

575.1

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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
. 115478
2 119991
3 150003
4 426034
5 152742
6 152901
7" 152846
8 61022,
9 119991
*e-mail: 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].
 I
 () (),
 [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.

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.

13 Y- R I,

[44, 45].

Haplomatch [44].

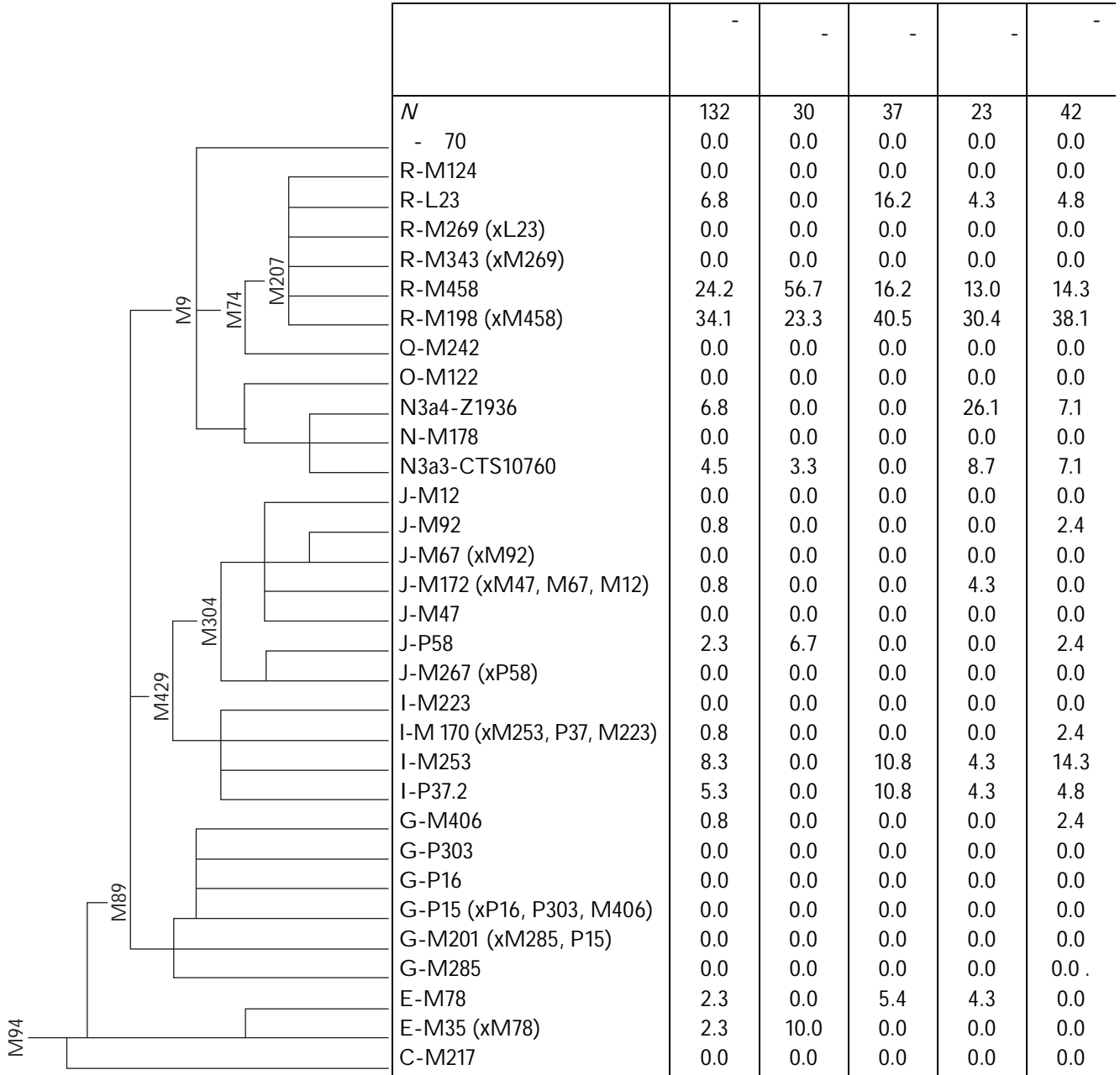
(. 3).

GeneGeo, [46–48].

(N= 132)

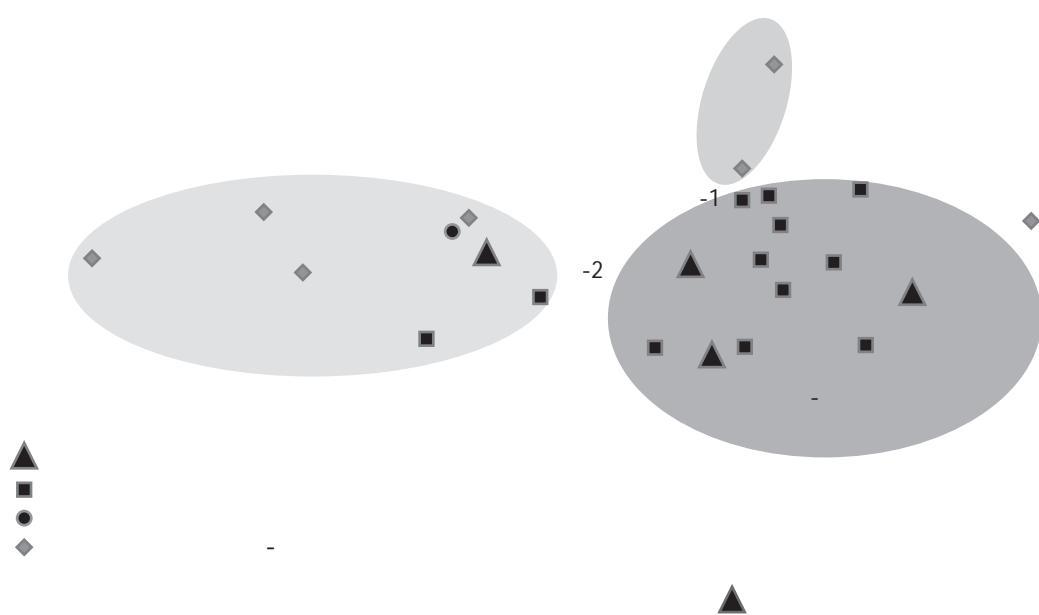
()
 : R-M198 (xM458) (34%); R-M458 (24%);

Y- (%)



[14, 50].

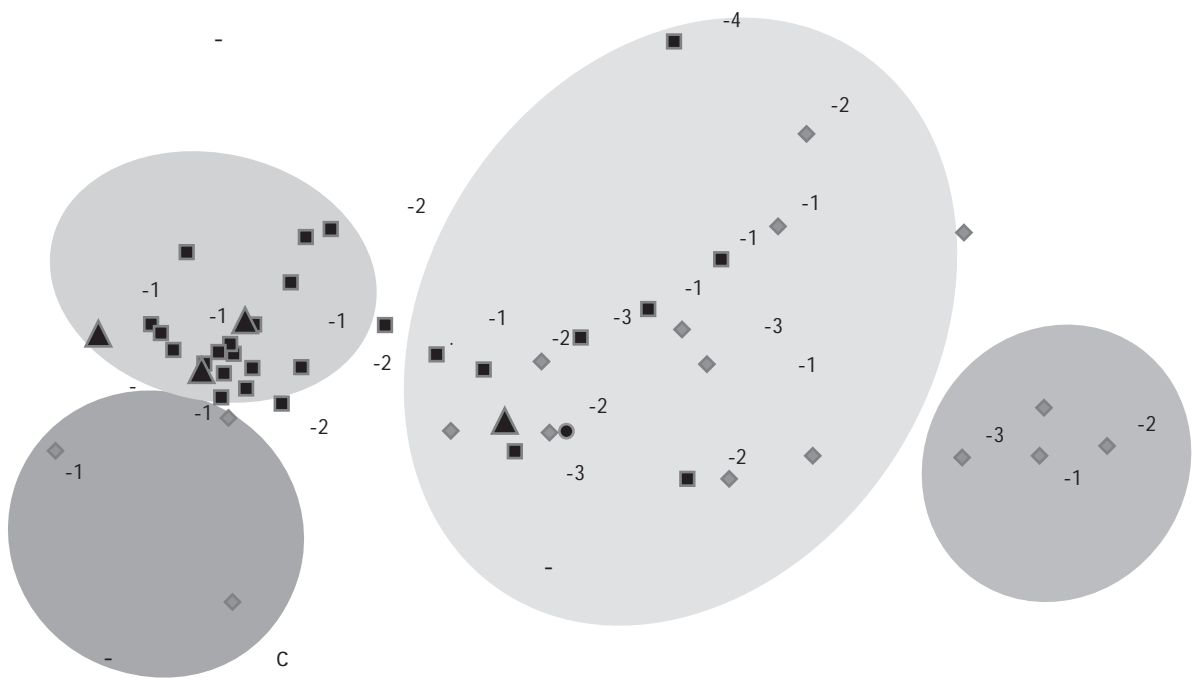
(.4)



.2. $\rho = 0.086$; $\rho = 0.102$. 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 (

[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. 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 (= 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, -
 - -2; [31] - -2, -2; [32] - -2, -3; [33] - -3. : [30] - -

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

R-M458

R- 458 (. 5)

R-M458

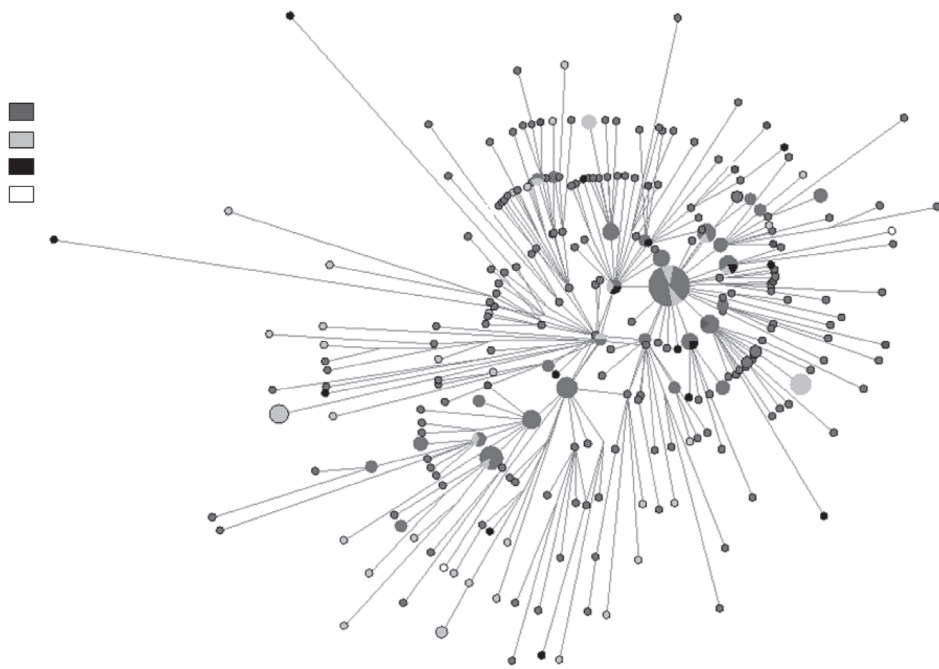
(. 4,C)

(. 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,

Haplomatch [44]

(.4,D)

C O

N

N3a3-CTS10760,

N-M178,

– R-M198 (xM458), R-M458,
N-M178 (35%).
N-M178

[21].

50%) [17].

(35–

() , N-M178, N3a4-Z1936

— , — , —

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

N3a3-CTS10760, N3a4-Z1936

N3a4-Z1936, (26%) N3a4-Z1936

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

(.4,E),

N: N3a4-Z1936.

16-06-00303_ N-M178

R-M198 (38%), R-M458 N-M178. 14-14-00827.

(14%) N-M178

: N3a3-CTS10760 () N3a4-Z1936 () [21].

N3a4-Z1936

N-M178. — R-M198, R-M458,

1. // : 2001.
2. . 436—467.
3. III. 2007. 215 .
4. IV. : , 2015. 313 .
5. . 2006. 3. . 38—51. " "

2015. 2(19). 7–61. //
6. // IX–X
7. // IX–X
8. // IX–X
9. // XI–XIII
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Is There a Finno-Ugric Component in the Gene Pool of Russians from Yaroslavl Oblast? Evidence from Y-Chromosome

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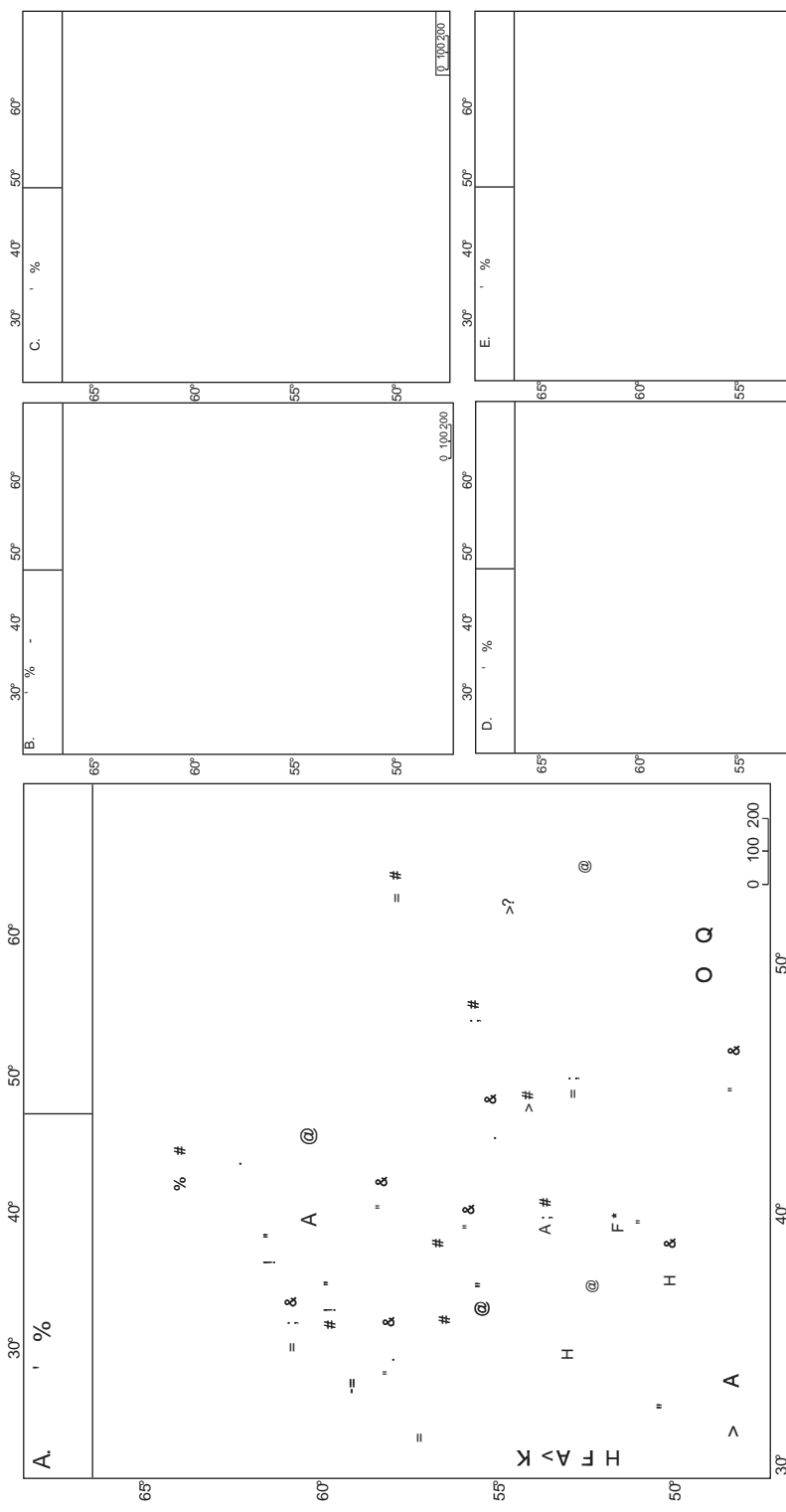
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The Upper Volga region was an area of contacts of Finno-Ugric, Slavic, and Scandinavian speaking populations in the 8th–10th centuries AD. However, their role in the formation of the contemporary gene pool of the Russian population of the region is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



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