O2. Molecular epidemiology of HIV-1 in Iceland

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Background
The molecular epidemiology of HIV-1 in Iceland has not been characterized so far. Detailed analyses of the dynamics of HIV-1 spread can give insight for prevention of virus spread. The objective of the current project was to study the molecular epidemiology of HIV-1 in Iceland.

Methods
Partial HIV-1 pol sequences (1020 bp) were generated from 230 Icelandic samples collected between 1996 and 2013, representing 77% of all HIV-1 infected individuals reported in Iceland between 1985 and 2012. Maximum likelihood phylogenies based on Icelandic and reference sequences were reconstructed for determination of HIV-1 subtype/circulating recombinant form (CRF) and transmission clusters representing domestic spread of HIV-1 in Iceland. Timing and demographic growth patterns were determined by a Bayesian approach in BEAST.

Results
HIV-1 infection in Iceland was dominated by subtype B (63%, n=145) followed by subtypes C (10%, n=23), CRF01_AE (10%, n=22), A1 (7%, n=15) and CRF02_AG (7%, n=15). The majority of the Icelandic subtype B sequences clustered with sequences of Western European, North American and Eastern European origin. Trend analysis showed a significant increase in HIV-1 non-subtype B variants in Iceland over the study period (p=0.004, two-tailed linear-by linear test for association). Overall, 61% of the Icelandic subtype B sequences were part of transmission clusters, with intravenous drug use being the risk group with the highest proportion (92%) of clustering sequences, followed by heterosexuals (74%) and MSM (41%). The time to the most recent common ancestor of the oldest subtype B cluster in Iceland dated back to 1976 (mean estimate, highest posterior density interval: 1971-1980). HIV-1 subtype B has been introduced to Iceland on at least 71 different times, of which 14 of these introductions have led to domestic spread. Three of these 14 Icelandic subtype B transmission clusters were defined as active clusters at the end of the study period. The phylogenetic analysis also showed that HIV-1 non-subtype B have been introduced in Iceland on at least 73 times resulting in five occasions of domestic spread of which three clusters were still being active at study closure. The increase in the incidence of HIV-1 in Iceland among IVDU was revealed to be due to two separate outbreaks. The time to the most recent common ancestor of the first IVDU outbreak was dated to 1999 (mean estimate, highest posterior density interval: 1997-1999) and showed a rapid exponential increase in the number of effective infections between 2008 and 2010 following a lag phase of approximately 9 years. A similar pattern was seen also for the second IVDU cluster that was dated back to 2005 (mean estimate, highest posterior density interval: 2003-2007) and displaying an exponential increase in effective infections between 2010 and 2011 after a lag phase of approximately 5 years.

Conclusions
A variety of HIV-1 subtypes and CRFs were prevalent in Iceland between 1985-2012, with subtype B being the dominant form both in terms of prevalence and domestic spread. Phylodynamic analysis showed that HIV-1 subtype B was introduced in Iceland from multiple geographical locations during

multiple time-points in the 1970s and this pattern subsequently continued. An increase in the number of infections occurred in the beginning of 2000 especially among IVDU which warrants preventive interventions.