

575.1

?

Y-

© 2017 . . . . . 1,2, . . . . . 3, . . . . . 4, . . . . . 5, . . . . . 6,  
. . . . . 7, . . . . . 1,2, . . . . . 1, . . . . . 1,2, . . . . . 1,2, . . . . . 8,  
. . . . . 2, . . . . . 9, . . . . . 1,2, . . . . . 1,2, . . . . . 1, \*  
. . . . . 7  
2 . . . . . 115478  
3 . . . . . 119991  
4 . . . . . 150003  
5 . . . . . 426034  
6 . . . . . 152742  
7" . . . . . ( . . . . . ), 152901  
8 . . . . . " . . . . . , 152846  
9 . . . . . 61022,  
. . . . . 119991  
\*e-mail: [balanovska@mail.ru](mailto:balanovska@mail.ru)  
10.06.2016 .

VIII–X .

STR SNP Y-  
(N = 132 ).  
R-M198( 458). R-M458. N-M178. N-M178  
: N3a3-CTS10760, N3a3-CTS10760 N3a4-Z1936,  
N3a4-Z1936,  
) ( - ), ( -  
: , Y- , SNP, STR,

DOI: 10.7868/S0016675817030043

VIII–X . . . . . [1].  
. . . . . X–XI . . . . .  
( ) ( - ) [2–5].  
:

( IX ) [6],  
 ( ) - XVII .  
 IX [7].  
 ( ) ( ),  
 [7-9]. [22].  
 ( )  
 Y- [10-16]. 2013-2015  
 Y- " "  
 [17] ( )  
 [18, 19],  
 (N = 132 )  
 Y- [19] (N = 23), (N = 42), (N = 37)  
 (N = 30), (N = 23).  
 ( N-M178 [14, 20]. )  
 N-M178, [21]. " "  
 Y-



J-M12, J-M47, L-M20, L-M27, L-M317, L-M357, NO-M214, N-M178, N3a3-CTS10760, N3a4-Z1936, O-M175, O-M122, QR-M45, Q-M242, R-M207, R-M198, R-M458, R-M343, R-M269, R-L23, R-M124, T-M70. 15

17 STR  
 Y-  
 Y-filer PCR Amplification Kit (Applied Biosystems) ABI 3130xl (Applied Biosystems) Gene Mapper (Applied Biosystems). : DYS19, DYS385a, DYS385b, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438, DYS439, DYS448, DYS456, DYS458, DYS635, GATAH4.

N-M178 (11%),  
 - N3a3-CTS10760 N3a4-Z1936.

10%: I-M253 (8%); R-L23 (7%); I-P37 (5%); E-M35 (2%); E-M78 (2%); J-P58 (2%); G-M406 (1%); I-M170 (xM253, M223, P37) (1%); J-M172 (1%); J-M92 (1%).

- R-M198  
 (xM458), R-M458, N-M178 - 70%,  
 I - 80%  
 ( . 1).

[17]  
 [19].

Y-base, [18–20, 26–42].

0  
 ( N-M178, I-M170, R-M269 N-M198, . .),

DJ  
 [17] Statistica 6.0 (StatSoft. Inc., 2001) [43].

16 Y-  
 ( . 2),

16 A-M91, B-M60, C-M130, D-M174, E-M35, G-M201, I-M170 (xM253, M223, P37.2), I-M253, I-M223, I-P37.2, J-M267, J-M172, N-LLYG, R-M198 (xM458), R-M458, R-M269.

( . ) .

4 13 :  
 C-M130, DE-P205, G-L116, H-M69, I-M170, J-M304, L-M11, N-M231, O-M175, Q-M242, R1-M173, R2-L261, T-L206.

-

STR Y-  
 Network 4.1.1.2 (Fluxus Technology Ltd., www.fluxus-engineering.com) Network Publisher (Fluxus Engineering, Clare, U.K.) reduced median.

).

[44, 45].

13 Y- R I,

Haplomatch [44].

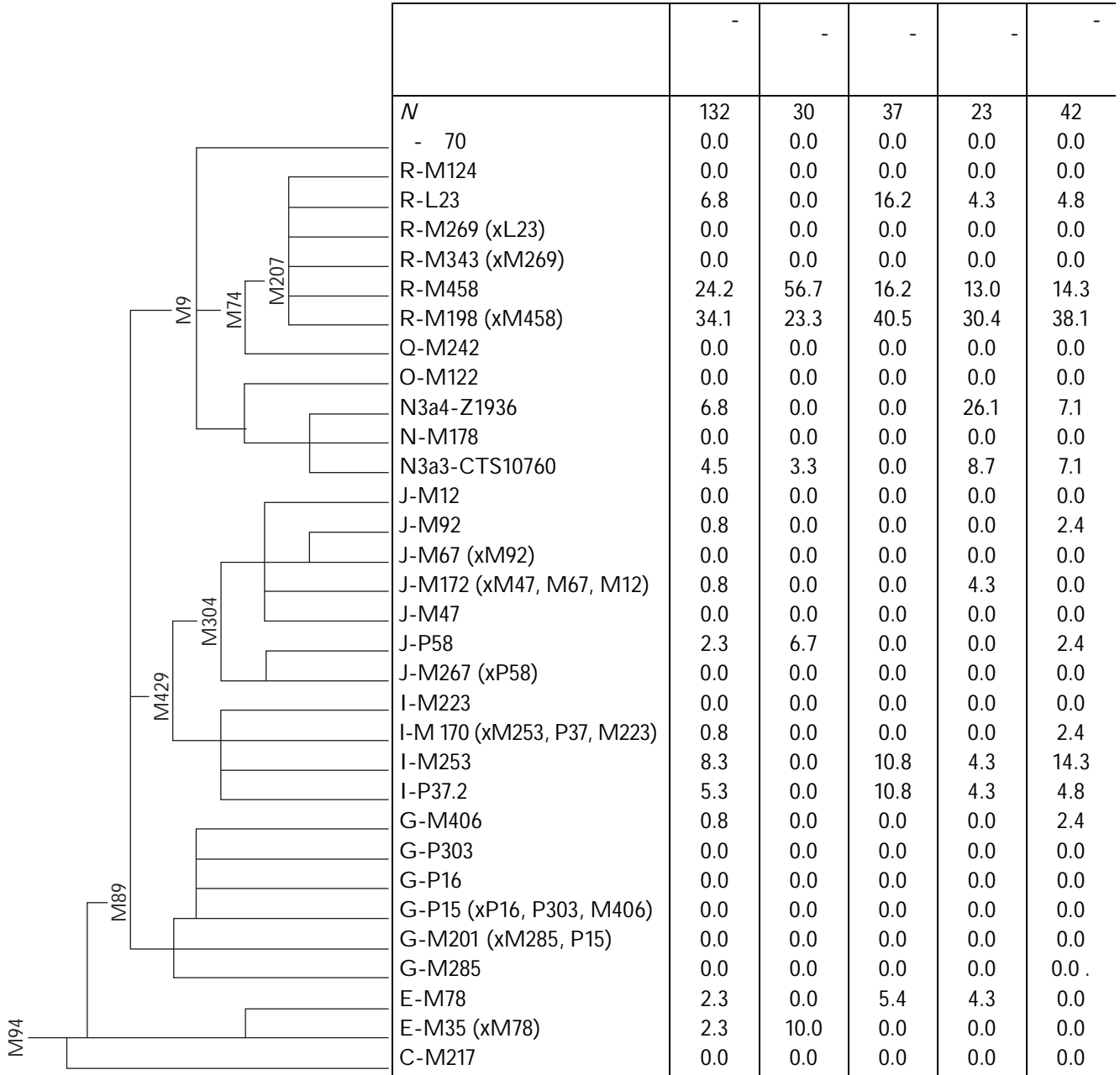
( . 3).

GeneGeo, [46–48].

(N= 132)

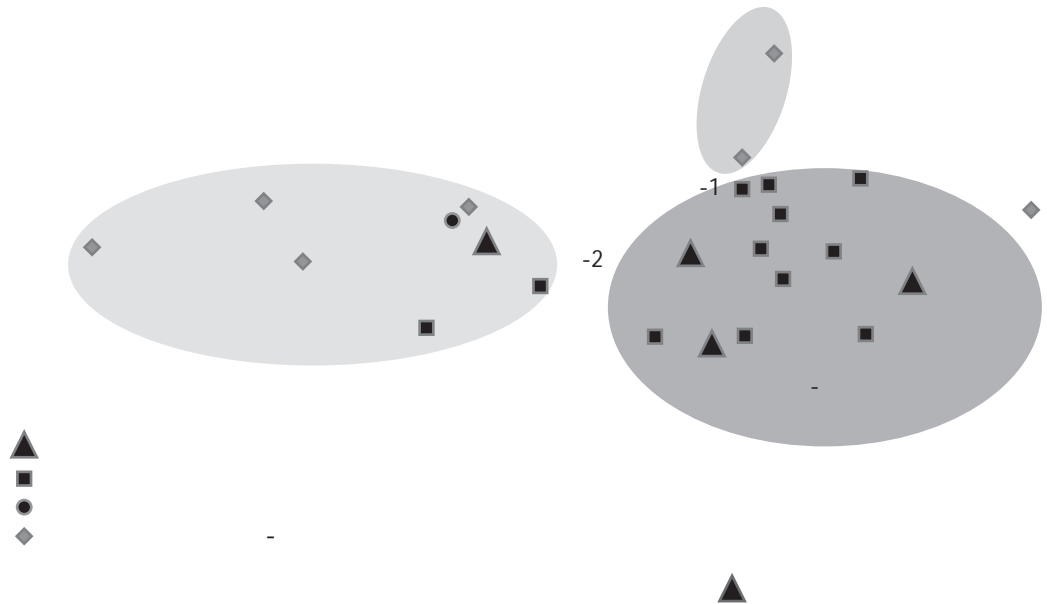
( : R-M198 (xM458) (34%); R-M458 (24%);

Y- (%)



[14, 50].

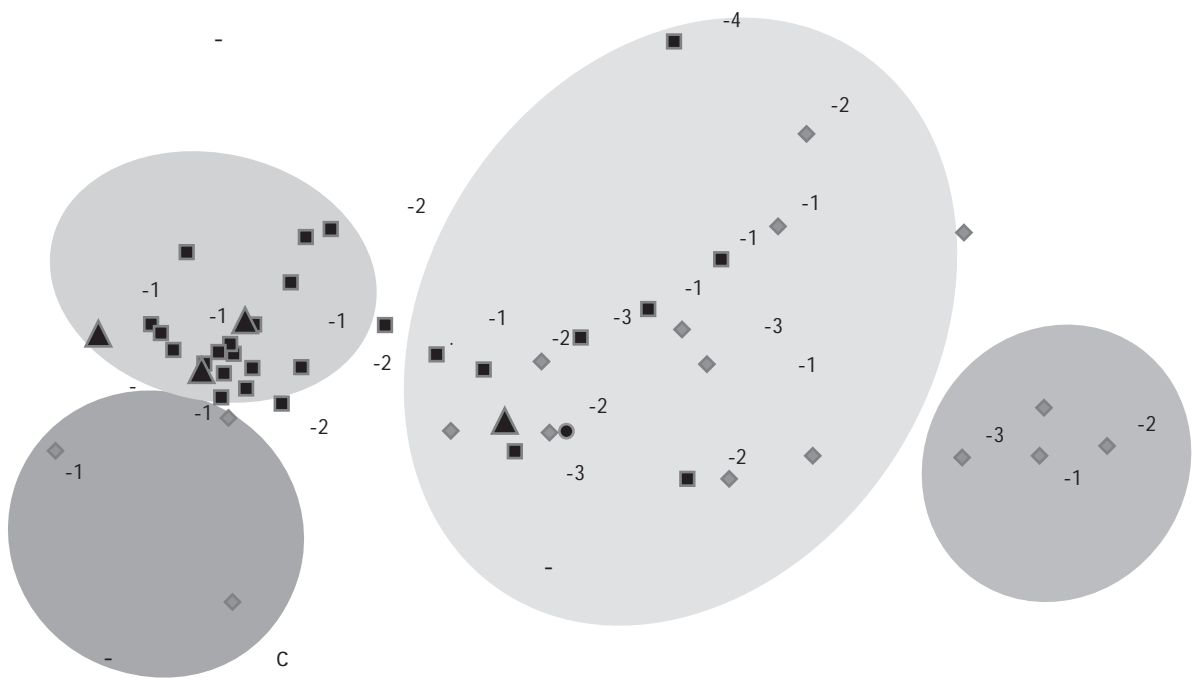
(.4)



.2.  $\frac{1}{16}$  : A-M91, B-M60, C-M130, D-M174, E-M35, G-M201, I-M170 (xM253, M223, P37.2), I-M253, I-M223, I-P37.2, J-M267, J-M172, N-LLYG, R-M198 (xM458), R-M458, R-M269 ( $= 0.086$ ;  $= 0.102$ ).

[27] — ; : [17] — , -1, -2, ; [20, 28, 29, 32, 39] — ; [20, 29, 31, 32, 34, 37, 39] — ; [20, 29, 39, 40] — ; [20, 29, 32, 34-42] — ; [20,

(.4,A) — ( ) .  
 , , 1478 .  
 ( .4,B):  
 ( , ),  
 ( ) ,  
 [49].  
 ( ) ,  
 ( ) :



3. Q-M242, R1-M173, R2-L261, T-L206 (13 : C-M130, DE-P205, G-L116, H-M69, I-M170, J-M304, L-M11, N-M231, O-M175, = 0.034; = 0.038). : [17] - -  
 -2, -1, -2, -1; [18] - -3, -2, -1, -2, -1, -1, -  
 -1, -1; [20, 28, 29, 32, 39] - ; [32] - ; [26] - -1; [27] - ; [28] - -4, -2, -2, -2, -  
 -1; [20, 29, 39, 40] - ; [20, 29, 32, 34-42] - ; [30] -  
 -2; [31] - -2, ; [32] - -2, -3; [33] - -3. : , -  
 , [20, 39] - .

[50]. 11-15% [17, 50].

R-M458

R- 458 ( . 5)

R-M458

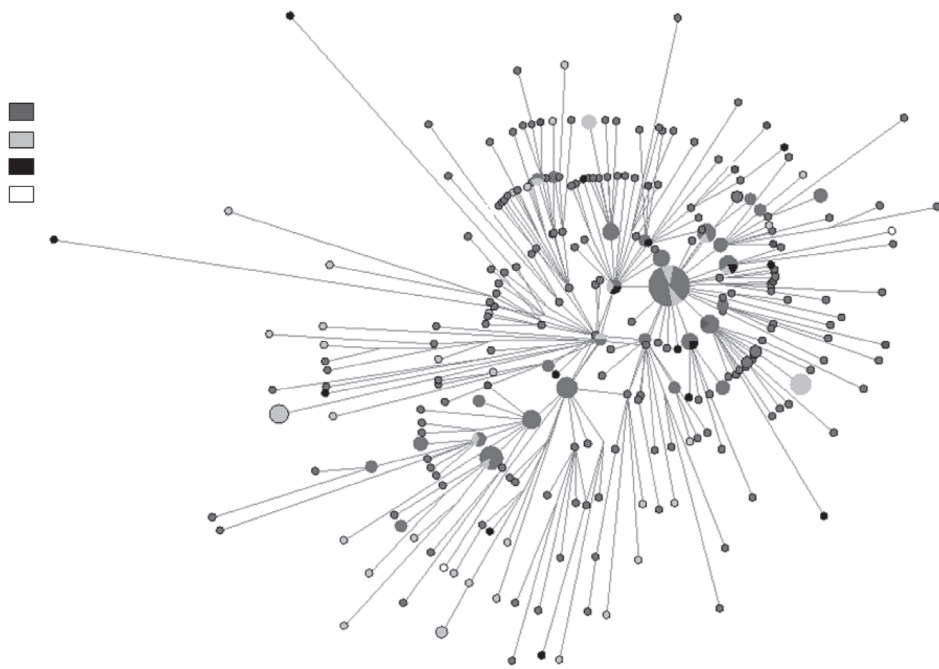
( . 4,C)

( . 4,C),

R-M458. (60%)

R-M458

J-P58 (6.7%) -



.5. R-M458. [45, 46].

J-P58, R-M198 (xM458) (40%), R-M458 (16%), R-M269 (16%), N-M178, ( .4,D)

Haplomatch [44]

C O N N3a3-CTS10760, N-M178, R-M198 (xM458), R-M458, N-M178 (35%), N-M178 (35-50%) [17].

[21].



( ) , N-M178, N3a4-Z1936

( ), Y- [21]. N-M178 ( )

N3a3-CTS10760, N3a4-Z1936 ( 26%)

N3a4-Z1936, [21]. N-M178 ( ) N3a4-Z1936.

( .4,E),

N: N3a4-Z1936.

16-06-00303\_ N-M178

14-14-00827.

R-M198 (38%), R-M458 N-M178. (14%)

N-M178 1. //

: N3a3-CTS10760 ( ) N3a4-Z1936 ( ) [21]. 436–467. 2001.

2. III. 2007. 215

N3a4-Z1936 3. IV. 2015. 313

4. //

N-M178. R-M198, R-M458, 2006. 3. 38–51.

5. " "

2015. 2(19). 7–61. //
6. // IX–X
7. // IX–X
8. // IX–X
9. // XI–XIII
10. *Pliss L.1., Timša L.1., Rootsi S. et al.* Y-chromosomal lineages of Latvians in the context of the genetic variation of the Eastern-Baltic region // *Ann. Hum. Genet.* 2015. V. 79. 6. P. 418–430. doi 10.1111/ahg.12130
11. *Balanovsky O., Zhabagin M., Agdzhoyan A. et al.* Deep phylogenetic analysis of haplogroup G1 provides estimates of SNP and STR mutation rates on the human Y-chromosome and reveals migrations of Iranic speakers // *PLoS One.* 2015. V. 10(4): e0122968. doi 10.1371/journal.pone.0122968
12. *Zalloua P.A., Xue Y., Khalife J. et al.* Y-chromosomal diversity in Lebanon is structured by recent historical events // *Am. J. Hum. Genet.* 2008. V. 82. P. 873–882. doi 10.1016/j.ajhg.2008.01.020
13. *Zalloua P.A., Platt D.E., El Sibai M. et al.* Identifying genetic traces of historical expansions: Phoenician footprints in the Mediterranean // *Am. J. Hum. Genet.* 2008. V. 83. P. 633–642. doi 10.1016/j.ajhg.2008.10.012
14. // ? ?
15. // Y
16. //
17. *Balanovsky O., Rootsi S., Pshenichnov A. et al.* Two sources of the Russian patrilineal heritage in their Eurasian context // *Am. J. Hum. Genet.* 2008. V. 82. P. 236–250. doi 10.1016/j.ajhg.2007.09.019
18. *Roewer L., Willuweit S., Krüger C. et al.* Analysis of Y chromosome STR haplotypes in the European part of Russia reveals high diversities but non-significant genetic distances between populations // *Int. J. Legal Med.* 2008. V. 122. 3. P. 219–223. doi 10.1007/s00414-007-0222-2
19. //
20. *Rootsi S., Zhivotovsky L.A., Baldovic M. et al.* A counter-clockwise northern route of the Y-chromosome haplogroup N from Southeast Asia towards Europe // *Hum. Genet.* 2007. V. 115. 2. P. 204–211.
21. *Ilumäe A.-M., Reidla M., Chukhryaeva M. et al.* Human Y-chromosomal haplogroup N: A non-trivial time-resolved phylogeography that cuts across language families // *Am. J. Hum. Genet.* 2016. V. 99(1). P. 163–173. doi 10.1016/j.ajhg.2016.05.025
22. //
23. //
24. //
25. //
26. *Karlsson A.O., Wallerström T., Götherström A. et al.* Y-chromosome diversity in Sweden – a long-time perspective // *Eur. J. Hum. Genet.* 2006. V. 14. 8. P. 963–970.
27. *Kushniarevich A., Sivitskaya L., Danilenko N. et al.* Uniparental genetic heritage of belarusians: encounter of rare middle eastern matrilineages with a central European mitochondrial DNA pool // *PLoS One.* 2013. V. 8(6):e66499. doi 10.1371/journal.pone.0066499
28. *Mirabal S., Regueiro M., Cadenas A.M. et al.* Y-chromosome distribution within the geo-linguistic landscape of northwestern Russia // *Eur. J. Hum. Genet.* 2009. V. 17. 10. P. 1260–73.
29. *Myres N.M., Rootsi S., Lin A.A. et al.* A major Y-chromosome haplogroup R1b Holocene era founder effect in Central and Western Europe // *Eur. J. Hum. Genet.* 2011. V. 19. 1. P. 95–101.
30. *Pimenoff V.N., Comas D., Palo J.U. et al.* Northwest Siberian Khanty and Mansi in the junction of West and East Eurasian gene pools as revealed by uniparental markers // *Eur. J. Hum. Genet.* 2008. V. 16. 10. P. 1254–1264. doi 10.1038/ejhg.2008.101
31. *Semino O., Passarino G., Oefner P.J. et al.* The genetic legacy of Paleolithic *Homo sapiens sapiens* in extant Europeans: a Y chromosome perspective // *Science.* 2000. V. 290. 5494. P. 1155–1159. doi 10.1126/science.290.5494.1155
32. *Tambets K., Rootsi S., Kivisild T. et al.* The western and eastern roots of the Saami—the story of genetic “outliers” told by mitochondrial DNA and Y chromosomes // *Am. J. Hum. Genet.* 2004. V. 74. 4. P. 661–682. doi 10.1086/383203
33. *Wells R.S., Yuldasheva N., Ruzibakiev R. et al.* The Eurasian heartland: a continental perspective on Y-chromosome diversity // *Proc. Natl Acad. Sci. USA.* 2001.

- V. 98. 18. P. 10244–10249. doi 10.1073/pnas.171305098
34. Rosser Z.H., Zerjal T., Hurler M.E. et al. Y-chromosomal diversity in Europe is clinal and influenced primarily by geography, rather than by language // *Am. J. Hum. Genet.* 2000. V. 67. P. 1526–1543.
35. Rootsi S., Magri C., Kivisild T. et al. Phylogeography of Y-chromosome haplogroup I reveals distinct domains of prehistoric gene flow in Europe // *Am. J. Hum. Genet.* 2004. V. 75. 1. P. 128–137.
36. Rootsi S., Myres N.M., Lin A.A. et al. Distinguishing the co-ancestries of haplogroup G Y-chromosomes in the populations of Europe and the Caucasus // *Eur. J. Hum. Genet.* 2012. V. 20. 12. P. 1275–1282.
37. Cruciani F., La Fratta R., Trombetta B. et al. Tracing past human male movements in northern/eastern Africa and western Eurasia: new clues from Y-chromosomal haplogroups E-M78 and J-M12 // *Mol. Biol. Evol.* 2007. V. 24. 6. P. 1300–1311. doi 10.1093/molbev/msm049
38. Underhill P.A., Myres N.M., Rootsi S. et al. New Phylogenetic Relationships for Y-Chromosome Haplogroup I: Reappraising Its Phylogeography and Prehistory / Eds Mellars P., Boyle K., Bar-Yosef O., Stringer C. Cambridge, UK: Rethinking the Human Revolution. McDonald Institute for Archaeological Research, 2007. P. 33–42.
39. Underhill P., Myres N., Rootsi S. et al. Separating the post-Glacial coancestry of European and Asian Y-chromosomes within haplogroup R1a // *Eur. J. Hum. Genet.* 2010. V. 18. 4. P. 479–484. doi 10.1038/ejhg.2009.194
40. Lappalainen T., Koivumäki S., Salmela E. et al. Regional differences among the Finns: a Y-chromosomal perspective // *Gene.* 2006. V. 376. 2. P. 207–215.
41. Lappalainen T., Laitinen V., Salmela E. et al. Migration waves to the Baltic Sea region // *Ann. Hum. Genet.* 2008. V. 72. 3. P. 337–348.
42. Heinrich M., Braun T., Sängler T. et al. Reduced-volume and low-volume typing of Y-chromosomal SNPs to obtain Finnish Y-chromosomal compound haplotypes // *Int. J. Legal. Med.* 2009. V. 123. 5. P. 413–418. doi 10.1007/s00414-009-0358-3
43. StatSoft, Inc. STATISTICA (data analysis software system). version 62001. www.statsoft.com
44. Haplomatch STR Y- // 2016. 5. 595–604. doi 10.1134/S1022795416050045
45. Balanovsky O., Dibirova K., Dybo A. et al. Parallel evolution of genes and languages in the Caucasus region // *Mol. Biol. Evol.* 2011. V. 28(10). P. 2905–2920. doi 10.1093/molbev/msr126
46. Haak W., Balanovsky O., Sanchez J.J. et al. Ancient DNA from European early Neolithic farmers reveals their near eastern affinities // *PLoS Biol.* 2010. V. 8. 11. doi 10.1371/journal.pbio.1000536
47. // +, 2012. 158–166.
48. 2015. 254
49. , 2015. 49–53, 141–162.
50. Kushniarevich A., Utevska O., Chuhryaeva M. et al. Genetic heritage of the Balto-Slavic speaking populations: a synthesis of autosomal, mitochondrial and Y-chromosomal data // *PLoS One.* 2015. V. 10(9): e0135820. doi 10.1371/journal.pone.0135820

## Is There a Finno-Ugric Component in the Gene Pool of Russians from Yaroslavl Oblast? Evidence from Y-Chromosome

M. I. Chukhryaeva<sup>a, b</sup>, E. S. Pavlova<sup>c</sup>, V. V. Napolskich<sup>d</sup>, E. V. Garin<sup>e</sup>, A. S. Klopov<sup>f</sup>, S. N. Temnyatkin<sup>g</sup>, V. V. Zaporozhchenko<sup>a, b</sup>, A. G. Romanov<sup>a</sup>, A. T. Agdzhoyan<sup>a, b</sup>, O. M. Utevska<sup>h</sup>, N. V. Markina <sup>b</sup>, S. M. Koshel<sup>i</sup>, O. P. Balanovsky<sup>a, b</sup>, and E. V. Balanovska<sup>a, \*</sup>

<sup>a</sup>Research Centre for Medical Genetics, Moscow, 115478 Russia

<sup>b</sup>Vavilov Institute of General Genetics, Russian Academy of Sciences, Moscow, 119991 Russia

<sup>c</sup>Demidov Yaroslavl State University, Yaroslavl, 150003 Russia

<sup>d</sup>Institute of Social Communications, Udmurt State University, Izhevsk, 426034 Russia

<sup>e</sup>Papanin Institute for Biology of Inland Waters, Russian Academy of Sciences, Yaroslavlskaya oblast, Borok, 152742 Russia

<sup>f</sup>Mologa Territory Museum (Rybinsk Museum Reserve), Yaroslavlskaya oblast, Rybinsk, 152901 Russia

<sup>g</sup>Ethnographic Museum of Katskari, Yaroslavlskaya oblast, Martynovo, 152846 Russia

<sup>h</sup>Karazin Kharkiv National University, Kharkiv, 61022 Ukraine

<sup>i</sup>Department of Cartography and Geoinformatics, Lomonosov Moscow State University, Moscow, 119991 Russia

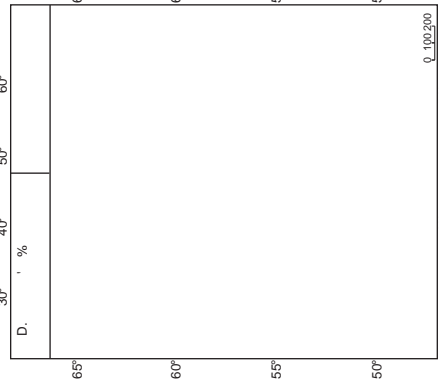
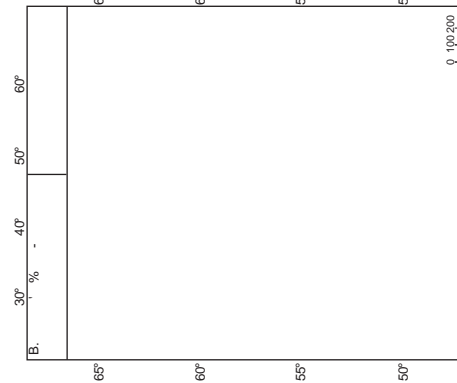
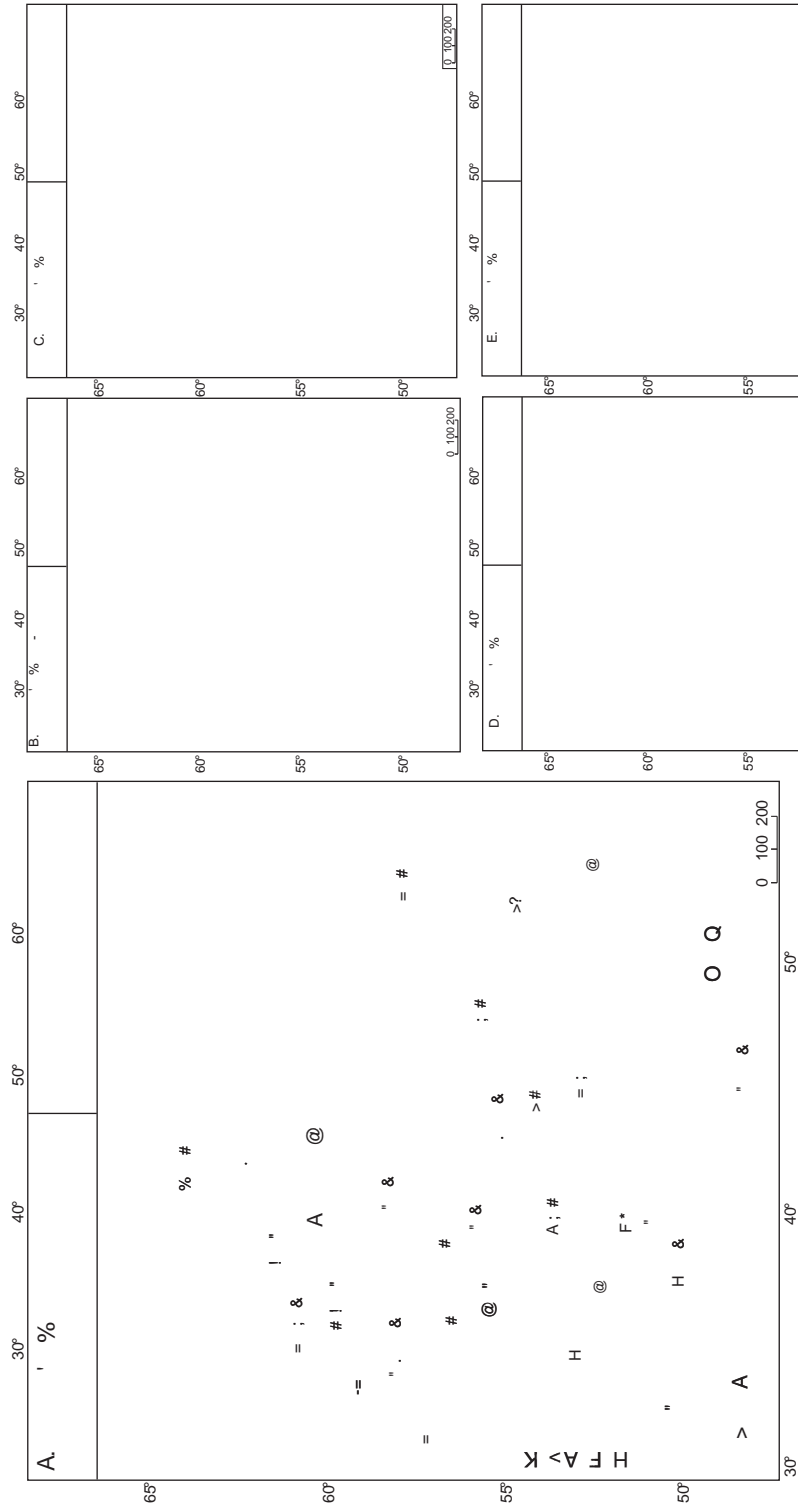
\*e-mail: balanovska@mail.ru

The Upper Volga region was an area of contacts of Finno-Ugric, Slavic, and Scandinavian speaking populations in the 8th–10th centuries AD. However, their role in the formation of the contemporary gene pool of the Russian population of the region is largely unknown. To answer this question, we studied four populations

of Yaroslavl oblast ( $N = 132$ ) by a wide panel of STR and SNP markers of the Y-chromosome. Two of the studied populations appear to be genetically similar: the indigenous Russian population of Yaroslavl oblast and population of Katskari are characterized by the same major haplogroup, R-M198(xM458). Haplogroup R-M458 composes more than half of Sitskari's gene pool. The major haplogroup in the gene pool of the population of the ancient town of Mologa is N-M178. Subtyping N-M178 by newest "genome-era" Y-SNP markers showed different pathways of entering this haplogroup into the gene pools of Yaroslavl Volga region populations. The majority of Russian populations have subvariant N3a3-CTS10760; the regular sample of Yaroslavl oblast is equally represented by subvariants N3a3-CTS10760 and N3a4-Z1936, while subvariant N3a4-Z1936 predominates in the gene pool of Molog population. This N3a4-Z1936 haplogroup is common among the population of the north of Eastern Europe and the Volga-Ural region. The obtained results indicate preservation of the Finno-Ugric component in the gene pool of population of Mologa and a contribution of Slavic colonization in the formation of the gene pool of the Yaroslavl Volga region populations and make it possible to hypothesize the genetic contribution of the "downstream" (Rostov-Suzdal) rather than "upstream" (Novgorod) Slavic migration wave. English translation of the paper published in Russian Journal of Genetics, 2017, Vol. 53, No. 3, is available ONLINE by subscription from: <http://www.springer.com/>, <http://link.springer.com/journal/11177>.

*Keywords:* gene pool, genogeography, Y-chromosome, SNP, STR, Russians, Yaroslavl oblast, Finno-Ugric peoples, Merya, Sitskari, Katskari, Mologzhane.





.4. <B... %  
 D ... & \*\* \*  
 \* \* \*  
 & # .  
 <E... %  
 +/ % \*\* ; .  
 <C... \* ;  
 ...  
 % #  
 <