

Description of a new clade within subtype 1 of Betaarterivirus suid 1 (PRRSV1) causing severe outbreaks in Spain

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During the first half of 2020, a series of unusually virulent PRRS outbreaks were reported in north-eastern Catalonia, close to the Spanish-French border (Baliellás 2022). According to the reports from swine veterinarians the outbreaks were characterized by: i) high abortion rates sustained for several weeks (up to 50%), even in vaccinated herds, ii) cases of sow mortality (up to 15% of the stock present in some farms), and iii) high mortality in suckling piglets and in nurseries (20-50%). Additionally, the performance of pigs surviving in the nurseries seemed to be seriously affected, with poor growth for several weeks. Incidental reports suggested that affected piglets had severe lymphopenia. The analysis performed indicated that the virus produced an intense viremia (Ct values below 15 for some weeks) and nasal shedding was very high and sustained (4-5 weeks).

Two years later, the virus has spread to neighboring areas (Baliellás, 2022). Some reports from the field suggest that the severity of the cases is attenuating, although this point is difficult to confirm without a large-scale case study.

Recently, the analyses carried out in our laboratory identified the strain responsible as a mosaic isolate, with a backbone related to a highly virulent strain previously reported in Italy (Canelli et al. 2017). However, the current strain has incorporated segments of other PRRSV1 by recombination. Moreover, the strain has undergone an extreme diversification in the last two years, generating a whole new clade within PRRSV1 (Fig.1, Martín-Valls et al. 2022).

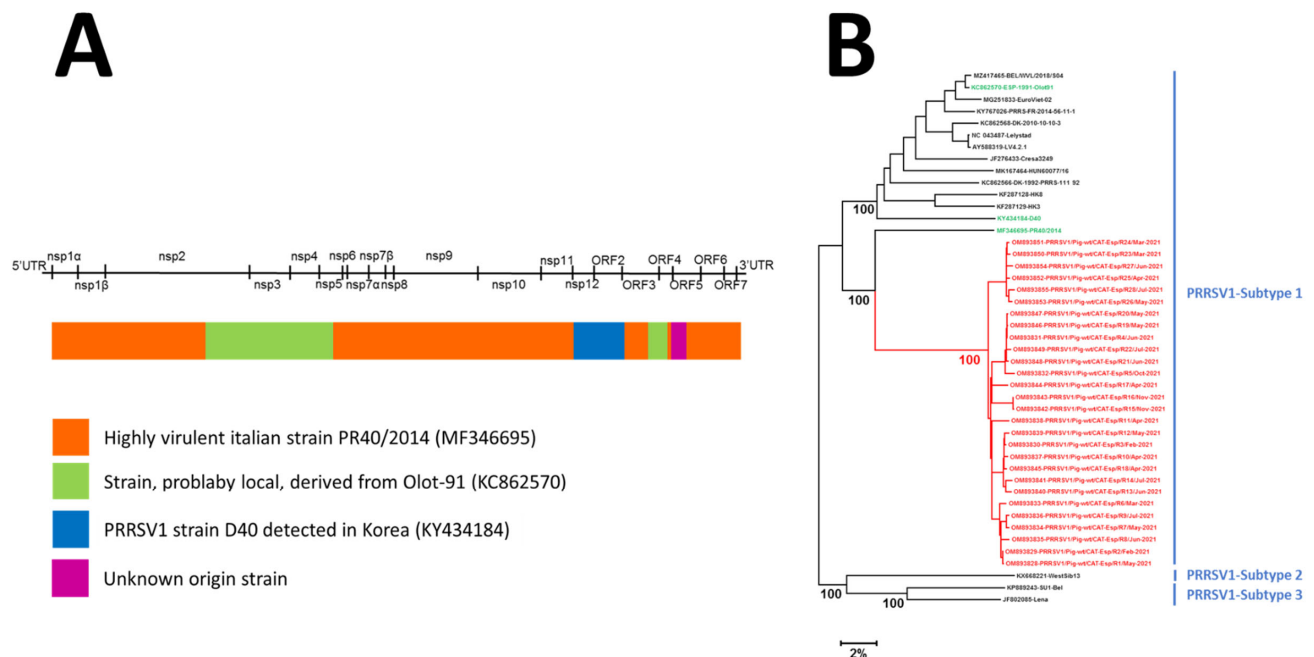


Figure 1. A, recombinant pattern in the new PRRSV1 clade described, including the segments associated to every parental strain; **B**, Maximum Likelihood phylogenetic tree build up using the whole genome and the general-time-reversible model. The confidence of the main internal branches, based on 100 bootstrap replicates, was indicated. In blue, three PRRSV1 subtypes are marked, the recombinant clade described in this report is highlighted in red and the three parental strains identified are colored in green.

References

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