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## Genetic and pathogenic characterization of a Russian subtype 2 PRRSV-1 isolate

Anton G. Yuzhakov<sup>a†\*</sup>, Sergei A. Raev<sup>a\*</sup>, Andrei N. Skrylev<sup>b</sup>, Alexander M. Mishin<sup>a</sup>, Tatiana V. Grebennikova<sup>a</sup>, Oleg A. Verkhovsky<sup>a</sup>, Alexei D. Zaberezhny<sup>c</sup>, Ivan Trus<sup>d</sup>, Hans J. Nauwynck<sup>d</sup>, Taras I. Aliper<sup>c</sup>

<sup>a</sup>Laboratory of Virology, Diagnostics and Prevention Research Institute for Human and Animal Diseases, Moscow, Russia

<sup>b</sup>Siberian Agrarian Group, Tomsk, Russia

<sup>c</sup>All-Russian Research Institute of Experimental Veterinary Medicine named Ya. R. Kovalenko, Moscow, Russia

<sup>d</sup>Laboratory of Virology, Faculty of Veterinary Medicine, Ghent University, Merelbeke, Belgium

\*These authors contributed equally to this work

†Corresponding author

Email addresses:

AGY: anton\_oskol@mail.ru, +7 926 100 66 56

SAR: raevsergey@mail.ru

ANS: shan.70@yandex.ru

AMM: doktor-mishin@mail.ru

TVG: t\_grebennikova@mail.ru

OAV: info@dpri.ru

ADZ: zaberezhny@mail.ru

IT: ivan.trus@ugent.be

HJN: hans.nauwynck@ugent.be

TIA: aliper@narvac.com

### Highlights

- The full genome sequence of the subtype 2 PRRSV-1 WestSib13 strain is determined
- Demonstrated significant difference in pathogenicity between subtype 1 and 2 strains of European PRRSV
- Demonstrated the unusual virological and clinical outcome (high level viremia without fever) of the novel WestSib13 strain

## Abstract

Porcine reproductive and respiratory syndrome virus (PRRSV) causes reproductive failure and respiratory problems. Data about the virulence and pathogenicity of subtype 2 PRRSV-1 strains are limited. The main purposes of this investigation were to characterize the full genome sequence of the subtype 2 PRRSV-1 WestSib13 strain and to compare the pathogenicity with that of the subtype 1 PRRSV-1 Lelystad strain. Comparison of the whole genome sequence of the WestSib13 strain with that of PRRSV-1 prototype strains revealed a 76.2% (subtype 1 Lelystad virus) and 79.0% (subtype 3 Lena virus) identity, respectively

The virulence and pathogenicity of the European subtype 2 PRRSV strain WestSib13 and the European subtype 1 PRRSV strain Lelystad were compared in 3-week-old piglets upon inoculation of  $10^{5.4}$  TCID<sub>50</sub> of virus. Non-infected animals (control group) as well as animals infected with the Lelystad strain were clinically healthy until 14 days post challenge. In contrast, animals infected with the WestSib13 strain demonstrated dyspnea starting from the 3 day post-inoculation (dpi). All piglets in this group died between 5 to 8 dpi. During that period, fever was not observed in