**The history of livestock trade in relation to the emergence of SRLVs**

We tried to find the ancient ancestors. That part of the project didn’t pan out exactly as we had hoped. The fact is that majority of circulating strains in Lebanon are similar to those found globally, though there is some evidence of higher diversity in the background. This doesn’t contradict the theory that the divergent SRLV subtypes found in remnant sheep reflect an ancient dispersal with early agriculture but doesn’t confirm it either.

The global livestock trade has strengthened connections between geograpohically distant regions and this allowed certain strains to predominate. If ancient strains of SRLV that are indigenous to

Similarly, the introduction of vaccines for small ruminant diseases, particularly some of the experimental vaccines trialed in the early 20th century (49), could potentially have facilitated spread and emergence of SRLVs.

Viruses that cause chronic, persistent infections have circulated in animals for millions of years (1, 2). However, many human pathogens are known to have emerged within the far shorter timeframe of recorded history. This reflects the role of human activities – particularly the development of efficient global transport networks - in enabling viral emergence (3). In the case of blood-borne viruses such as human immunodeficiency virus type 1 (HIV-1) and hepatitis C virus (HCV), other anthropogenic factors (e.g. iatrogenic transmission associated with unsafe injections) are also proposed to have played an important role (3-6). The same or similar combinations of anthropogenic factors are likely to have impacted the emergence of blood-borne viral infections in domestic species as well, but this has not been explored in equivalent depth.

Domestic sheep and goats have occupied an important place in human culture for thousands of years (21, 22). Thus, disease ecology in these species has been directly impacted by human activities, and the emergence of SRLVs in sheep and goats can be examined in the context of this relatively well-documented history.

Spread of B1 from a Swiss epicenter could have been preceded by the introduction of novel SRLV diversity into the Swiss small ruminant population during the early 20th century. The fact that B1 is predominantly associated with goats, whereas the most closely related subtype (B2) has primarily been isolated from sheep, suggests a possible role for sheep to goat transmission in its emergence. The burgeoning interest in exotic sheep breeds during this period (exemplified by the introduction of Karakul to Switzerland (37)), likely brought many region-specific breeds of small ruminant into contact for the first time. Potentially, this may have introduced viruses from small ruminant populations in elsewhere in Europe (e.g. in the regions where B2 and B3 genotypes are also found) into Swiss small ruminant populations.

*Karakul sheep and the emergence of pandemic SRLV-A*

SRLV-A can confidently be stated to have been present in Europe since at least 1933, because the Icelandic epidemic from which the prototypic SRLV-A strain was derived was definitively traced to an importation of Karakul sheep in this year (11). Karakul are ‘fat-tailed’ sheep, and are among the oldest domesticated sheep breeds (21, 33). The breed is native to Central Asia, and arrived in Iceland via the Institute for Animal Breeding, in Halle, Germany. Karakul sheep were originally exported to Halle from Bukhara in Uzbekistan in 1903 (34). Interest in Karakul at the time was not restricted to Germany – a Karakul herd to the United States in the same decade (35), facilitated by the personal intervention of President Theodore Roosevelt.

In Germany, interest in Karakul focused on assessing their suitability for rearing in arid regions of Africa that were at that time German colonies (34). The breed was introduced to the South West Africa (SWA) (present day Namibia) by German colonists, and quickly spread as it became the basis of a profitable pelt industry (36). In subsequent years, German Karakul were also introduced to several European countries, including Switzerland (37), Italy (34), and Greece (38). From Mussolini’s Italy, Karakul were further exported to the Italian colonies in East Africa (34). During the 1940s the Halle flock were transported East as they were incorporated into German plans for settlement of Poland and Ukraine (34, 39).

*Swiss dairy goats and the emergence of pandemic SRLV-B*

In addition, global spread of SRLV-B1 is conspicuously associated with Swiss dairy goat breeds in general, and the Saanen breed in particular (**Table S2**). Many of the first reported outbreaks of SRLV infection in goats involved this popular breed, which was first exported from Switzerland in the late 19th century, and has subsequently been introduced to many countries throughout the world (45). However, given that (i) SRLV infection is known to cause disease in Saanen and other Swiss dairy goat breeds, and; (ii) these breeds have been exported from Switzerland since the late 19th century, but neither epidemiological; genetic evidence support the virus having spread this early (45), It seems unlikely that Swiss dairy goats are the ancestral hosts of SRLV-B1.

called Jord1 (**Figure 1d**). The Jord1 genome was similar in structure to previously characterized SRLVs. The putative Gag protein contained YPXL and PS/TAP late domain motifs that are conserved across all SRLV genotypes, as well as an additional YPXL domain found in genotypes A and E only. Putative accessory protein genes found in other SRLVs were also identified: a Rev protein encoding an arginine rich putative nuclear export signal, and a Vif protein encoding an elongin BC-binding region (28, 29). A lysine-specific tRNA primer-binding was identified between the 5’ LTR and *gag* gene.

We therefore tentatively named the lineage represented by Jord1 ‘SRLV-F’. These results indicate that all currently circulating SRLV genotypes are to some extent mosaics of one another. If the SRLV-C and E strains reflect ancient variants, as their distribution suggests, then the interconnected, recombinant ancestry of these SRLV genotypes with other genotypes would imply the existence of parental strains that co-circulated during the early dissemination of Neolithic agro-pastoralism (16, 30).

Importantly, none of the above-mentioned diseases have ever been described as occurring in the Karakul breed itself. Current evidence indicates that Lentiviruses, including some SRLVs (40), are relatively apathogenic in populations with which they have longer-term associations (41). This would account for the failure to detect disease during quarantine of Karakul exported from Halle to Iceland subsequently in the German Karakul flock (42, 43). A delay in the emergence of disease following introduction of virus via Karakul (**Figure 4**) is consistent with the requirement for transmission to susceptible breeds, and the slow course of disease associated with SRLV infection.

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