

Feline Leukemia Virus (FeLV) sequence analysis and endogenous FeLV quantification in Iberian lynxes (*lynx pardinus*)

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With less than 200 specimens remaining, the Iberian lynx (*lynx pardinus*) is considered the most endangered felid species in the world and is listed as critically endangered by the World Conservation Union. Fourteen of 77 free-ranging lynxes tested during the last four years were positive for Feline Leukemia Virus (FeLV) provirus; 11 of them for FeLV p27 antigen as well. Direct PCR sequencing of the proviral envelope gene from 10 p27-positive animals revealed a common origin and a strong similarity to the FeLV-A 61E strain at DNA level. In addition, FeLV subtypes -B and -C were not detectable in any of the animals. The absence of FeLV-B, a recombinant between FeLV-A and endogenous FeLV (enFeLV) which is present in about 1/3 of FeLV-positive healthy cats, pushed us to determine the enFeLV loads in Iberian lynxes. Surprisingly, while in domestic and wild cats the amount of enFeLV sequences ranges from 1 to 100 copies/cell, only 5 of the 77 lynxes were positive for enFeLV by real-time PCR and this was limited to far less than one copy/cell, most probably because of the presence of slightly cross-reactive sequences. Thus, absence of recombinant FeLV type B proviruses may be due to absence of type I and II enFeLVs. Data available on the time frame (6 of the 14 FeLV positive lynxes died in 2007 and were positive for both FeLV provirus and p27), co-infections and outcome of the FeLV-infection suggest that the FeLV involved is of high virulence to Iberian lynxes. If this is a result from the combination of factors like the genetic background and an aggressive FeLV variant or due to one of these factors alone is still to be elucidated.