

# Preliminary mitochondrial DNA analysis of a 10<sup>th</sup> century medieval population in Capidava (Constanța, Romania)

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### Introduction

Capidava is an archaeological site located in the South-Eastern part of Romania (Dobrudja), near the Danube River a location, theoretically on the route of migratory populations, especially in medieval times. Recently, human remains belonging to 9 individuals were recovered from the graves outside the walls of Capidava fortress.



#### Methodology

The whole process of obtaining ancient genetic information was carried out following strict guidelines in laboratories designated for working solely with ancient DNA in order to avoid contamination risk with exogenous DNA (Willerslev and Cooper, 2005).

After DNA extraction from bone samples using a phenol/chloroform protocol (Hervella et al., 2012; Hagelberg and Clegg, 1991; Ginther et al., 1992), four overlapping segments of the mtDNA control region's first hypervariable segment (HVS I) were amplified by PCR (Gabriel et al., 2001).

Also, two blank controls for each extraction series were included, as well as negative PCR controls for each amplification to screen for possible contamination. Subsequently, amplicons were cloned (CloneJet PCR Cloning, Thermo Scientific) and for each successful sample a minimum of five clones have been sequenced (Macrogen, Netherlands).



this period Dobrudja was alternatively dominated by several populations it is difficult to determine based only on the archaeological record whether the skeletons excavated from Capidava belong to a local population or to migratory population groups, and specifically to which ones (Pinter et al., 2011).



**Results and discussion** 

**Fig. 4.** Human remains from individual M1 (Pinter et al., 2011)



**Individual M1** 

- No discernible mutation versus rCRS
- Probable haplogroup H
- Clones have miscoding lesions due to DNA degradation



Fig. 7. Possible migratory routes relevant for the identified mutations (https://maps.google.ro/) Turkic lineage Slavic lineage

- Possible haplogroup H (HV3) with 16069T/16111T or haplogroup J
- 16111T and was associated by Malyarchuk et al, 2008 with HV3 in a Slavic population
- Transition 16111 C  $\rightarrow$  T was found 483 times in MITOMAP
- 16111T was not found in literature data associated with mutations 16069T and 16126C
- Mutation 16111T appears for the first time in any samples analyzed in our lab
- 16267T, a rare mutation (only 4 registered sequences in MITOMAP) and 16129A were associated by Malyarchuk et al, 2010 with western Eurasian haplogroup (H1,H) found in individuals from the Republic of Tatarstan, Mishars (turkic populations)
- "Mishars are one of two major groups among the Volga Tatars"
- 16267T appear for the first time in any samples analyzed in our lab
- Mutation 16129A appeared in 2 modern samples analyzed in our lab in conjunction with other HVR1 mutation which diagnosed haplogroup I

		-	1	16060	16070	16080	16090	16100	16110	16120	16130	16140	16150	16160
CRS			CCACCC	AGTATTO	GACTCACCCAT	CAACAACCGC	TATGTATTTC	<b>GTACATTACT</b>	GCCAGCCACO	CATGAATATTO	STACGGTACCA	TAAATACTTG	ACCACCTGT	AGTACATA
HVRI A	D M3	3 Сар			T						. c	T		
HVRI A	D M3	3 Cap			T				T					
HVRI A	D M3	3 Cap			T						. c			
HVRI A	D M3	3 Cap			<b>T</b>						. c			
HVRI A	D M3	3 Cap			T				T					
HVRI A	D M3	3 Cap			<b>T</b>						. c			
HVRI A	. мз	Cap			<b>T</b>						. c			
HVRI A	. мз	Cap			T						. C			
3anda1	. HVF	RI ÂB			<b>T</b>				T					G
3anda1	. HVF	RI AB			T						. C			
3anda1	. HVF	RI AB			T			G	T					
Banda2	HVE	RI AB			T						. C			
Banda2	HVE	RI AB			T				T					
3anda2	HVE	RI AB			T				T					

Fig. 8. Sequences alignment for M3



## Conclusion

If 16111T, 16129A and 16267T mutations will be confirmed for M3 and M4 it could possible reveal:

1. Both M3 and M4 originate from migrants of the Volga-Ural region

2. Admixture of Slavic and Turkic elements predates the migration towards west (prior to 10th century AD)

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