

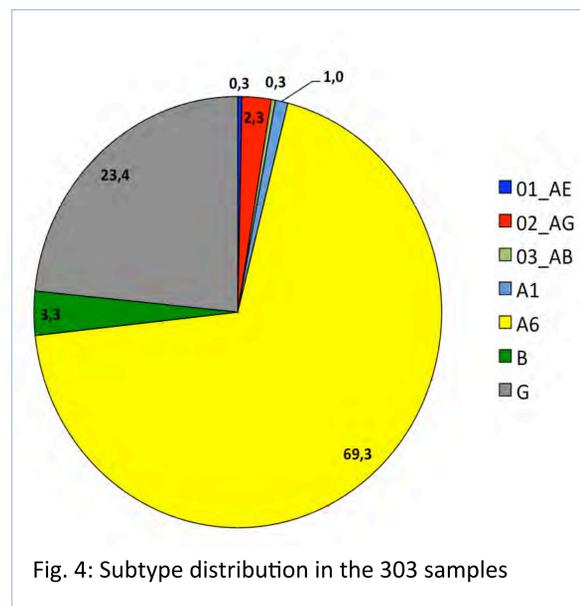
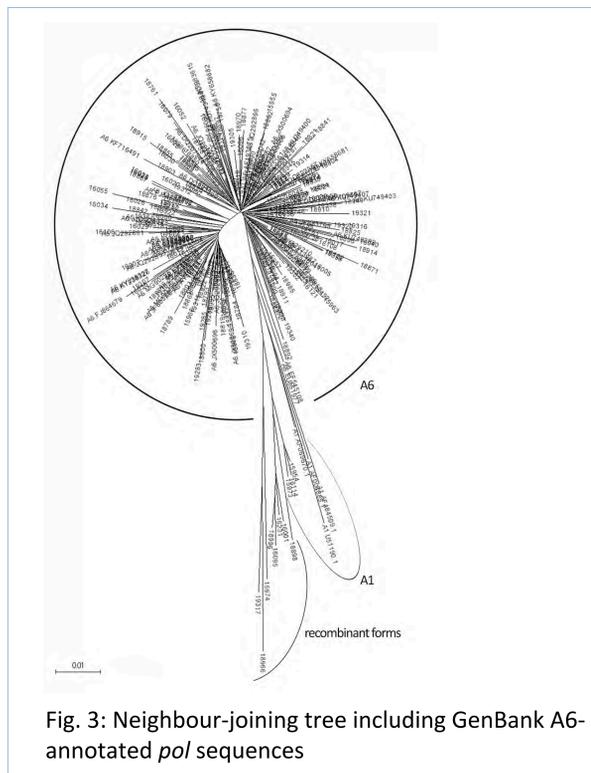
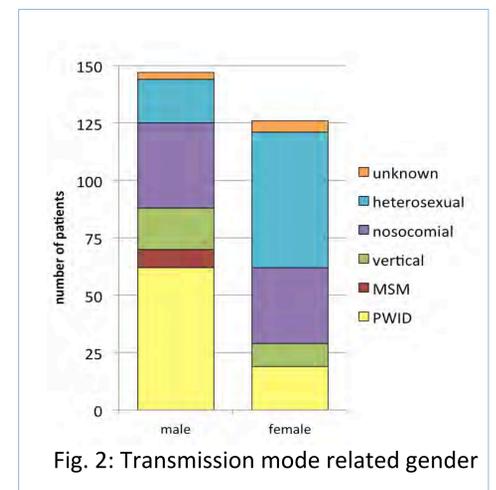
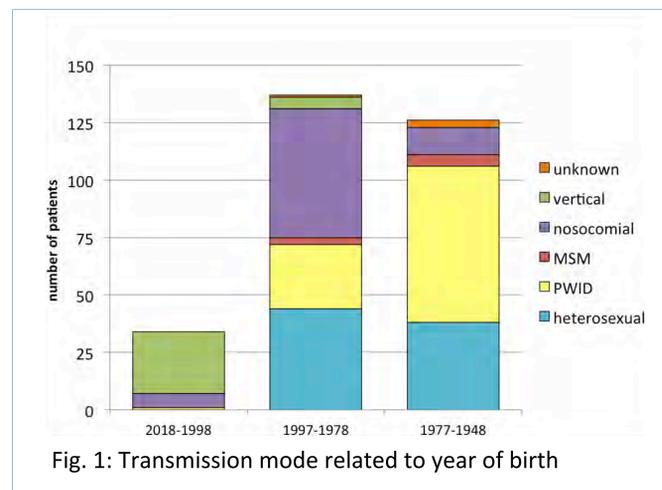
Madita Schlösser¹, Vladimir Kartashev^{2,3}, Visa Mikkola¹, Andrey Shemshura⁴, Dmitry Kolpakov², Alexander Suladze², Tatiana Tverdokhlebova², Sergey Saukhat³, Rolf Kaiser¹, Eva Heger¹, Elena Knops¹, Michael Böhm¹, Katharina Hutt¹, and Saleta Sierra¹

¹Institute of Virology, University of Cologne, 50935 Cologne, Germany; ²Russian Southern Federal Center for HIV Control, Rostov-na-Donu 34400, Russia; ³Rostov State Medical University, Rostov-na-Donu 344022, Russia; ⁴Krasnodar Clinical Center for HIV Control, Krasnodar 350015, Russia

Background: In East Europe and Central Asia HIV-1 infection rate has risen by 57% in 2000-2015, with currently 1.5 million HIV-infected people, whereof 1.16 million live in Russia. Russia shows an HIV-1 landscape with predominant subtype A1/A6 throughout the land and subtype G cohort in the South. Resistance testing at baseline and after failure of ART is not routinely performed. Epidemiology and resistance data are still limited and not accessible through international databases.

Methods: We collected samples and epidemiological data from 328 patients taking care in South Russia to describe epidemiology in this region. Protease-reverse transcriptase (PRRT) and integrase (IN) sequences were used for subtyping, and resistance-associated-mutations (RAMs) and drug susceptibility analysis.

Results: 97 patients (32.0%) were persons who inject drugs (PWID), 82 (27.1%) got infected by heterosexual contacts, 75 (28.4%) corresponded to the nosocomial infection occurred in South Russia at the end of the 80s, 32 (10.6%) were infected vertically, 8 (2.6%) were men having sex with men (MSM), and for 9 (3.0%) the transmission route was not known. Year of birth was known for 297 patients (Fig. 1). 126 (42%) were female, 147 (49%) male and 27 (9%) unknown (Fig. 2).

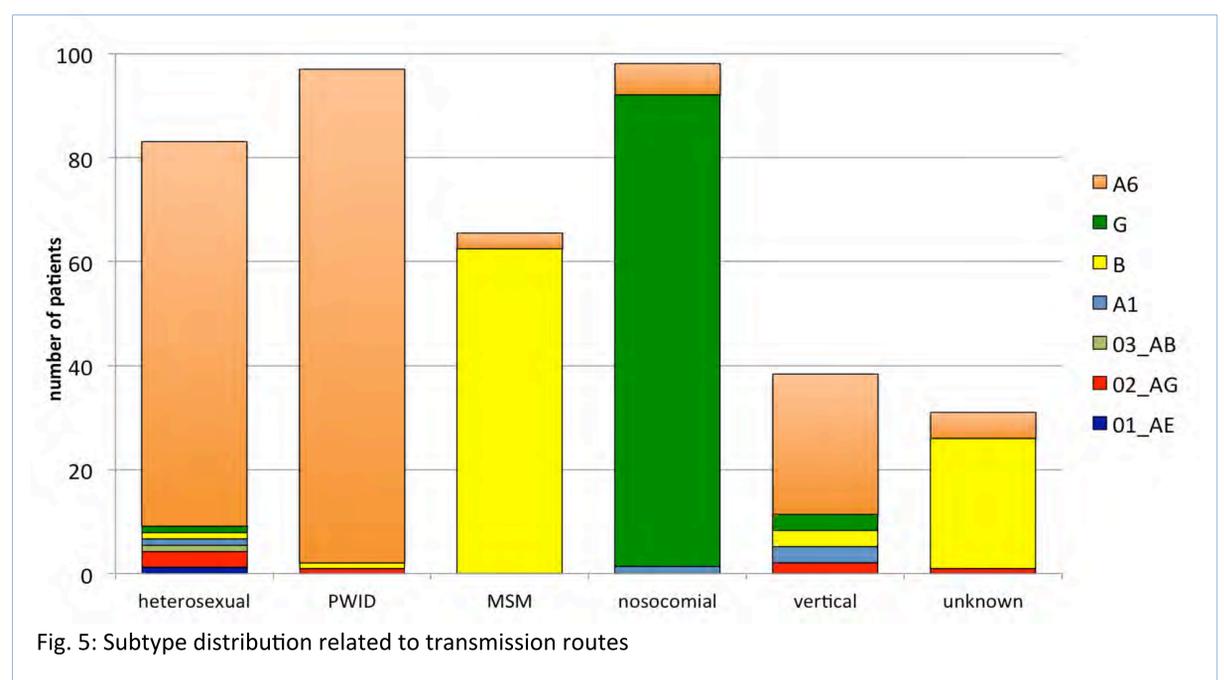


303/328 samples could be amplified. For A6 Subtype detection (A6 is not included in the geno2pheno system and the Stanford HIVdb PROGRAM), all *pol* sequences annotated as A6 in GenBank as well as four A1 reference sequences were retrieved. These sequences were aligned to our samples and a Neighbour-joining tree was generated (Fig. 3). 210 of our samples were classified as A6. The rest of the samples were subtyped using the geno2pheno system and the Stanford HIVdb PROGRAM. The final subtype distribution is showed in Fig. 4.

There were no significant differences in the subtype distribution regarding gender, but significant differences were found in subtype distribution among transmission routes (Fig. 5).

Subtype B correlated with MSM transmission. Subtype G correlated with nosocomial infections and was detected only in patients born before 1991 with only one exception.

261 PRRT, 16 RT and 61 IN sequences were analysed with the Stanford HIVdb PROGRAM tools for RAM detection. 248 PR sequences were obtained, where 228 (91.9%) displayed no major PI-RAMs and 20 (8.1%) showed 1-5 major mutations. Most frequently found RAMs were M46I, I54V and L90M (Table 1). 273 RT sequences could be analysed: 147 (53.8%) displayed no NRTI-RAMs and 126 (46.2%) samples showed 1-7 mutations, with A62V and M184V being the most highly prevalent. 198 RT samples (72.5%) contained no NNRTI mutations and 75 (27.5%) showed 1-5 NNRTI-RAMs; K103N, E138A and G190S were most commonly found.



Conclusions: HIV-1 subtype distribution in Russia is different to West- and Central-Europe, with predominant subtype A1/A6 throughout the land and subtype G cohort in the South. In addition, the proportion of PR sequences displaying major PI-RAMs in our study is similar to that described for West- and Central-Europe therapy-experienced patients, while the prevalence of NRTI- and NNRTI-RAMs is larger in Russia than in Western Europe. Efforts to increase the implementation of routine HIV-1 resistance testing will improve therapy efficacy and Russian epidemiology knowledge.