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).

Fig. 1: Transmission mode related to year of birth
Fig. 2: Transmission mode related gender

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).

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.