Coding-Complete Genome Sequence of an African Swine Fever Virus Strain Liv13/33 Isolate from Experimental Transmission between Pigs and Ornithodoros moubata Ticks

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libraries. The libraries for sequencing were prepared using the Ion Xpress plus fragment library kit and Ion Xpress barcode adapters 1-96 kit (Thermo Fisher Scientific). Magnetic beads from the Agencourt AMPure XP kit (Beckman Coulter, Villepinte, France) were used for DNA purification steps. The resulting reads were cleaned with Trimmomatic version 0.36 (options: ILLUMINACLIP: oligos.fasta: 2:30:5:1: true; LEADING: 3; TRAILING: 3; MAXINFO: 40:0.2; MINLEN: 36) and were first de novo assembled using the SPAdes version 3.10.0 (option: – careful -t 12 -m 50) and MIRA version 4.0.2 (option: IONTOR_SETTINGS -ASSEMBLY:mrpc/1/H11005 100) programs. In parallel, reads were mapped on three reference ASFV genomes of genotype I (BA71 [GenBank accession no.KP055815], Mkuzi 1979 [AY261362], and Benin97/1 [AM712239]) using Burrows-Wheeler Aligner software version 0.7.15-r1140 (option: mem -M). For each library, contigs produced by the different methods were scaffolded to generate a single consensus sequence validated by an additional BWA alignment.

De novo assemblers and alignment software could not deal with inverted terminal repeats (ITRs) present in the ASFV genomes (7); the obtained sequence was thus probably shorter than that in reality. A comparison of the 11 genomes obtained showed fewer than 7 nucleotide differences that were mainly in ITRs and up to 34 gaps located in mononucleotide repeats A or T (Table 1). The coding-complete genome sequence of Liv13/33 with the best coverage (72.09X) was isolated from tick OmLF2 (Table 1). This sequence of 188,277 bp (G+C content of 38.4%) harbored 228 open reading frames (ORFs) annotated with the help of Prokka (Galaxy version 1.13) based on the annotations of genomes available on the African Swine Fever Virus Database (http://asfvdb.popgenetics.net/), which proposed the most complete and homogeneous revised annotation (8).

Data availability. The coding-complete genome sequence of isolate OmLF2 has been deposited in GenBank under the accession no. MN913970. Raw data from the 11 isolates for this project can be found in the GenBank SRA under accession no. PRJNA587575.

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| Isolate | Host | Total no. of produced reads | Total no. of mapped reads | Mean coverage on reference sequence OmLF2 | No. of nucleotide differences/gaps compared to reference sequence OmLF2 | BiSample accession no. | SRA accession no. |
|---------|------|----------------------------|--------------------------|----------------------------------------|---------------------------------------------------------------------|------------------------|------------------|
| 6517IM  | SPF pig inoculated by the intramuscular route | 7,629,638 | 26,960 | 18.70 | 2/17 | SAMN13195023 | SRS6053714 |
| 6524IM  | SPF pig inoculated by the intramuscular route | 8,281,778 | 23,558 | 14.67 | 1/5 | SAMN13195024 | SRS6053715 |
| 6540IM  | SPF pig inoculated by the intramuscular route | 11,118,211 | 47,712 | 32.69 | 0/6 | SAMN13195025 | SRS6053707 |
| OmlF1   | Infected O. moubata tick | 8,013,796 | 33,325 | 19.54 | 6/30 | SAMN13191038 | SRS6053706 |
| OmlF2   | Infected O. moubata tick | 13,675,689 | 129,761 | 72.16 | Reference | SAMN13191036 | SRS6053705 |
| OmlF3   | Infected O. moubata tick | 5,526,024 | 27,692 | 16.83 | 7/34 | SAMN13191040 | SRS6053708 |
| OmlM1   | Infected O. moubata tick | 7,096,453 | 29,221 | 18.93 | 2/5 | SAMN13191039 | SRS6053709 |
| OmlM2   | Infected O. moubata tick | 3,742,020 | 33,372 | 21.39 | 0/8 | SAMN13191042 | SRS6053710 |
| 6573T   | SPF pig infected by ticks | 12,708,781 | 26,414 | 17.14 | 1/10 | SAMN13194022 | SRS6053712 |
| 6594T   | SPF pig infected by ticks | 7,616,042 | 25,491 | 17.81 | 0/10 | SAMN13195022 | SRS6053713 |
| 693T    | SPF pig infected by ticks | 9,392,643 | 29,607 | 21.65 | 3/9 | SAMN13191126 | SRS6053711 |

*The mean coverage corresponds to the mean number of reads mapped on the sequence of reference by position.

*GenBank accession no. MN913970.
REFERENCES

1. Quembo CJ, Jori F, Vosloo W, Heath L. 2018. Genetic characterization of African swine fever virus isolates from soft ticks at the wildlife/domestic interface in Mozambique and identification of a novel genotype. Trans-bound Emerg Dis 65:420–431. https://doi.org/10.1111/tbed.12700.

2. Dixon LK, Wilkinson PJ. 1988. Genetic diversity of African swine fever virus isolates from soft ticks (Ornithodoros moubata) inhabiting warthog burrows in Zambia. J Gen Virol 69:2981–2993. https://doi.org/10.1099/0022-1317-69-12-2981.

3. Wilkinson PJ, Pegram RG, Perry BD, Lemche J, Schels HF. 1988. The distribution of African swine fever virus isolated from Ornithodoros moubata in Zambia. Epidemiol Infect 101:547–564. https://doi.org/10.1017/S09502688000029423.

4. Lubisi BA, Bastos ADS, Dwarka RM, Vosloo W. 2005. Molecular epidemiology of African swine fever in East Africa. Arch Virol 150:2439–2452. https://doi.org/10.1007/s00705-005-0602-1.

5. Simulundu E, Lubaba CH, Van Heerden J, Kajihara M, Matala L, Chambaro HM, Sinkala Y, Munjita SM, Munang’andu HM, Nalubamba KS, Samui K, Pandey GS, Takada A, Mweene AS. 2017. The epidemiology of African swine fever in “nonendemic” regions of Zambia (1989–2015): implications for disease prevention and control. Viruses 9:236. https://doi.org/10.3390/v9090236.

6. Pereira de Oliveira R, Hutet E, Paboeuf F, Duhayon M, Boinas F, Perez de Leon A, Filatov S, Vial L, Le Potier MF. 2019. Comparative vector competence of the Afrotropical soft tick Ornithodoros moubata and Palearctic species, O. erraticus and O. verrucosus, for African swine fever virus strains circulating in Eurasia. PLoS One 14:e0225657. https://doi.org/10.1371/journal.pone.0225657.

7. Dixon LK, Chapman DA, Netherton CL, Upton C. 2013. African swine fever virus replication and genomics. Virus Res 173:3–14. https://doi.org/10.1016/j.virusres.2012.10.020.

8. Zhu Z, Meng G. 2019. ASFVdb: an integrative resource for genomics and proteomics analyses of African swine fever. bioRxiv https://doi.org/10.1101/670109.