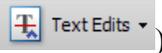
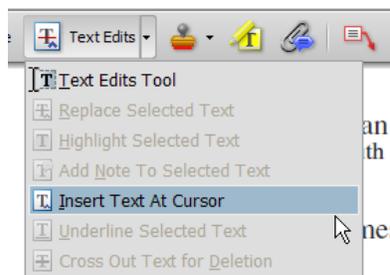


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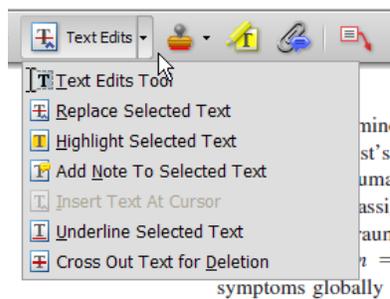
To facilitate electronic transmittal of corrections, we encourage authors to utilize the comments and notes features in Adobe Acrobat. The PDF provided has been “comment-enabled,” which allows you to utilize the comments and notes features, even if using only the free Adobe Acrobat reader (see note below regarding acceptable versions). Adobe Acrobat’s Help menu provides additional details on the tool. When you open your PDF, the comments/notes/edit tools are clearly shown on the tool bar (though icons may differ slightly among versions from what is shown below).

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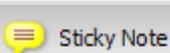
- Use the **Text Edits tool** () to insert, replace, or delete text.
 - To **insert text**, place your cursor at a point in text and select “Insert Text at Cursor” from the text edits menu. Type your additional text in the pop-up box.



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- To **delete text**, highlight the text to be deleted and select “Cross Out Text for Deletion” from the text edits menu (see graphic above).

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- Use the **Callout tool** () to point directly to changes that need to be made. Try to put the callout box in an area of white space so that you do not obscure the text, as in the example below.

Table 5
Experiment 4: Comparative Optimism as a Function of Self-Presentation and Event Valence

	Event					
	Positive		Negative		Total	
Self-presentation	<i>M</i>	<i>SD</i>	<i>M</i>	<i>SD</i>	<i>M</i>	<i>SD</i>
Public/student	3.46	0.13	3.60	0.10	3.53	0.12
Public/expert	2.66	0.12	2.78	0.13	2.73	0.13
Control	2.39	0.11	2.46	0.09	2.43	0.11
Total	2.84	0.47	2.95	0.50		

The first column's entries should be flush left (except for "Total", which should be indented one em-space), as in Tables 1 and 2 previously.

- Use the **Highlight tool** () to indicate font problems, bad breaks, and other textual inconsistencies. Describe the inconsistencies with the callout tool (shown) or a sticky note. One callout (or sticky note) can describe many changes.

$$du/dt = -\lambda v^\alpha = -\lambda u$$

$$du/u = -\lambda dt$$

$$u_t = ue^{-\lambda t}$$

Close up minus sign to lambda (3 times, highlighted)

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Complete Genome Sequence of the Goatpox Virus Strain Gorgan, Isolated from a Commercial Live-Attenuated Vaccine

AQ: au Elisabeth Mathijs,^a Frank Vandebussche,^a Andy Haegeman,^b Ahmad Al-Majali,^{c,d} Kris De Clercq,^b Steven Van Borm^a

AQ: aff Molecular Platform, Veterinary and Agrochemical Research Centre, Ukkel, Belgium^a; Viral Diseases, Vesicular and Exotic Diseases, Veterinary and Agrochemical Research Center, Ukkel, Belgium^b; Jordan Bio-Industries Centre (JOVAC), Amman, Jordan^c; Faculty of Veterinary Medicine, Jordan University of Science and Technology, Irbid, Jordan^d

AQ: A This is a report of the complete genome sequence of the goatpox virus strain Gorgan, which was isolated from a commercial live-attenuated vaccine (Caprivac, Jordan Bio-Industries Centre).

Received 19 August 2016 Accepted 20 August 2016 Published XXX

Citation Mathijs E, Vandebussche F, Haegeman A, Al-Majali A, De Clercq K, Van Borm S. 2016. Complete genome sequence of the goatpox virus strain Gorgan, isolated from a commercial live-attenuated vaccine. *Genome Announc* 4(5):e01113-16. doi:10.1128/genomeA.01113-16.

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AQ: B Capripox disease is an economically important disease in small domestic ruminants that is caused by goatpox virus (GTPV) and sheeppox virus (SPPV), which belong to the *Poxviridae* family, *Capripoxvirus* genus. The disease is present in central and north Africa, the Middle East, and various parts of Asia, with occasional incursions in southern Europe. Vaccination plays a key role in controlling the spread of the disease and is mainly based upon the use of live-attenuated vaccines. The genomic characterization of the virus strains that compose these vaccines, along with *in vivo* experimentations, will give insight into the mechanism of attenuation for vaccine strains and will improve our understanding of vaccination failure observed in the field (1). Here, we report the complete genome sequence of the GTPV strain Gorgan, isolated from a commercial live-attenuated vaccine (Caprivac, Jordan Bio-Industries Centre).

AQ: C

DNA was purified from a freeze-dried vaccine pellet dissolved in 3 ml of phosphate-buffered saline using the Puregene Core Kit A (Qiagen) according to the manufacturer's instructions. Pre-sequencing enrichment was performed through an in-house long-range PCR methodology covering the entire genome with overlapping ~5.5-kb amplicons. All amplicons were pooled in an equimolar manner. P6-C4 sequencing was performed on 1 single-molecule real-time (SMRT) cell on a PacBio RSII sequencer (Pacific Biosciences) at the Genomics Core UZ Leuven (Leuven, Belgium).

Consensus amplicon sequences were obtained from the reads using the LAA protocol (default parameters; Pacific Biosciences) in SMRT Portal version 2.3.0 (Pacific Biosciences). The amplicons were further assembled using iAssembler software version 1.3.2 (2). Discrepancies with previously published GTPV genomes were confirmed by Sanger sequencing. The protein-coding genes were predicted by NCBI's ORF-Finder (<http://www.ncbi.nlm.nih.gov/orffinder>) and by GATU relative to GTPV Pellor reference sequence NC_003027 (3).

Consensus amplicon sequences were assembled into a single double-stranded, linear DNA sequence of 148,146 bp, with an average G+C content of 25.33%. The GTPV strain Gorgan iso-

lated from the Caprivac vaccine contains a 143,732-bp central coding region flanked by two identical terminal-inverted repeats of 2,144 bp. In comparison with GTPV strain Pellor, the Gorgan strain genome is characterized by 2 single-nucleotide substitutions (N/D in GTPV_gp34 and N/D in GTPV_gp63) and a large deletion of 1,593 bp disrupting two putative genes (GTPV_gp137 and GTPV_gp138).

Accession number(s). The complete genome sequence of GTPV strain Gorgan (Caprivac vaccine) has been deposited in GenBank under the accession number [KX576657](https://ncbi.nlm.nih.gov/nucl/KX576657).

ACKNOWLEDGMENTS

We thank Maria Vastag and Orkun Ozhelvaci for their technical assistance. We thank the Jordan Bio-Industries Centre for providing the Caprivac vaccine sample.

The research that yielded these results was funded by the Bill and Melinda Gates Foundation (grant agreement; investment ID OPP1126866), the European Union FP7 project RAPIDIA-FIELD (grant number FP7-289364), the Belgian Federal Public Service of Health, Food Chain Safety and Environment through the contract "RT 15/3 LUMPY SKIN 1" and the Veterinary and Agrochemical Research Centre (CODA-CERVA), Ukkel, Belgium.

FUNDING INFORMATION

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