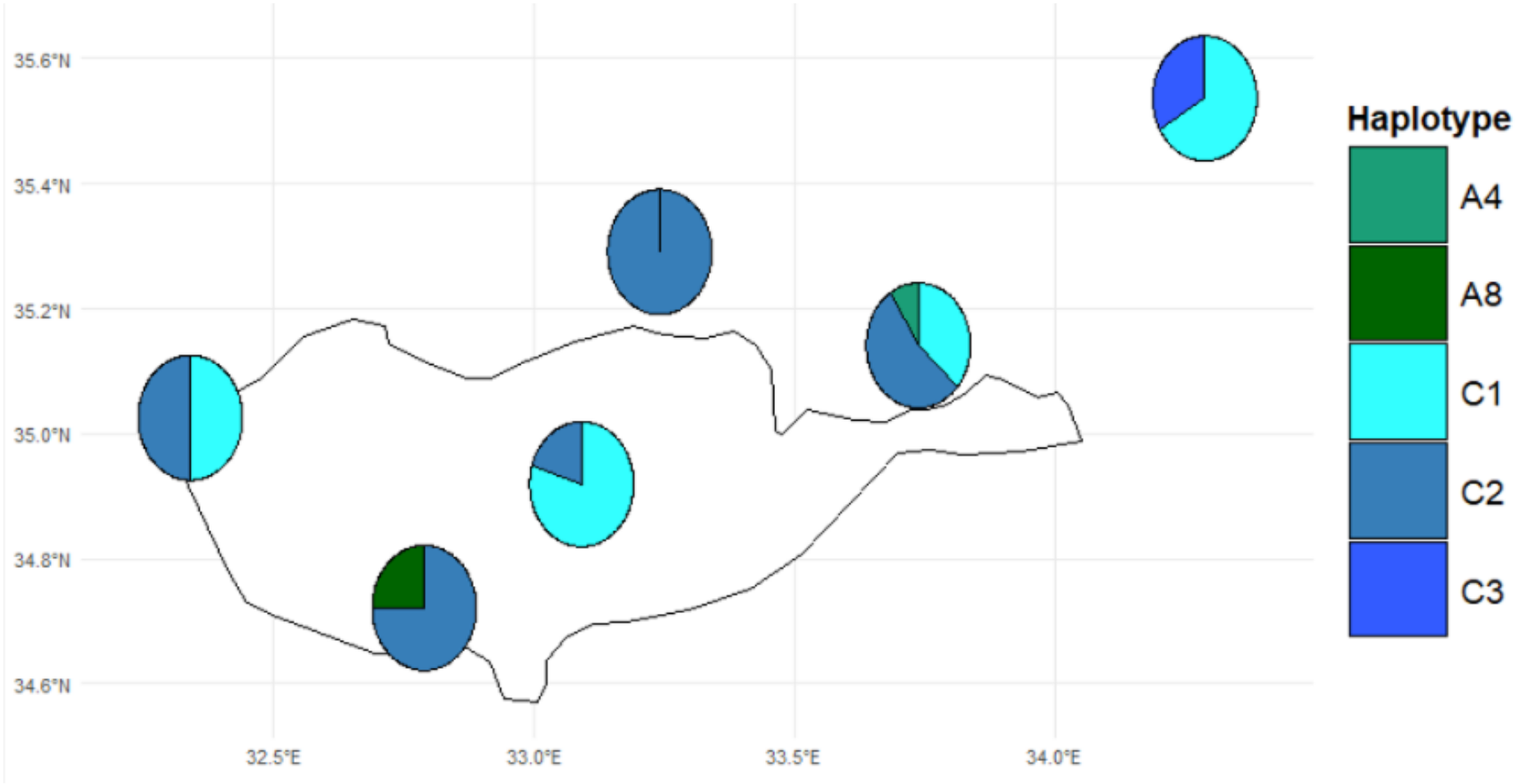
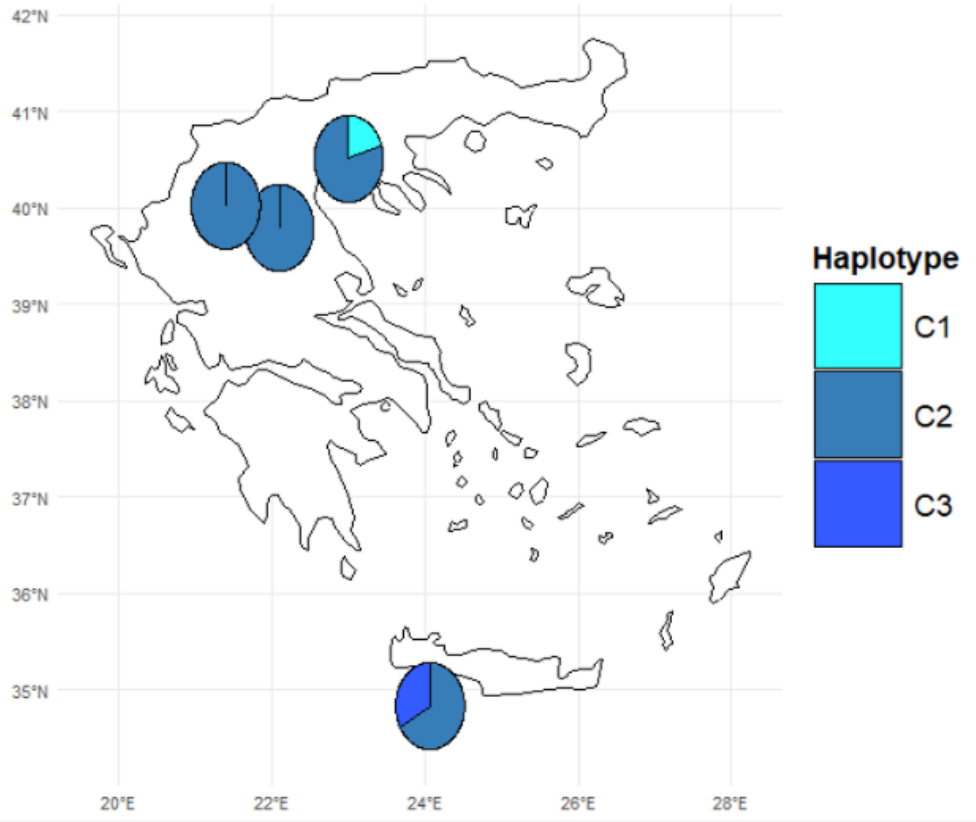


Dominant Haplotype: C2

70°N
60°N
50°N
40°N
30°N
20°N
10°N
20°W
0°
20°E
40°E
60°E

Greece

- Sample No. 13
- Overall Haplotype Diversity Index: 0.29



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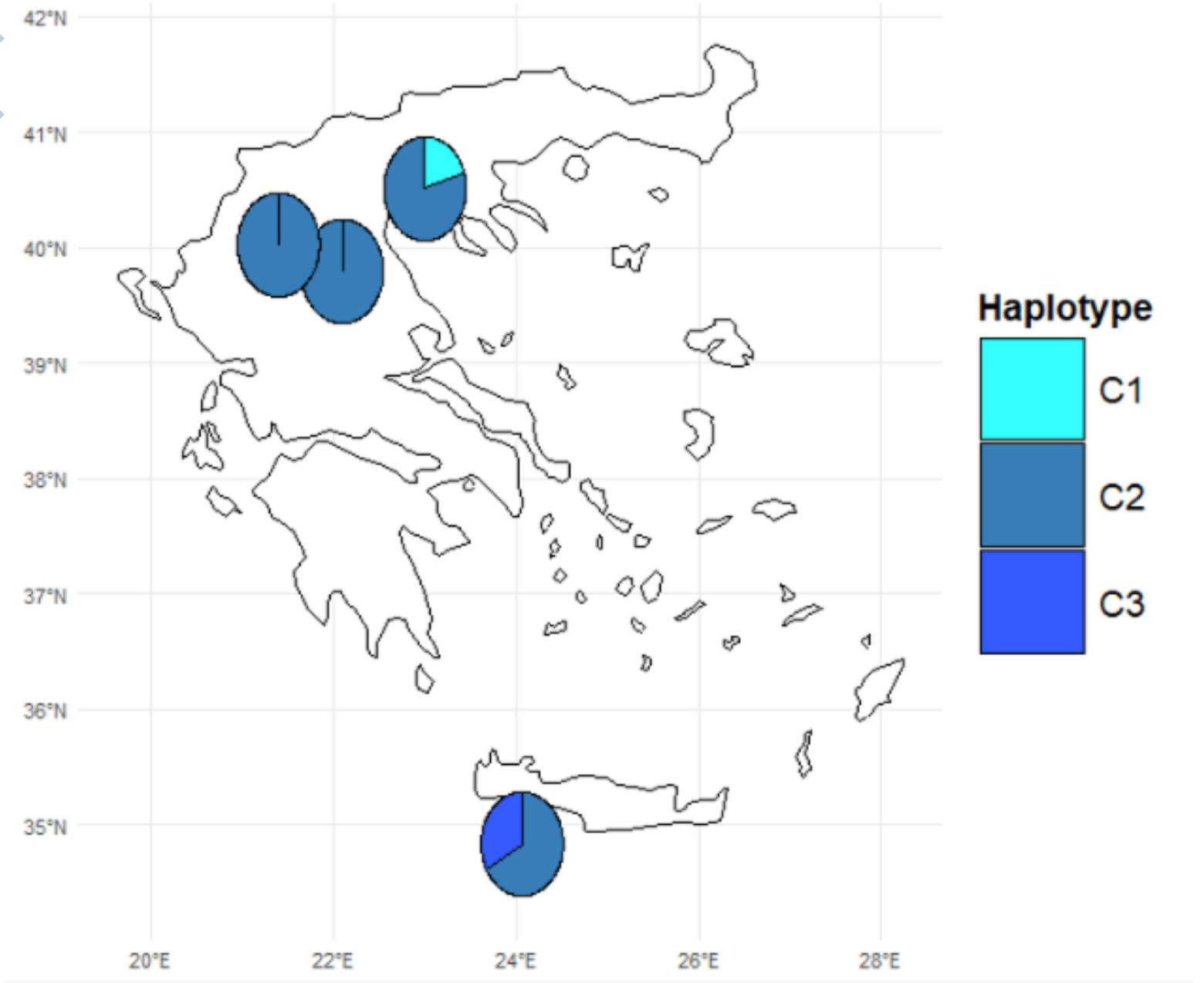
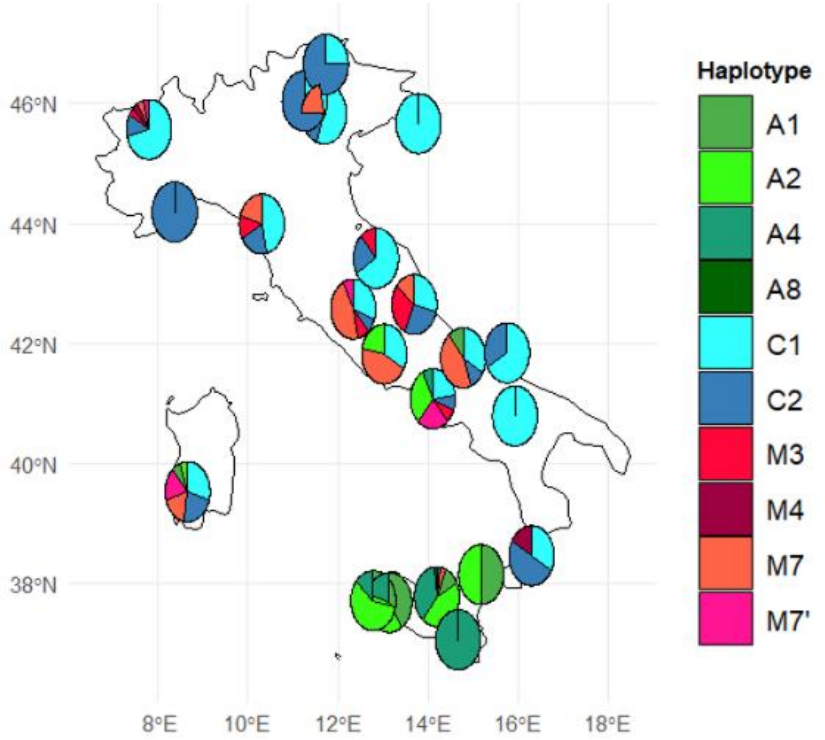


Dominant Haplotype: C2

70°N
60°N
50°N
40°N
30°N
20°N
10°N
20°W
0°
20°E
40°E
60°E

Italy and Sicily

- Sample No. in Italy 235
- Overall Haplotype Diversity Index in Italy: 0.69



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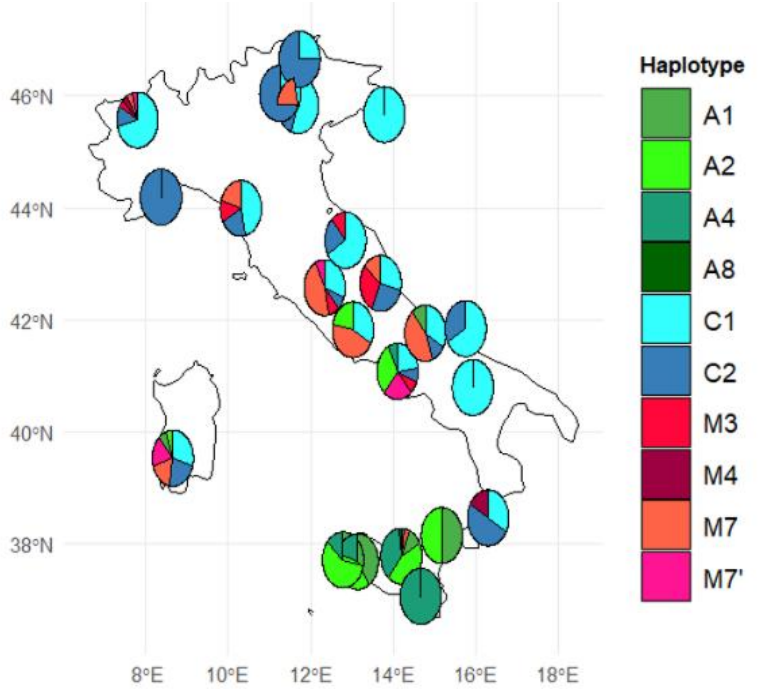
Italy and Sicily

- Sample No. in Sicily 64
- Overall and Native Haplotype Diversity Index in Sicily 0.68 and 0.65 respectively



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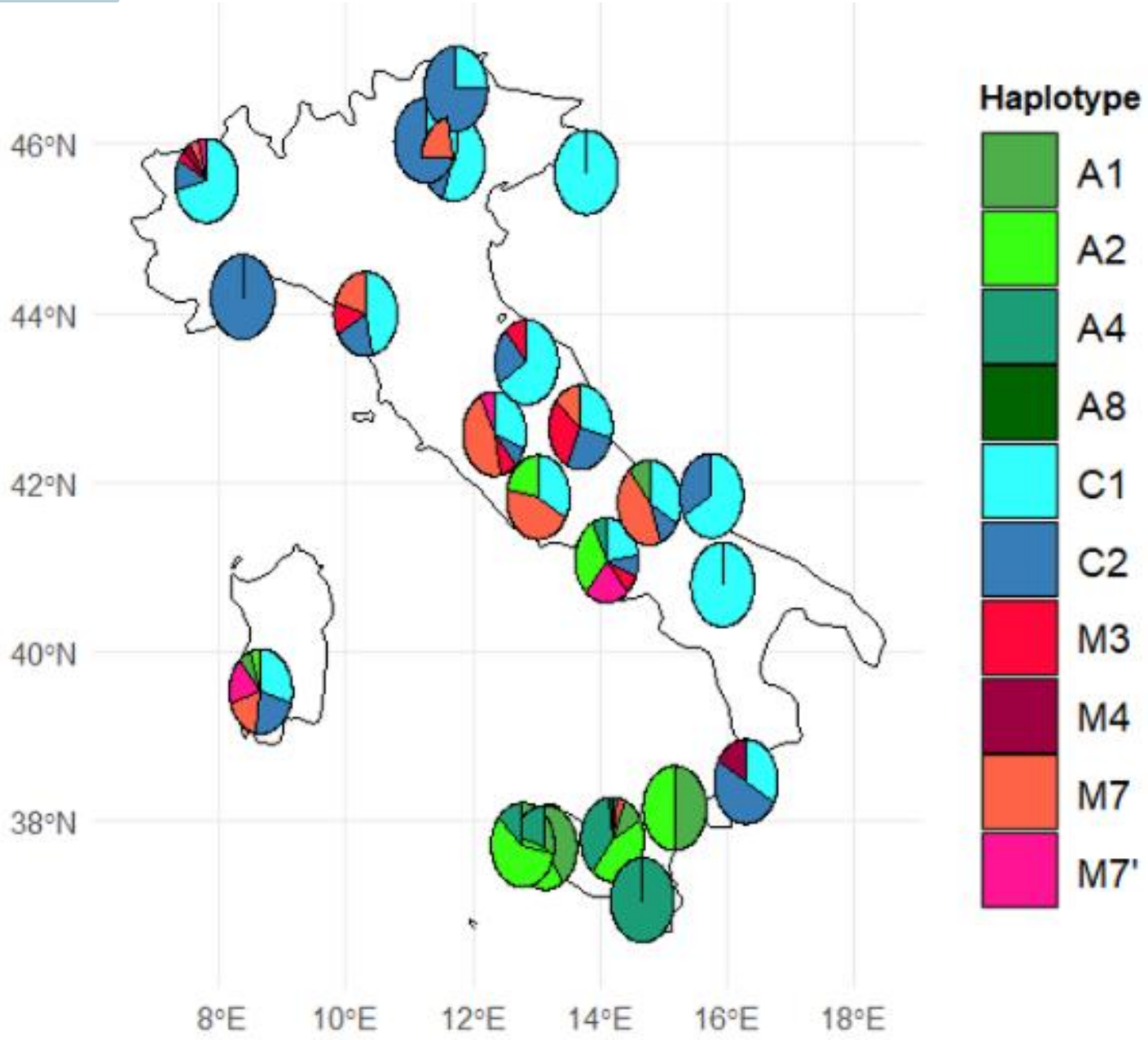


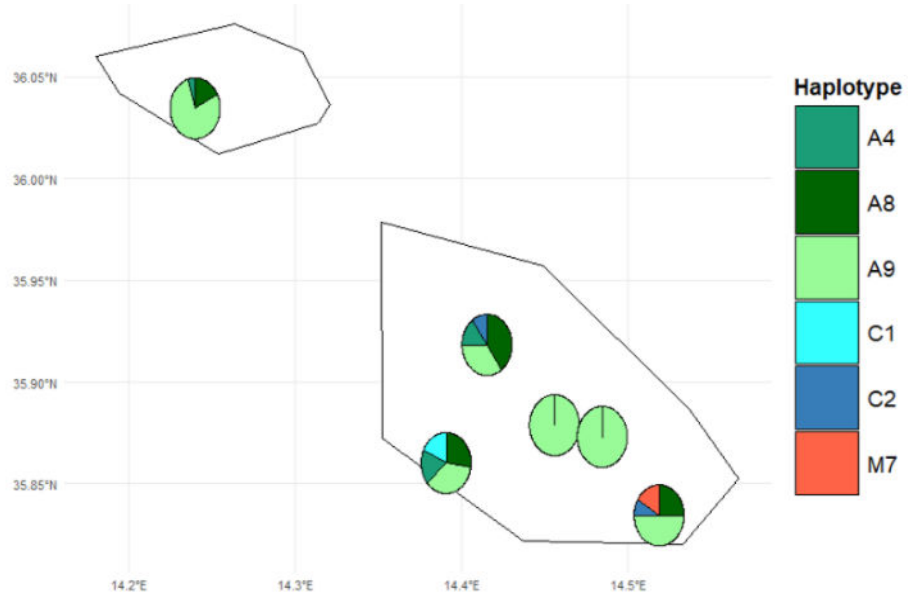
Dominant Haplotype – Italy: C1

Dominant Haplotype – Sicily: A2

70°N
60°N
50°N
40°N
30°N
20°N
10°N
20°W
0°
20°E
40°E
60°E

Malta

- Sample No. 68
- Overall Haplotype Diversity Index: 0.63
- Native Haplotype Diversity Index: 0.54



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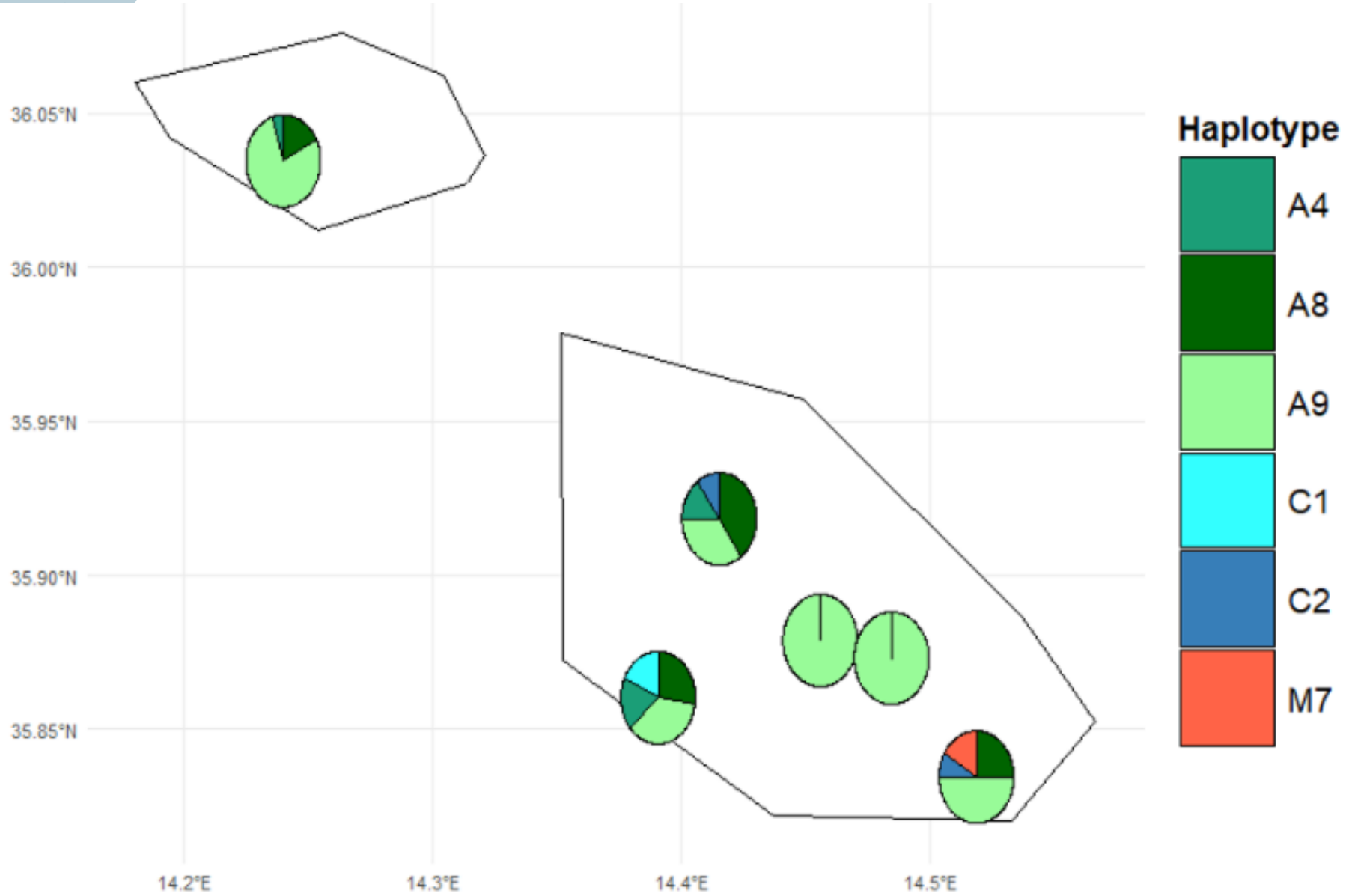
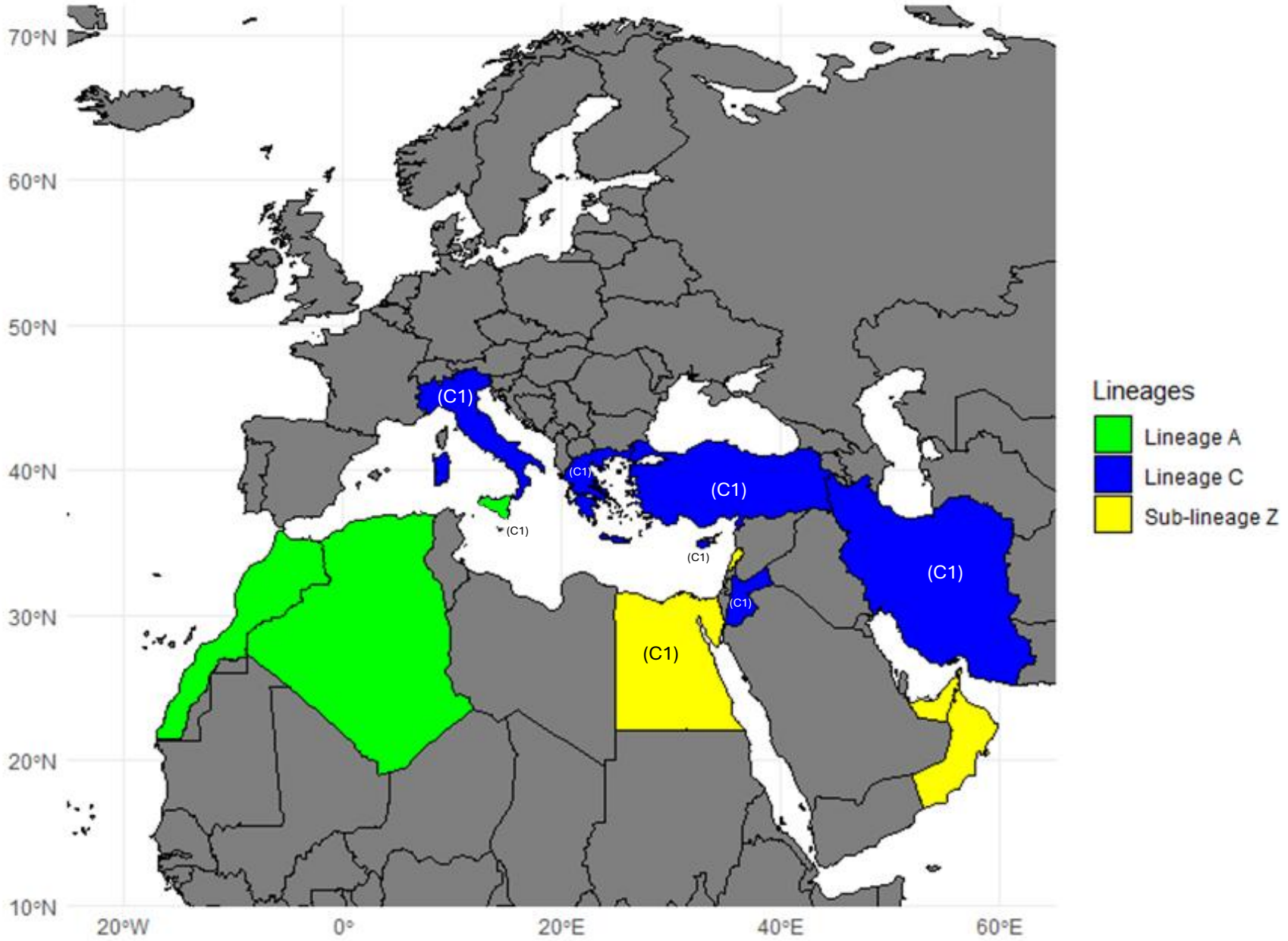
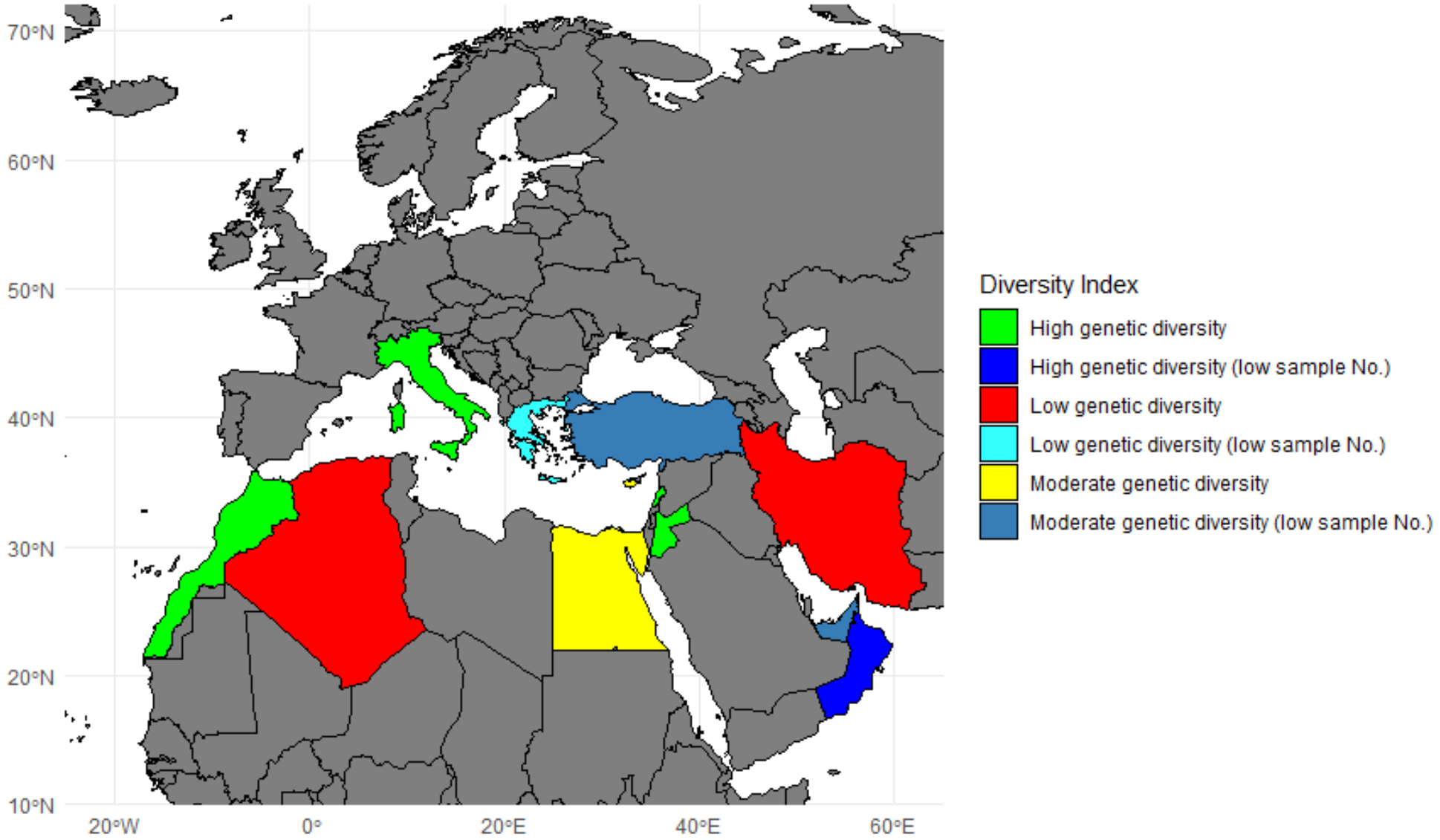


Dominant Haplotype: A9

Overall Lineages

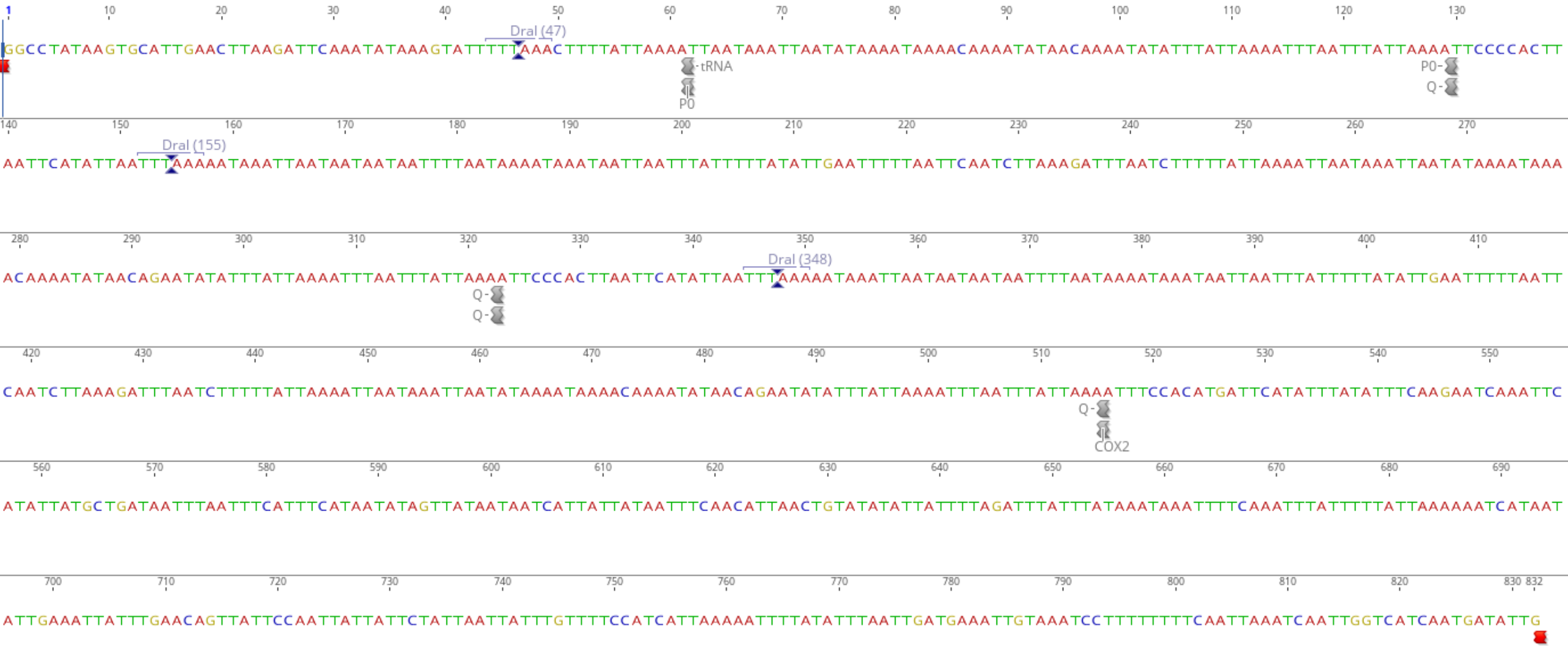


Diversity Indices (Native Haplotypes Only)



Conservation Implications

- Native bee populations show different proportions of haplotypes
- Haplotypes should be represented in breeding programmes


1
10
20
30
40
50
60
70
80
90
100
110
120
130
DraI (47)
GGCCTATAAGTGCATTGAACTTAAGATTCAAATATAAAGTATTTTTAAACTTTTATTAAAATTAATAAATTAATATAAAATAAAACAAAATATAACAAAATATATTTATTAAAATTTAATTTATTAAAATTCCCCACTT
tRNA
P0
P0
Q
140
150
160
170
180
190
200
210
220
230
240
250
260
270
DraI (155)
AATTCATATTAATTTAAAAATAAATTAATAATAATAATTTTAATAAAATAAATAATTAATTTATTTTTATATTGAATTTTTAATTCAATCTTAAAGATTTAATCTTTTTATTAAAATTAATAAATTAATATAAAATAAA
280
290
300
310
320
330
340
350
360
370
380
390
400
410
DraI (348)
ACAAAATATAACAGAATATATTTATTAAAATTTAATTTATTAAAATTCCCACTTAATTCATATTAATTTAAAAATAAATTAATAATAATAATTTTAATAAAATAAATAATTAATTTATTTTTATATTGAATTTTTAATT
Q
Q
420
430
440
450
460
470
480
490
500
510
520
530
540
550
CAATCTTAAAGATTTAATCTTTTTATTAAAATTAATAAATTAATATAAAATAAAACAAAATATAACAGAATATATTTATTAAAATTTAATTTATTAAAATTTCCACATGATTCATATTTATATTTCAAGAATCAAATTC
Q
COX2
560
570
580
590
600
610
620
630
640
650
660
670
680
690
ATATTATGCTGATAATTTAATTTCATTTCATAATATAGTTATAATAATCATTATTATAATTTCAACATTAACTGTATATATTATTTTAGATTTATTTATAAATAAATTTTCAAATTTATTTTTATTAAAAAATCATAAT
700
710
720
730
740
750
760
770
780
790
800
810
820
830
832
ATTGAAATTATTTGAACAGTTATTCCAATTATTATTCTATTAATTATTTGTTTTCCATCATTAAAAATTTTATATTTAATTGATGAAATTGTAAATCCTTTTTTTTCAATTAAATCAATTGGTCATCAATGATATTG