

CONTENTS

ABSTRACT 9

ACKNOWLEDGEMENTS 11

1. Introduction 13

 1.1 Palaeogenomics as a tool for studying past populations 13

 1.2 Main prehistoric demographic events in a view of palaeogenomics 14

 1.2.1 Last Glacial Maximum 14

 1.2.2 Neolithic Transition 14

 1.2.3 Population influx from the Pontic Steppe 16

 1.2.4 Challenges in palaeogenomic applications 16

2. The skeletal material and its archaeological background 18

 2.1 Anthropological and archaeological background 18

 2.2 The Balkans in Meso-Neolithic Transition 18

 2.2.1 Lepenski Vir 19

 2.2.2 Vlasac 20

 2.2.3 Padina 20

 2.2.4 Ostrovul Corbului 20

 2.2.5 Vinča 21

 2.2.6 Grivac 24

 2.2.7 Sultana Malu Roşu 24

 2.3 Neolithic in NW Anatolia 24

 2.3.1 Aktopraklık 24

 2.3.2 Barcin Höyük 25

 2.3.3 Catalhöyük 26

 2.4 Isotopic analysis 26

3. Methods 29

 3.1 Sample Preparation 29

 3.2 Extraction 29

 3.3 Library preparation 30

 3.4 Quality assessment of samples 30

 3.5 Sex determination 30

 3.6 Quantitative real-time PCR 31

 3.7 Whole-genome sequencing 31

 3.8 Nuclear capture 31

 3.9 Mitochondrial capture 32

 3.10 Read processing 32

 3.11 Analysis of mitochondrial dataset 33

 3.11.1 Contamination rate 33

 3.12 Y chromosomal variation 33

 3.13 Nuclear data analysis 34

 3.13.1 f3-statistics 34

 3.13.2 D statistics 34

 3.13.3 Admixture proportions 34

4. Ancient DNA analysis 36

 4.1 Evaluation of Anatolian and Danubian extraction success rate and ancient DNA quality and quantity 36

 4.2 Sex determination 36

 4.3 Maternal insight into population makeup of Meso-Neolithic Balkans and NW Anatolia 38

 4.3.1 Mitochondrial haplogroups identified for Mesolithic individuals from the Danube Gorges (~9,500–6,200 cal BC) .. 38

 4.3.2 Mitochondrial haplogroups identified in the Transition period (~6,200–6,000/5,950 cal BC) of Lepenski Vir 38

 4.3.3 Mitochondrial haplogroups identified for Neolithic and post-Neolithic individuals from NW Anatolian and the Balkans 40

 4.3.4 Diversities indices comparison for farmers and hunter-gatherers 41

- 4.4 Quality of nuclear dataset obtained 46
- 4.5 Using f-statistics to infer shared drift in Anatolians and Danubians 47
 - 4.5.1 Mesolithic Danubian genomes compared to modern and ancient reference populations 47
 - 4.5.2 Differences among Danubian samples 51
 - 4.5.3 Placing Danubians in the context of other hunter-gatherer genomes 53
 - 4.5.4 Genetic structure of Western hunter-gatherers 55
 - 4.5.5 Relationship of Greek and Anatolian genome samples to other ancient and modern populations 56
 - 4.5.6 Genetic Structure of Aegean Neolithic populations 57
 - 4.5.7 The Aegean as the source for early farming populations in Europe 58
 - 4.5.8 The relationship between Neolithic Aegeans and Chalcolithic Anatolians 59
 - 4.5.9 Hunter-gatherer contributions to farming societies 68
 - 4.5.10 Differences between Danubian and WHG heritage in farming societies 69
 - 4.5.11 Patterns of allele correlations among Anatolian and Danubian capture samples and reference populations 71
 - 4.5.12 Intrapopulation genetic structure in Anatolia 73
 - 4.5.13 Intrapopulation genetic structure in the Danube Gorges 75
 - 4.5.14 Relationships between Danubians and Anatolians 76
 - 4.5.15 Confirming D statistics results on the capture dataset 90
- 4.6 Ancestral components of studied populations 90
 - 4.6.1 NW Anatolian samples form an ancestral cluster to Neolithic farmers in Europe 90
 - 4.6.2 CHG affinities to farmers 90
 - 4.6.3 Yamnaya signal in Late Neolithic 91
 - 4.6.4 Danubians during Neolithic Transition 91
- 4.7 Remarks on Y chromosomal variation 96
- 5. Discussion 98
 - 5.1 Population demographics during the spread of farming 98
 - 5.1.1 Western Anatolia as a core zone for Neolithic spread to Europe 98
 - 5.1.2 Neolithic NW Anatolians in a context of known regional genetic variation 99
 - 5.1.3 Mesolithic settlements in the Danube Gorges 99
 - 5.1.4 The Balkans in a time of change 100
 - 5.2 Implication for understanding of Neolithisation 101
 - 5.2.1 Summary of differences between sites 101
 - 5.2.2 Comparison to archaeological models 102
 - 5.2.3 Hypothesis of the Neolithic spread through the Aegean and the Balkans 103
 - 5.3 Methodological considerations 103
 - 5.3.1 Processing of old and damaged samples 103
 - 5.3.2 Sex determination 104
 - 5.3.3 Comparison to the context 104
 - 5.3.4 Different datasets could lead to different conclusions 105
- 6. Conclusion 107
- 7. References 108
- 8. Supplementary material 117
 - Supplementary Figures and Tables 117
 - Additional files 140