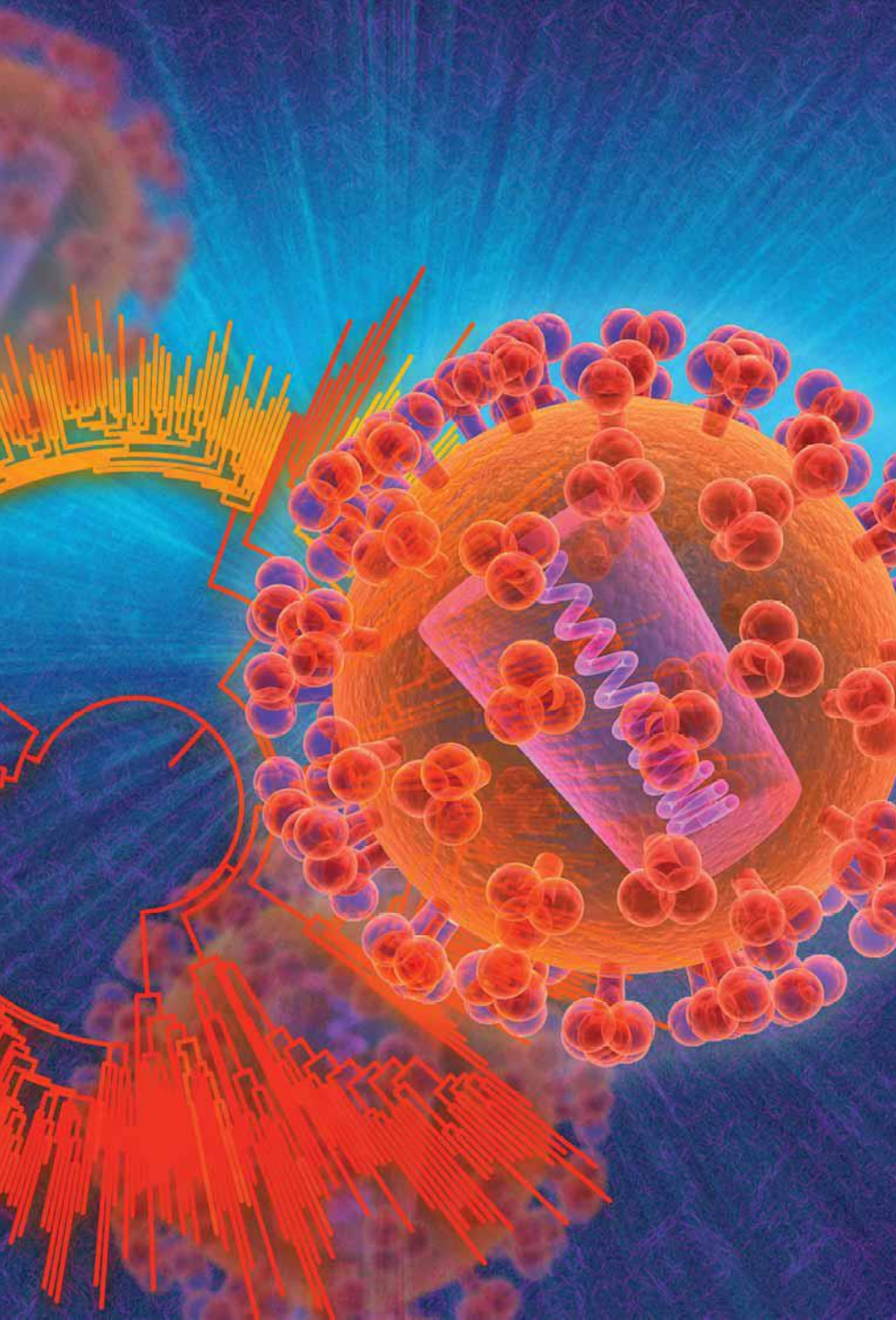
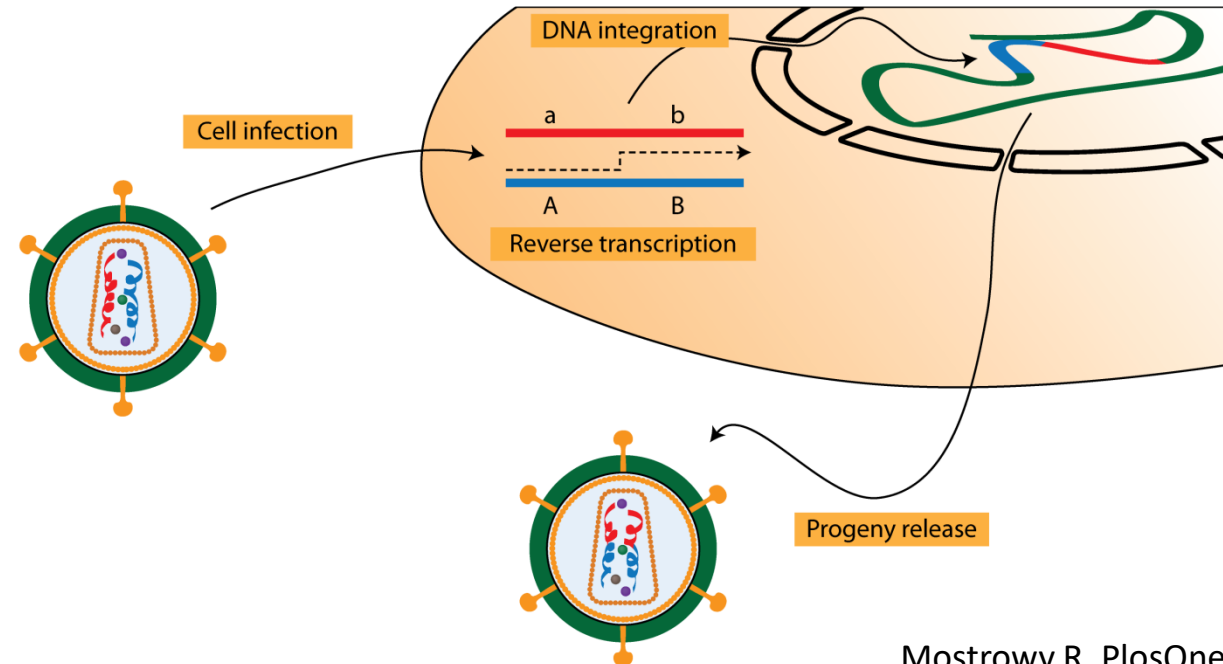




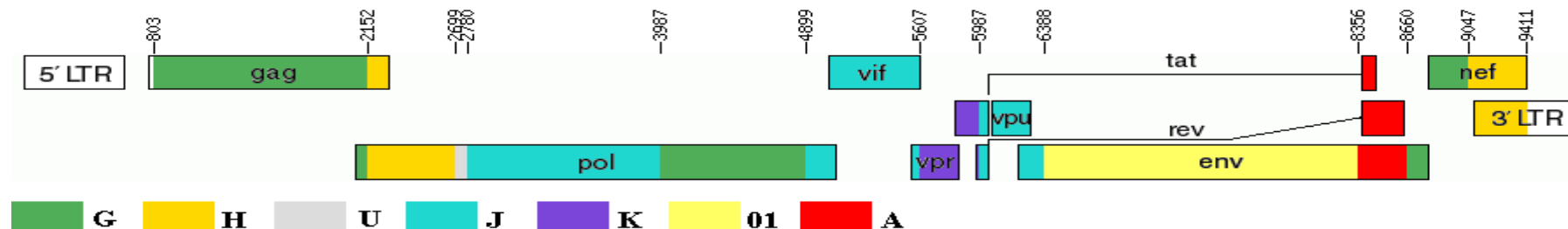
Epidemiologia moleculară a infecției HIV în România

Simona Paraschiv, Dan Otelea

Recombination – essential for HIV evolution and diversity



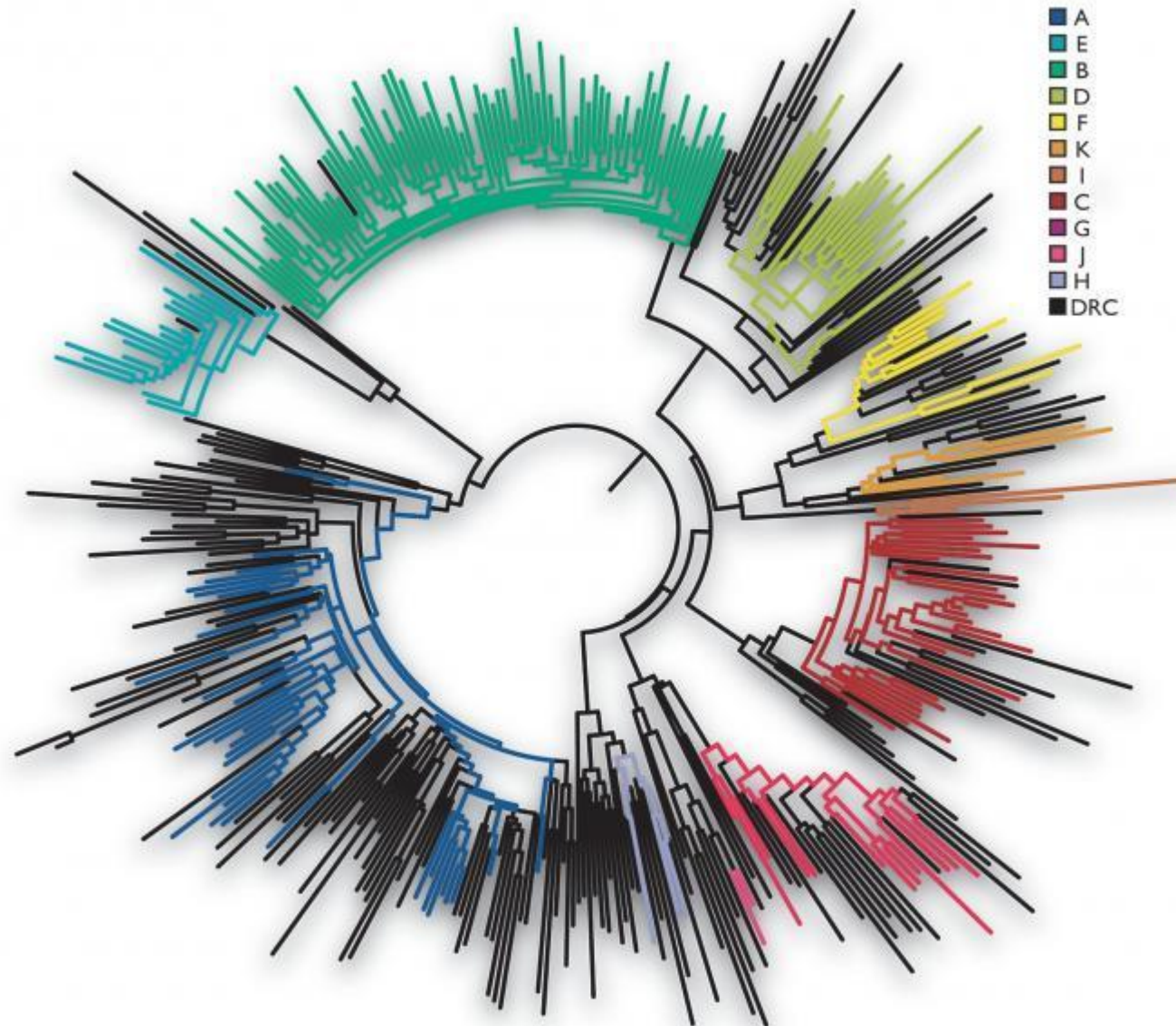
Mostrowy R, PlosOne, 2011



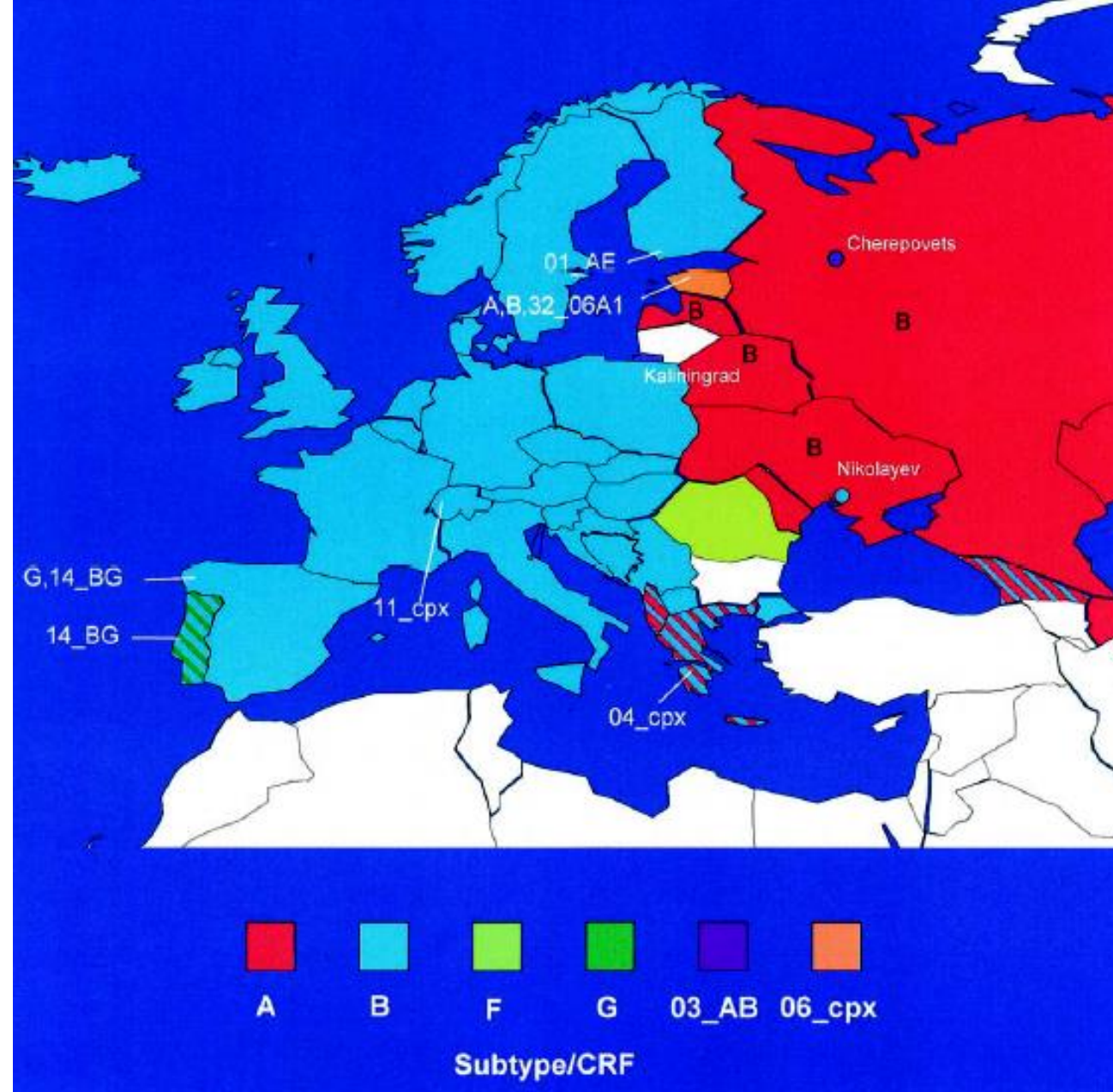
CRF27_cpx

<https://www.hiv.lanl.gov/components/sequence/HIV/crfdb/crfs.comp>

Diversity of HIV-1 group M



9 subtypes
132 CRFs
....URFs



Thomson MM, Najera R, 2007. Increasing HIV-1 Genetic Diversity in Europe. *J Infect Dis*; 196:1120–1124

Nosocomial HIV-1 transmission and primary prevention in Romania

C Apetrei, I Buzdugan, Irina Mitroi, Luminita Iancu, M Duca
Virus Laboratory, University of Medicine 16, Universitatii Street, Ro-6600,
Iasi, Romania; Sanitary Police Departments, Epidemiology Services,
Iasi and Vaslui Districts, Romania

SIR—Blank and colleagues (Aug 20, p 512) report the possibility of patient-to-patient transmission of HIV during medical care in a paediatric unit. The HIV epidemic among Romanian children has already been attributed to nosocomial transmission.¹⁻⁴ Since previous reports involved cross-sectional studies, we started a seroepidemiologic survey in 1992 in northeast Romania to establish the prevalence and incidence of HIV infection in life-care institutions for orphans and abandoned children. In 1992,

Vol 344 • October 8, 1994

Most of the Romanian HIV infected children (~10000 persons) were nosocomial infected with subtype F1 in the late 80s

The tragic situation was due to HIV-1-contaminated hospital equipment usage (needles, syringes) or contaminated blood products

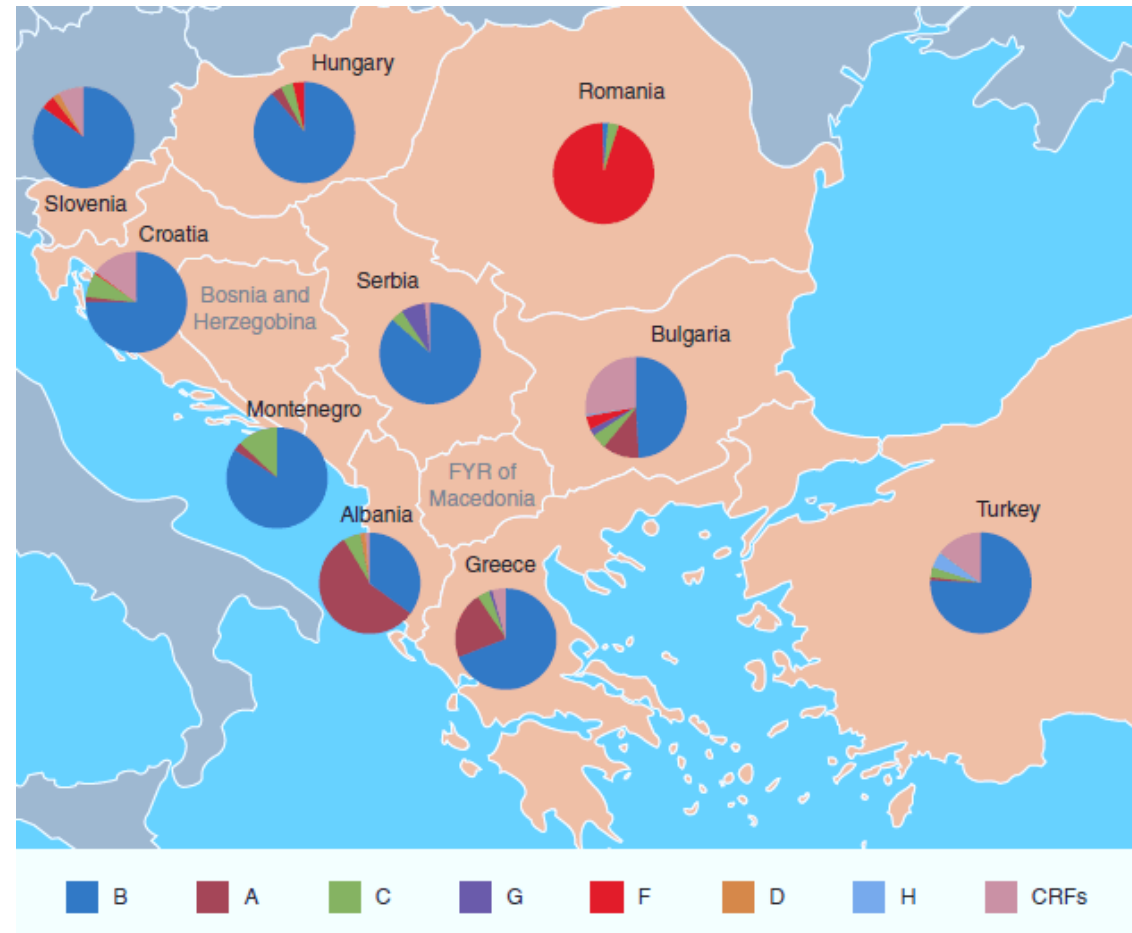
Click on image to zoom

Sequence Note

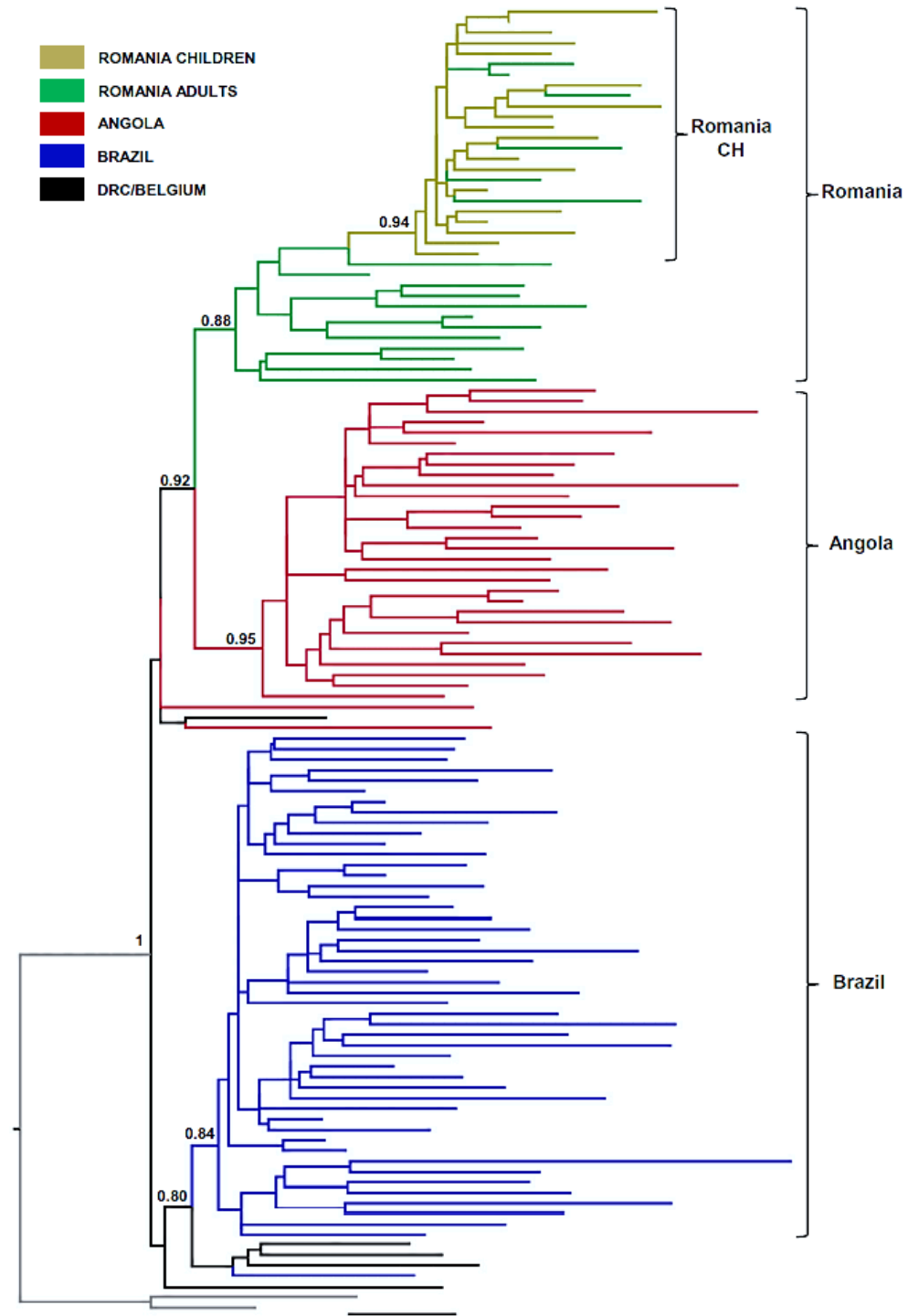
HIV Type 1 Subtype F Sequences in Romanian Children and Adults

CRISTIAN APETREI,^{1,2} IBTISSAM LOUSSERT-AJAKA,¹ GILLES COLLIN,¹ FRANCK LETOURNEUR,³
MIHAI DUCA,² SENTOB SARAGOSTI,³ FRANÇOIS SIMON,¹ and FRANÇOISE BRUN-VÉZINET¹

2003 - 2011 - 91% of the
sequenced HIV strains were
F1 subtype



Origin of subtype F



Phylogeographic analysis of subtype F1 epidemic in Romania: tracing back the origin of the epidemic

Nazle Mendonca Collaço Vêras^{1,2}, **Simona Paraschiv**³, Ana Maria Tudor³, Dan Otelea³ and Marco Salemi^{1,2}

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² Emerging Pathogens Institute, University of Florida, Gainesville, FL 32610, USA

³ National Institute for Infectious Diseases 'Matei Bals', Bucharest, Romania

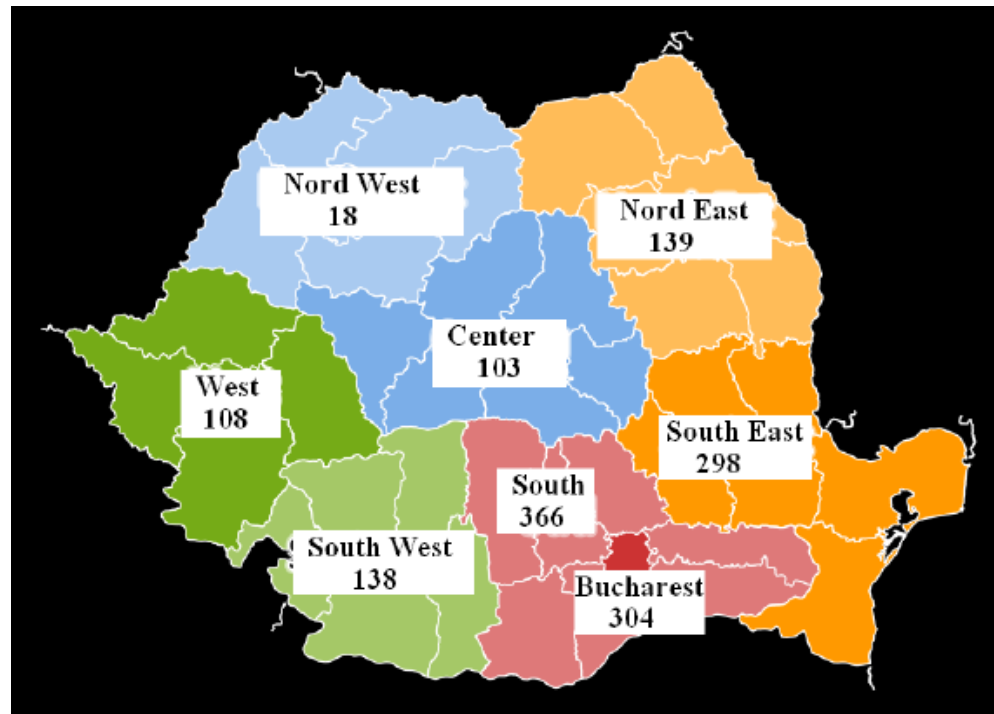
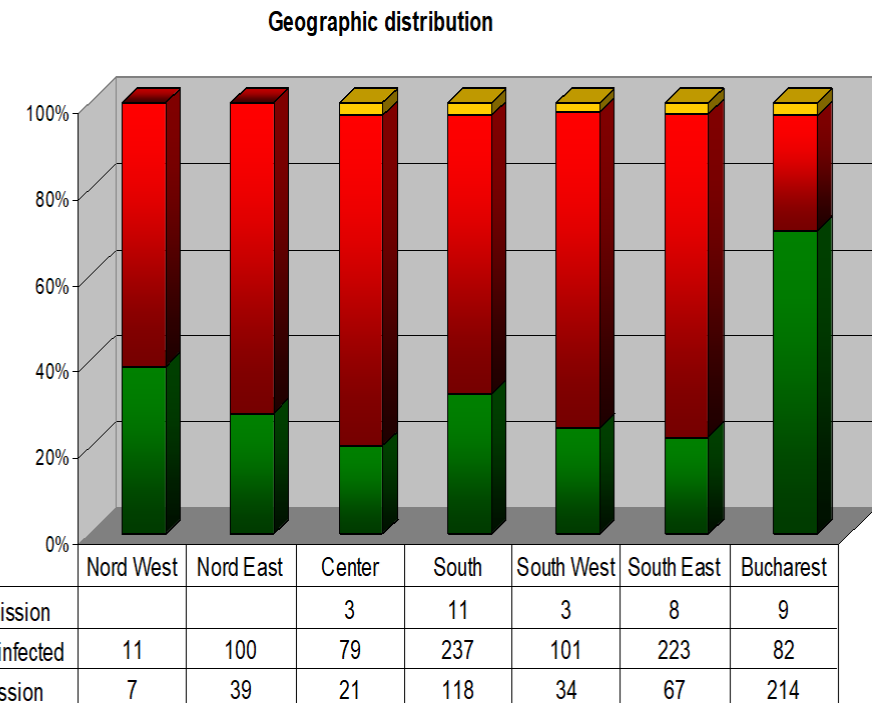
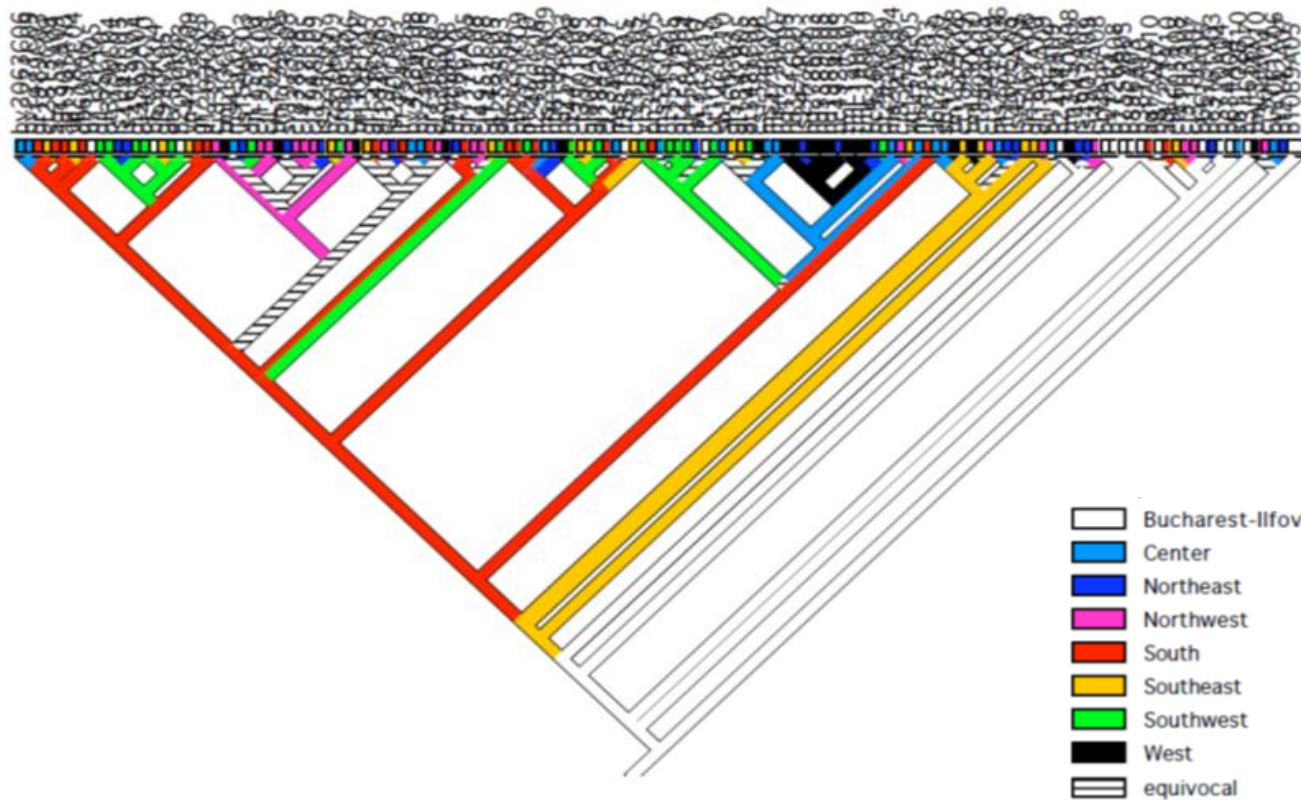


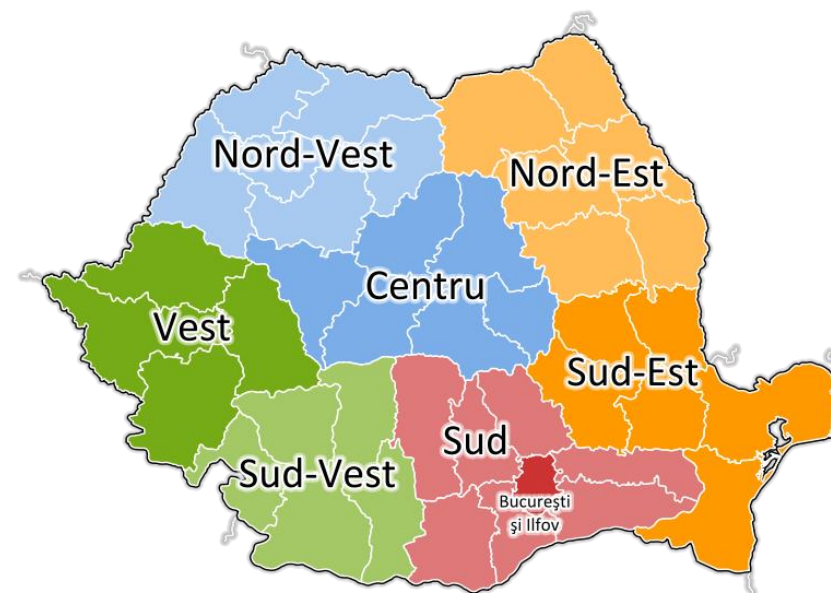
Figure 1. Geographic distribution of the studied patients





Bucharest - entry point of subtype F1

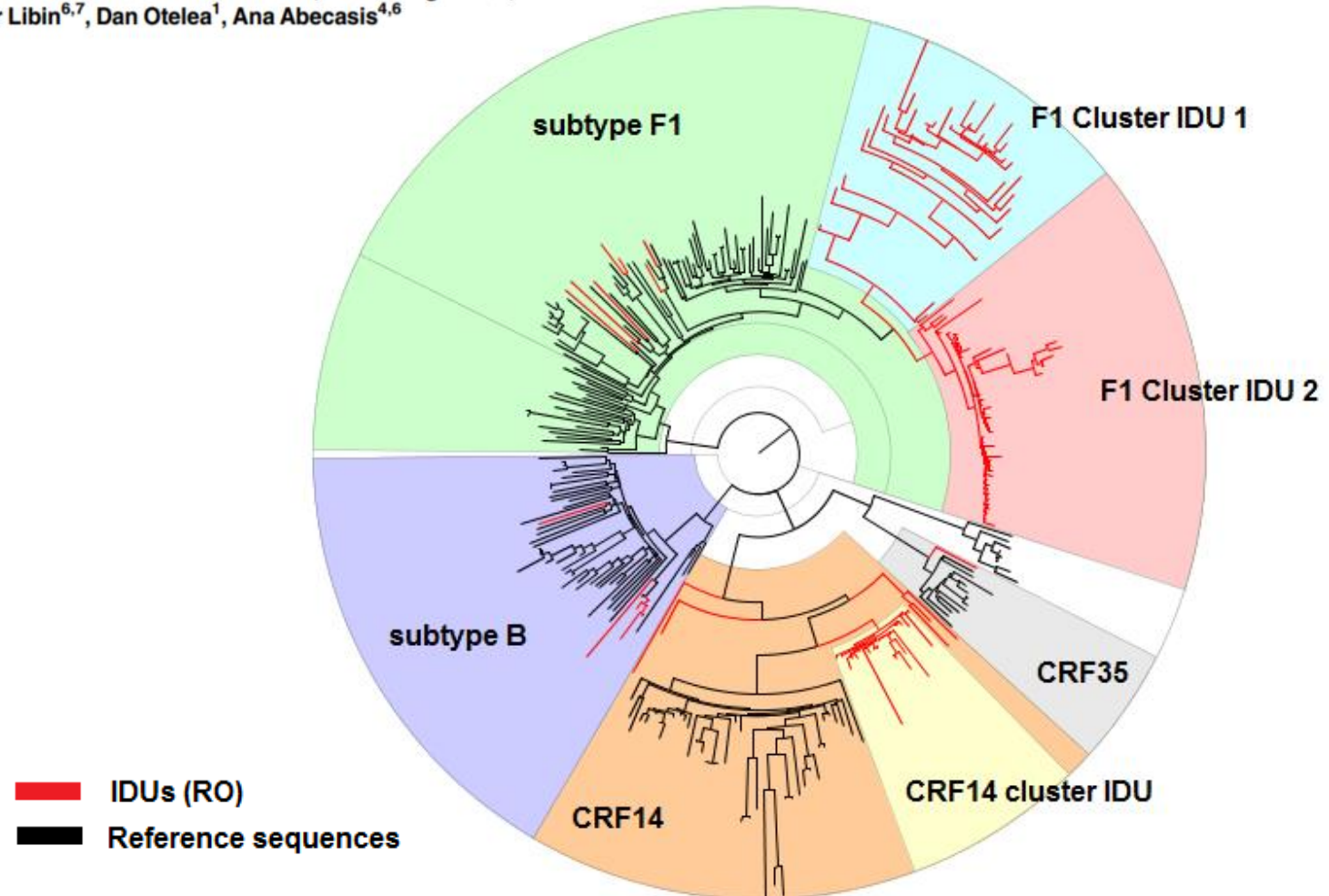
Spread across the country: Southeast, South to North



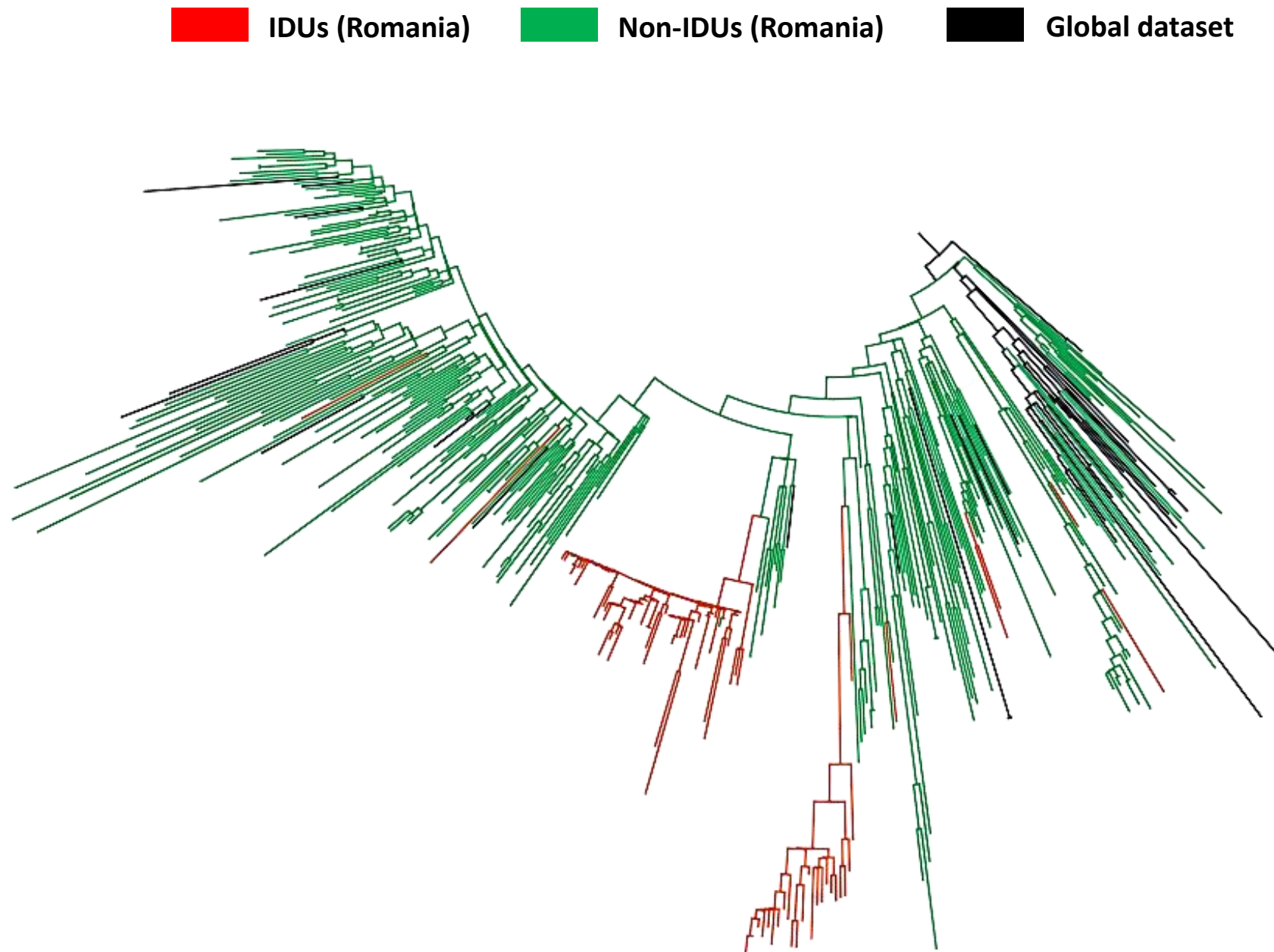
RESEARCH ARTICLE

Epidemic dispersion of HIV and HCV in a population of co-infected Romanian injecting drug users

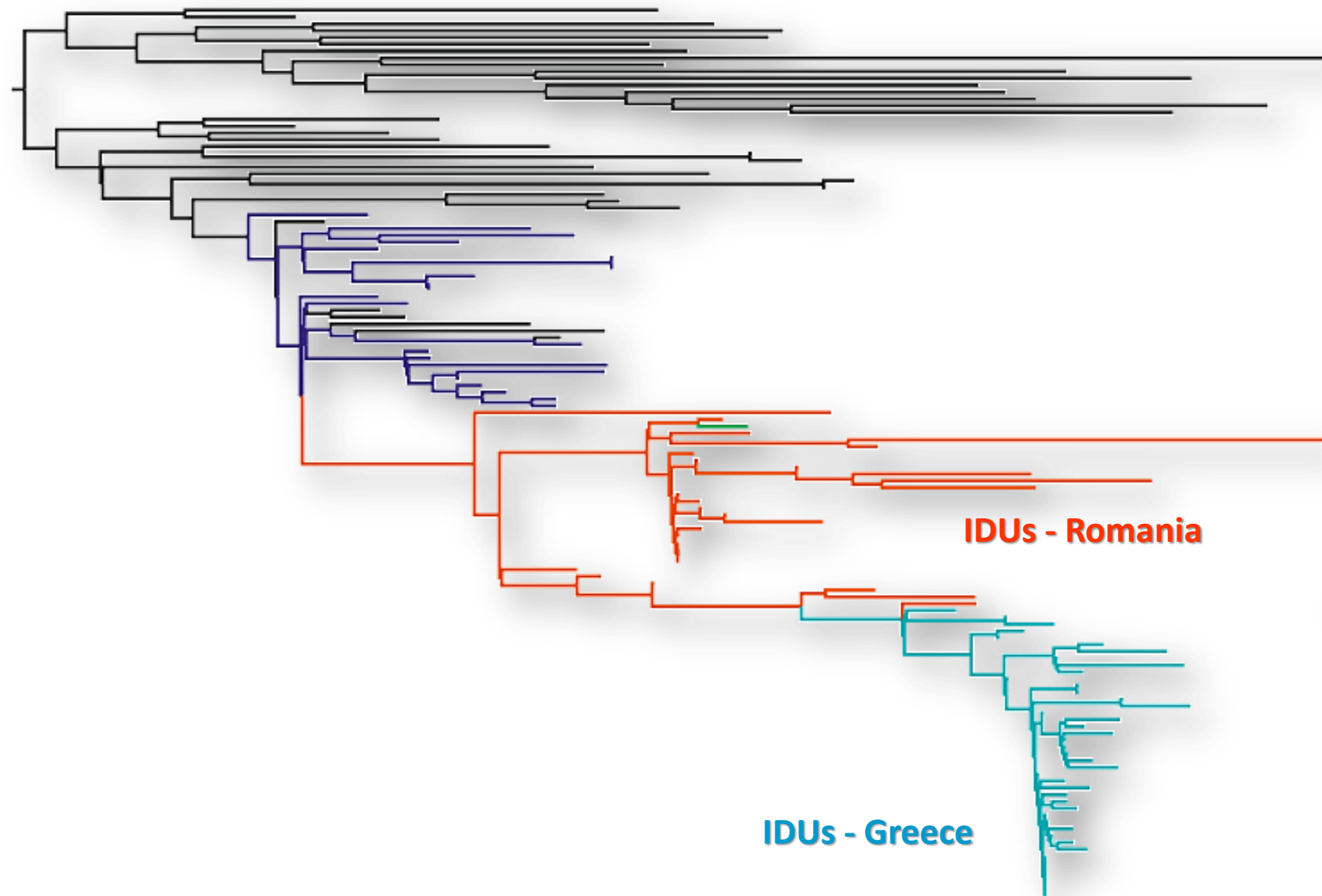
Simona Paraschiv^{1☯*}, Leontina Banica^{1☯}, Ionelia Nicolae¹, Iulia Niculescu^{2,3}, Adrian Abagiu², Raluca Jipa², Andrea-Clemencia Pineda-Peña^{4,5}, Marta Pingarilho⁴, Emil Neaga¹, Kristof Theys⁶, Pieter Libin^{6,7}, Dan Otelea¹, Ana Abecasis^{4,6}

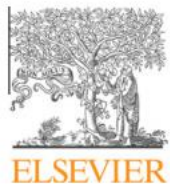


Subtype F



■ IDUs (Greece)
 ■ IDUs (Romania)
 ■ Non-IDUs (Romania)
 ■ Spain





Molecular typing of the recently expanding subtype B HIV-1 epidemic in Romania: Evidence for local spread among MSMs in Bucharest area ☆,☆☆

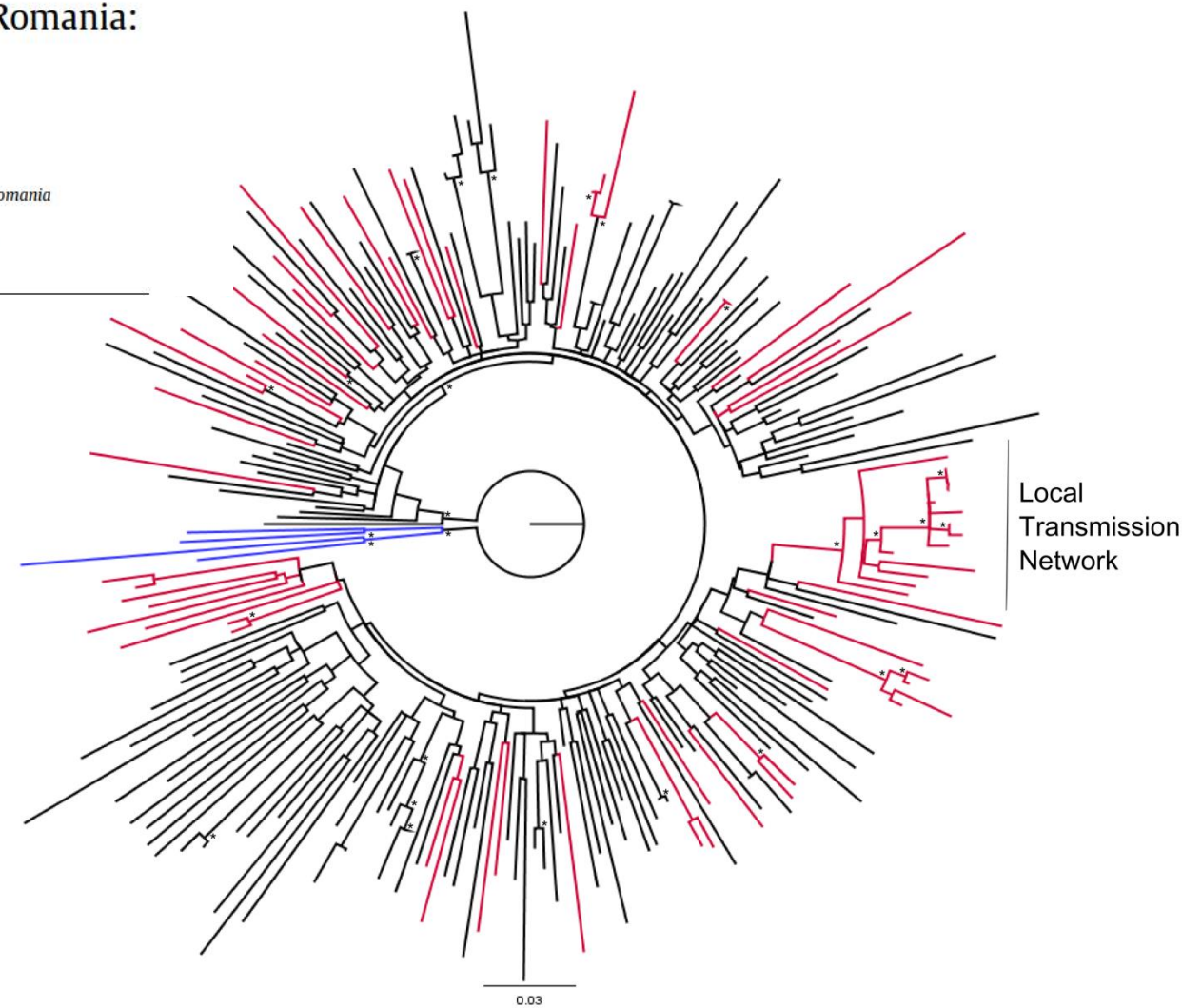
Simona Paraschiv^a, Dan Otelea^{a,*}, Ionelia Batan^a, Cristian Baicus^b, Gkikas Magiorkinis^{c,d}, Dimitrios Paraskevis^c

^a Molecular Diagnostics Laboratory, 'Prof. Dr. Matei Bals' National Institute for Infectious Diseases, Str. Calistrat Grozovici, Nr. 1, Sector 2, 021105 Bucharest, Romania

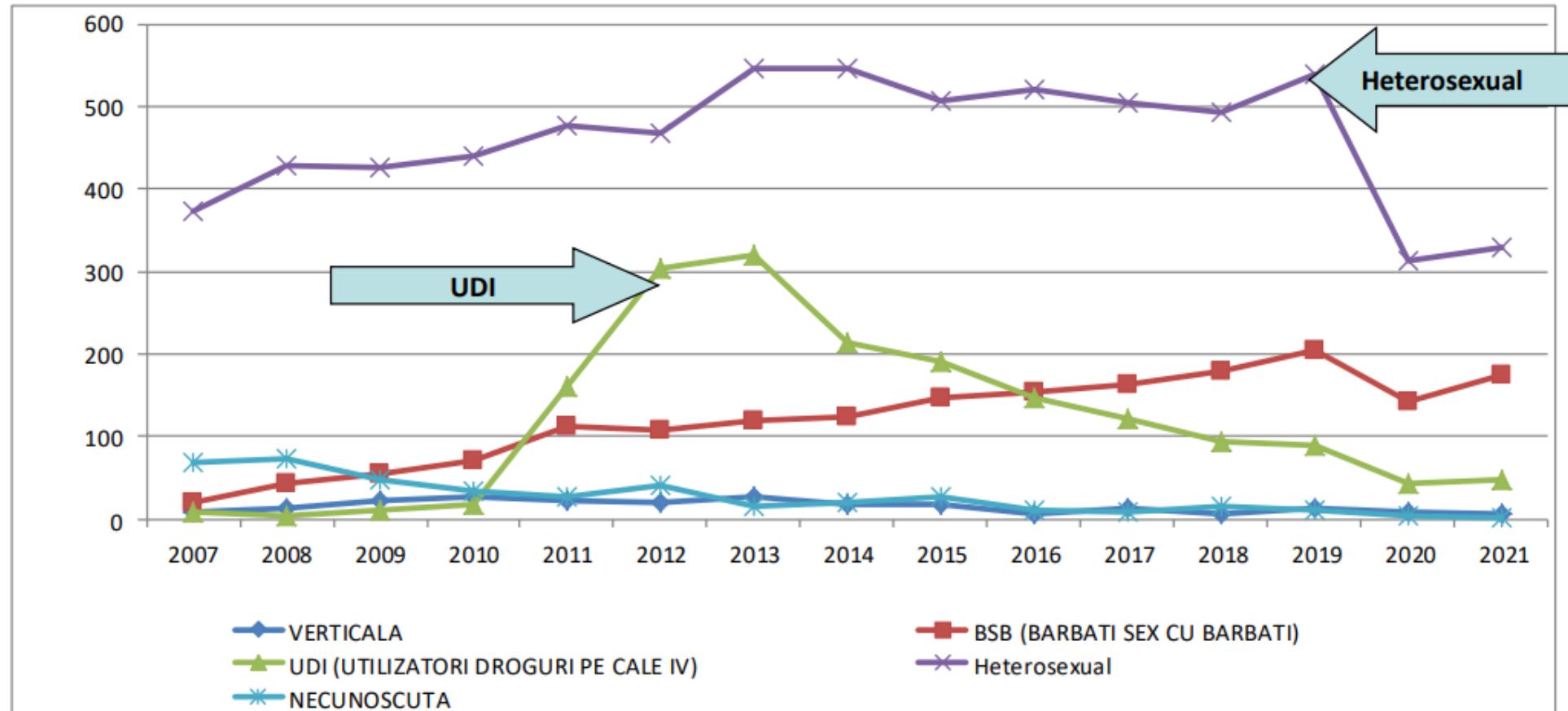
^b Department of Internal Medicine, Colentina Hospital, Bucharest, Romania

^c National Retrovirus Reference Center, Department of Hygiene and Epidemiology, Faculty of Medicine National and Kapodistrian, University of Athens, Greece

^d Department of Zoology, University of Oxford, Oxford, United Kingdom



Tendențele căilor de transmitere a HIV în România 2007-2021



HIV-1 subtype B spread through cross-border clusters in the Balkans: a molecular analysis in view of incidence trends

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Dubravka Salemovic^c, Djordje Jevtovic^c, Ivailo Alexiev^d,
Snjezana Zidovec-Lepej^e, Maja Oroz^e, Josip Begovac^f,
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Dan Otelea^j, Simona Paraschiv^j, Mario Poljak^k, Maja M. Lunar^k
and Maja Stanojevic^a

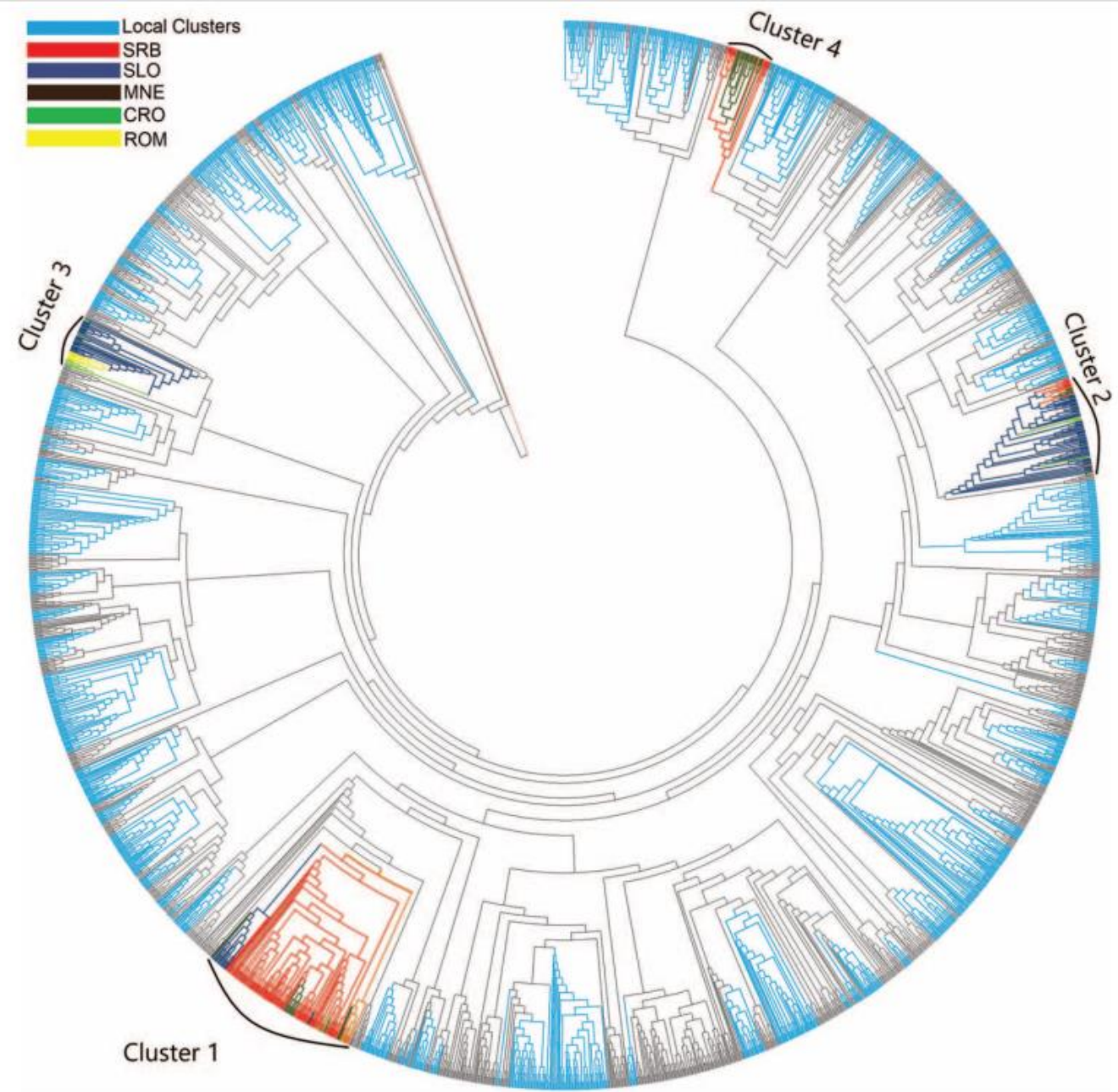


Fig. 1. ML phylogenetic tree of 2,415 subtype B *pol* sequences from the Balkans, from 1999–2019. Local transmission clusters are marked in blue. In cross-border clusters (clusters 1–4), sequences are marked according to country of origin: sequences from Serbia (SRB) in red; Slovenia (SLO) in violet; Montenegro (MNE) in brown; Romania (ROM) in yellow; Croatia (CRO) green.

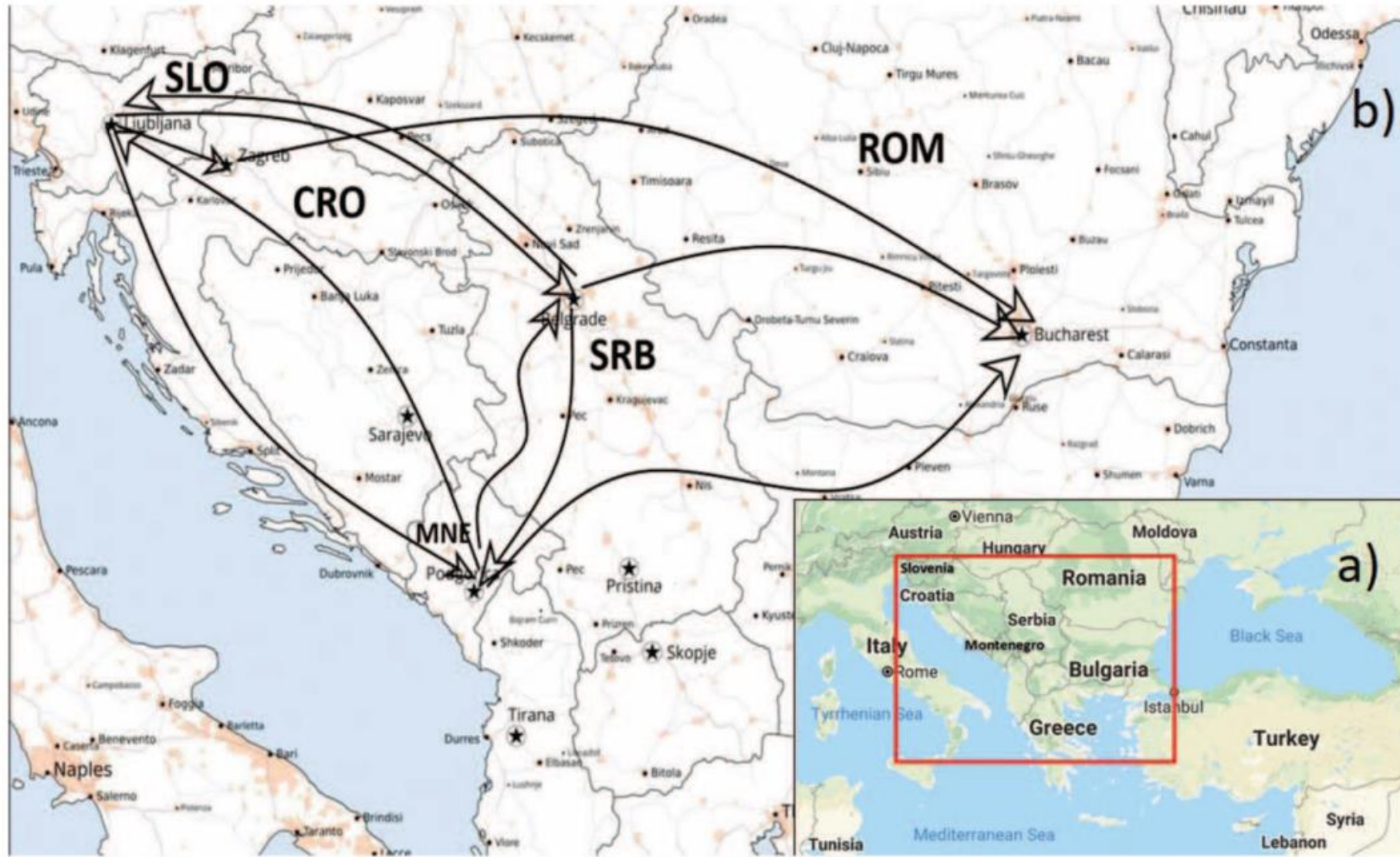
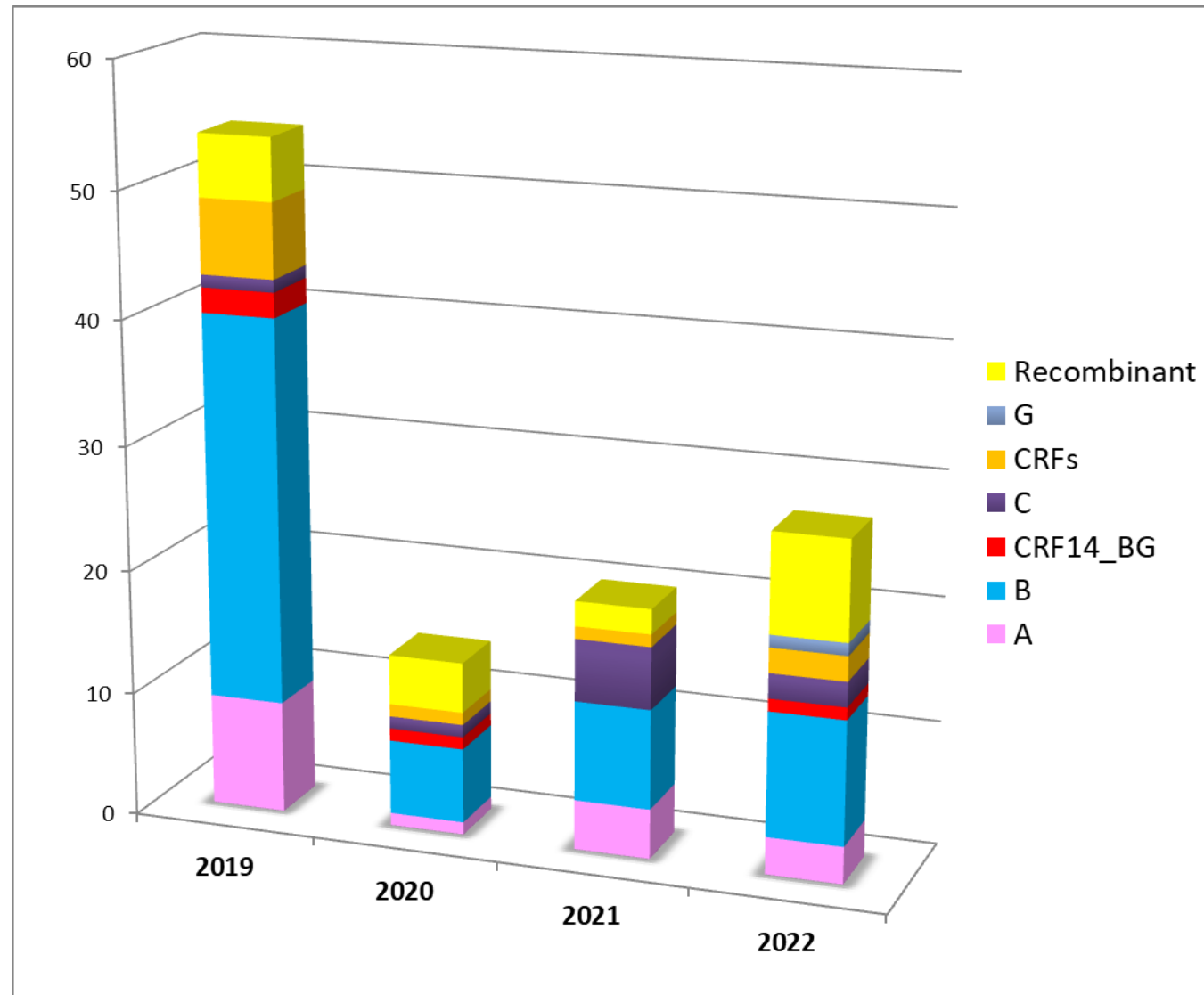


Fig. 3. (a) Map depicting location of Balkan countries in South East Europe; (b) phylogeographic analysis of subtype B dispersal among the countries that participated in cross-border cluster formation: SRB, CRO, SLO, MNE and ROM. Migration patterns supported by Bayes factor greater than 3 and posterior probability greater than 0.9 are shown. Abbreviations of participating Balkan countries: Romania (ROM), Greece (GR), Bulgaria (BLG), Serbia (SRB), Croatia (CRO), Slovenia (SLO), Montenegro (MNE).

Other subtypes than F1- 2019-2022



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