African Horse Sickness Caused by Genome Reassortment and Reversion to Virulence of Live, Attenuated Vaccine Viruses, South Africa, 2004–2014

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African horse sickness (AHS) is a hemorrhagic viral fever of horses. It is the only equine disease for which the World Organization for Animal Health has introduced specific guidelines for member countries seeking official recognition of disease-free status. Since 1997, South Africa has maintained an AHS controlled area; however, sporadic outbreaks of AHS have occurred in this area. We compared the whole genome sequences of 39 AHS viruses (AHSVs) from field AHS cases to determine the source of 3 such outbreaks. Our analysis confirmed that individual outbreaks were caused by virulent revertants of AHSV type 1 live, attenuated vaccine (LAV) and reassortants with genome segments derived from AHSV types 1, 3, and 4 from a LAV used in South Africa. These findings show that despite effective protection of vaccinated horses, polyvalent LAV may, paradoxically, place susceptible horses at risk for AHS.

African horse sickness (AHS) is a severe, often fatal disease of equids that is caused by AHS virus (AHSV), a member of the genus *Orbivirus,* family *Reoviridae* (*1*). The virus is transmitted to horses by biting midges in the genus *Culicoides* (*2*). Although AHS currently occurs only in sub-Saharan Africa, various species of *Culicoides* midges occur throughout the entire inhabited world, warranting concern that AHSV could spread into areas that are currently free of the virus (*1*,*3*–*5*). Furthermore, the global range of related *Culicoides*-transmitted orbiviruses, such as bluetongue virus, has expanded recently, probably in part as a result of climate change (*6*). In AHS-endemic temperate regions, such as those occurring throughout much of South Africa, the disease is most prevalent in late summer (*7*). Efforts to prevent the catastrophic impact of AHS began soon after the determination of its viral etiology in 1900, at which time it was only the second animal virus ever described (*8*,*9*). Presently, a polyvalent, live, attenuated vaccine (LAV) against AHSV (AHSV-LAV), which is produced by Onderstepoort Biological Products (Pretoria, South Africa) and provides broad protection against all 9 AHSV types (*10*), is used widely in South Africa and adjacent countries. This vaccine is supplied in 2 vials, each containing different combinations of AHSV types: combination 1 is trivalent and contains types 1, 3, and 4, whereas combination 2 is tetravalent and contains types 2, 6, 7, and 8 (*10*). Heterologous immunity is believed to provide protection to the 2 AHSV types, 5 and 9, that are not included in the vaccine.

AHS is the only equine disease for which the World Organisation for Animal Health (OIE) observes official recognition status, such that OIE member countries are required to have legally enforceable AHS control measures in place and are required to immediately notify OIE of any change to their country's AHS status (*11*). The Western Cape Province of South Africa, at the southern tip of the African continent, has historically been free from AHS, and for this reason, a legislatively defined AHS controlled area was created there in 1997 to facilitate movement of horses from South Africa. Within this area are an AHS free zone, consisting of the Cape Town metropolis; an AHS surveillance zone surrounding the free zone; and an outermost AHS protection zone (PZ) (Figure 1) (*12*). Movement of equids into and between these zones is strictly controlled. Vaccination with the polyvalent AHSV-LAV in the surveillance zone and free zone is allowed only with permission

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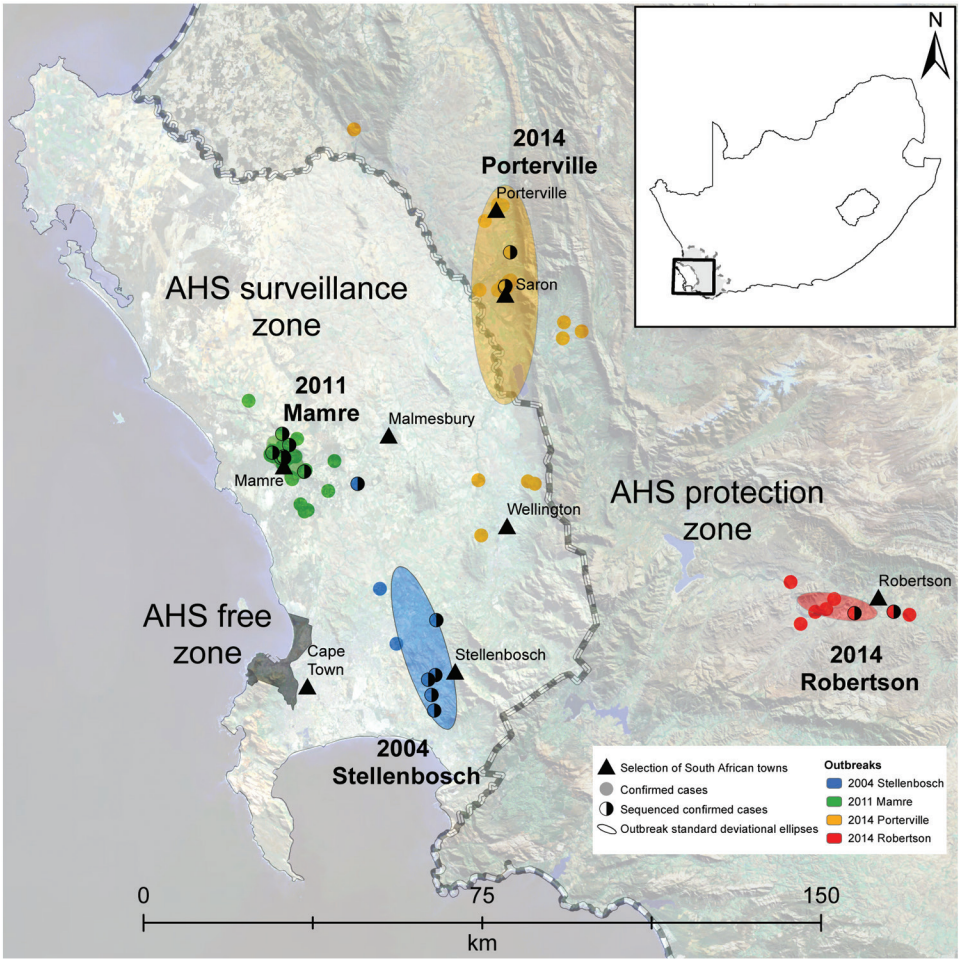

Figure 1. Locations of African horse sickness (AHS) outbreaks in Western Cape Province, South Africa, 2004–2014, including the spatial distribution of each of the AHS virus type 1 outbreaks that have occurred in the AHS controlled area since 1997. The AHS controlled area (shown in inset) is the combination of the AHS free, AHS surveillance, and AHS protection zones (also shown). Individual confirmed cases of AHS are indicated by solid dots. Half-shaded dots indicate confirmed cases for which samples were sent for sequencing (as opposed to confirmed cases that were not sequenced). The directional distribution of each outbreak is indicated by ellipses based on SD.

from the state veterinary service, and since March 2015, only during the period of low vector activity.

Since its creation in 1997, a total of 6 outbreaks of AHS in the AHS controlled area have been reported to OIE, in1999, 2004, 2006, 2011, 2013, and 2014 (*13*–*17*). Before the 2014 outbreak, these outbreaks were assumed to be caused by illegal movement of viremic animals into the controlled area, although the source was established for only 2 of these outbreaks: a type 7 virus for the 1999 outbreak in the surveillance zone and a type 5 virus for the 2006 outbreak in the PZ (Figure 1) (*18*,*19*). Because the source of the viruses responsible for the other outbreaks was never established, the goal of our study was to further characterize the epidemiology of AHSV type 1 (AHSV-1) outbreaks in the controlled area by 1) whole-genome sequencing of viruses from individual outbreaks (2004, 2011, and 2014); 2) phylogenetic comparison of these sequences with those of the polyvalent AHSV-LAV and AHSV reference strains; 3) analysis of outbreak viruses for genome segment reassortment; 4) analysis of single-nucleotide variants (SNVs) associated with attenuation of AHSV-LAV to determine whether vaccine-derived viruses have reverted to virulence; 5) correlation of epidemiologic and clinical findings with molecular findings; and 6) confirmation of the source of the virus strains responsible for the 2004, 2011, and 2014 outbreaks of AHS in the controlled area.

Materials and Methods

Virus Isolates

We sequenced complete genomes from 55 AHSV isolates collected during 1961–2014, including 39 field isolates of AHSV-1 from horses during the 2004 Stellenbosch (16 isolates), 2011 Mamre (7 isolates), 2014 Porterville (14 isolates), and 2014 Robertson (2 isolates) outbreaks of AHS in Western Cape Province of South Africa (Figure 1); AHSV LAV strains of types 1, 2, 3, 4, 6, 7, and 8; and Agricultural Research Council–Onderstepoort Veterinary Institute Laboratory reference strains for each of the 9 AHSV types. We included each of these virus isolates in the AHS genome sequencing Bioproject (http://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA271179) and identified each by a unique virus strain name (online Technical Appendix 1, http://wwwnc.cdc.gov/EID/article/22/12/16-0718-Techapp1.xlsx).

RNA Extraction, Identification, and Typing

We isolated individual viruses of each type included in the polyvalent AHSV-LAV independently, as previously described (*20*,*21*). We extracted genomic double-stranded RNA from all AHSV strains evaluated from virus-infected cells by using TRIzol reagent (Life Technologies, Johannesburg, South Africa). We identified and typed AHSV isolates by using group-specific (GS) real-time reverse transcription PCR (rRT-PCR) assays (*22*) and type-specific (TS) rRT-PCR assays targeting the gene encoding viral protein (VP) 2 (VP2) (*23*).

Genome Sequencing and Assembly

We prepared sequencing templates by using sequence-independent whole-genome RT-PCR amplification (*24*). We sequenced PCR amplicons on an Illumina MiSeq sequencer (Inqaba Biotechnical Industries, Pretoria, South Africa) by using the Nextera XT DNA sample preparation kit and 300-bp paired-end V3 Illumina chemistry. We analyzed Illumina sequence reads by using Geneious version 9 (http://www.geneious.com) (25). We used a combination of de novo assembly followed by mapping to obtain the full-length consensus genome sequences of each virus strain.

Phylogenetic Analysis

We aligned sequences of the concatenated whole virus genomes and individual genome segments by using MAFFT (http://mafft.cbrc.jp/alignment/software) (*26*) implemented within Geneious version 9 (*25*). We then used the Smart Model Selection program included in PhyML version 3 (http://www.atgc-montpellier.fr/phyml) (*27*) to identify the evolutionary models that best fit the individual sequence datasets by applying the corrected Akaike information criterion. We used the parameters from these models to construct maximum-likelihood trees by using PhyML version 3 (*27*) implemented within Geneious version 9 (*25*) with 1,000 bootstrap replicates to estimate branch support.

Genotype Group Analysis

We used RAMI (http://mbio-serv2.mbioekol.lu.se/rami.html) to analyze the concatenated whole genome sequence maximum-likelihood tree to genetically (and not evolutionarily) classify the sequences into genotype groups based on patristic distances (*28*). We ran RAMI with the patristic distance threshold set to 0.000459, enabling us to differentiate between genome sequences that differed from one another by as few as 16 nt variants.

Reassortment Analysis

We used Recombination Detection Program (RDP) version 4.63 (*29*) with default settings, except that we invoked the "scan for reassortment and recombination" setting to identify any reassortment between the gene segments of LAV strains of AHSV types 1, 3, and 4 and the 39 field isolate strains included in this study. We considered reassortment events detected by any of the 8 different recombination detection methods implemented in RDP (RDP, MAXCHI, and GENECONV methods in primary scanning mode and the BURT, Bootscan, CHIMAERA, SisScan, and 3SEQ methods in secondary scanning mode, each with a Bonferroni corrected p value cutoff of 0.05) to represent evidence of reassortment.

Nonsynonymous Single Nucleotide Variants

We aligned consensus concatenated whole virus genomes from 2 AHSV-1 laboratory strains (1/Lab/ZAF/62/OVI-HS29/62 and 1/Lab/ZAF/98/OBP-116) and the 39 field isolate strains by using MAFFT (*26*) and analyzed them by using the find variations/SNPs function in Geneious (*25*) with the find nonsynonymous polymorphisms only option enabled. We then compared the nonsynonymous SNVs in these sequences with the nonsynonymous SNVs previously associated with attenuation of AHSV-1 (*24*).

Results

Phylogenetic and Genotype Group Analysis

We used concatenated genome segments of 55 AHSV genomes to construct a maximum-likelihood phylogenetic tree incorporating best-fit substitution models (online Technical Appendix 2 Table 1, http://wwwnc.cdc.gov/EID/article/22/12/16-0718-Techapp2.pdf) to infer degrees of genetic relatedness (Figure 2). Genotype group analysis of patristic distances inferred from this maximum-likelihood tree by using RAMI (*28*) indicated that the AHSV strains isolated during the 2004, 2011, and 2014 outbreaks of AHS in the controlled area segregate into 3, 1, and 2 unique groups, respectively. Specifically, the groups were 1a, 1b, and 1c for the 2004 outbreak; 2 for the 2011 outbreak; 3a for the 2014 Porterville outbreak; and 3b for the 2014 Robertson outbreak (online Technical Appendix 2 Table 2). For the 2004 outbreak viruses, genotype group 1a includes 4 viruses that group closely with the AHSV-1-LAV strain, 1/Lab/ZAF/98/OBP-116; genotype group 1b includes 11 viruses that are also closely related to 1/Lab/ZAF/98/OBP-116; and genotype group 1c includes a single virus that segregates between 1/Lab/ZAF/98/OBP-116 and 4/Lab/ZAF/98/OBP-116. The Mamre outbreak viruses in genotype group 2 consist of 7 viruses that are all closely related to 1/Lab/ZAF/98/OBP-116. For the 2014 outbreak viruses, genotype group 3a includes 14 viruses that were all isolated from AHSV-infected horses in the Porterville area and genotype group 3b includes 2 viruses that were isolated from AHSV-infected horses in the Robertson area, with both groups of viruses being closely related to 1/Lab/ZAF/98/OBP-116.

Table 1. Attenuation-associated nonsynonymous SNVs of consensus sequences of genome segments of AHSV-1 viruses from 4 AHS outbreaks in the AHS controlled area of Western Cape Province, South Africa, 2004–2014, and reference strains*

Abbreviated strain name	Genome segment and amino acid position							Genotype group
	VP2 357	VP3 232	VP5 422	VP5 434	VP6 81	VP6 169	NS3 201	
1/E.cab-tc/ZAF/62/OVI-HS29/62	N	Y	S	T	A	R	M	
1/Lab/ZAF/98/OBP-116†	K	H	N	I	V	Q	K	
1/E.cab-tc/ZAF/04/Elb-E040019	‡			T§	A	R	E	1a
1/E.cab-tc/ZAF/04/Elb-E040020				T	A	R	E	1a
1/E.cab-tc/ZAF/04/Elb-E040021				T	A	R	E	1a
1/E.cab-tc/ZAF/04/Dkt-E040029				T	A	R	E	1a
1/E.cab-tc/ZAF/04/Tgd-E040031	N			T	A	R	¶	1b
1/E.cab-tc/ZAF/04/Elb-E040034	N			T	A	R	¶	1b
1/E.cab-tc/ZAF/04/Tgd-E040039	N			T	A	R	¶	1b
1/E.cab-tc/ZAF/04/Avt-E040043	N			T	A	R	¶	1b
1/E.cab-tc/ZAF/04/Avt-E040048	N			T	A	R	¶	1b
1/E.cab-tc/ZAF/04/Vdm-E040062	N			T	A	R	¶	1b
1/E.cab-tc/ZAF/04/Tgd-E040064	N			T	A	R	¶	1b
1/E.cab-tc/ZAF/04/Vdm-E040065	N			T	A		¶	1b
1/E.cab-tc/ZAF/04/Avt-E040066	N			T	A	R	¶	1b
1/E.cab-tc/ZAF/04/Avt-E040081	N			T	A	R	¶	1b
1/E.cab-tc/ZAF/04/Kbk-E040086	N			T	A	R	¶	1b
1/E.cab-tc/ZAF/04/Avt-E040061	N		¶	¶	A	R	¶	1c
1/E.cab-tc/ZAF/11/Mre-E110143_1				T	A	R	N	2
1/E.cab-tc/ZAF/11/Mre-E110180_WC44				T	A	R	N	2
1/E.cab-tc/ZAF/11/Mre-E110180_WC61				T	A	R	N	2
1/E.cab-tc/ZAF/11/Mre-E110180_WC165				T	A	R	N	2
1/E.cab-tc/ZAF/11/Mre-E110411_1				T	A	R	N	2
1/E.cab-tc/ZAF/11/Mre-E110418_1				T	A	R	N	2
1/E.cab-tc/ZAF/11/Mre-E110674_3				T	A	R	N	2
1/E.cab-tc/ZAF/14/Ptv-E140485_WC00522				T	A	R	¶	3a
1/E.cab-tc/ZAF/14/Ptv-E140485_WC00528				T	A	R	¶	3a
1/E.cab-tc/ZAF/14/Ptv-E140485_WC00533				T	A	R	¶	3a
1/E.cab-tc/ZAF/14/Ptv-E140485_WC00544				T	A	R	¶	3a
1/E.cab-tc/ZAF/14/Ptv-E140485_WC00555				T	A	R	¶	3a
1/E.cab-tc/ZAF/14/Srn-E140526_WC00481				T	A	R	¶	3a
1/E.cab-tc/ZAF/14/Srn-E140526_WC00482				T	A	R	¶	3a
1/E.cab-tc/ZAF/14/Srn-E140526_WC00488				T	A	R	¶	3a
1/E.cab-tc/ZAF/14/Srn-E140526_WC00491				T	A	R	¶	3a
1/E.cab-tc/ZAF/14/Srn-E140526_WC00493				T	A	R	¶	3a
1/E.cab-tc/ZAF/14/Srn-E140526_WC00502				T	A	R	¶	3a
1/E.cab-tc/ZAF/14/Ptv-E140536_WC00506				T	A	R	¶	3a
1/E.cab-tc/ZAF/14/Ptv-E140536_WC00507				T	A	R	¶	3a
1/E.cab-tc/ZAF/14/Ptv-E140536_WC00508				T	A	R	¶	3a
1/E.cab-tc/ZAF/14/Rbn-E140702_RB00008				T	A	R	¶	3b
1/E.cab-tc/ZAF/14/Rbn-E140816_RB00221				T	A	R	¶	3b

*AHS, African horse sickness; AHSV-1, AHS virus type 1; NS3, nonstructural protein 3; SNV, single-nucleotide variants; VP, viral protein.
†The changes in amino acids are indicated in comparison with the AHSV-1 live, attenuated vaccine-derived strain (1/Lab/ZAF/98/OBP-116) for relevant viral proteins.
‡Sequences that were identical to the consensus sequence of the vaccine-derived strain are indicated by an empty cell.
§Sequences that differed from the consensus sequence of the AHSV-1 live, attenuated vaccine-derived strain are indicated with the letter symbol of the relevant amino acid.
¶Indicates that these segments were not considered due to a recombination event that occurred with another vaccine-derived AHSV type.

Given that reassortment is a major feature of orbivirus evolution (*30*,*31*), we further explored the evolutionary relationships between the 55 AHSV sequences by constructing separate maximum-likelihood trees for each of the VP1, VP2, VP3, VP4, VP5, VP6, VP7, nonstructural (NS) protein 1 (NS1), NS2, and NS3 encoding genome segments (online Technical Appendix 2 Figures 1–10). For the segments encoding VP2, VP3, VP6, NS1, and NS2, viruses included in genotype groups 1a, 1b, 1c, 2, 3a, and 3b all group, with high degrees of associated bootstrap support, together with the AHSV-1-LAV strain, 1/Lab/ZAF/98/OBP-116. For the segments encoding VP1, VP4, and VP7, the viruses included in genotype groups 1a, 2, 3a, and 3b also group with 1/Lab/ZAF/98/OBP-116, whereas those in genotype groups 1b and 1c group with the AHSV-3-LAV strain, 3/Lab/ZAF/98/OBP-116. For the gene encoding VP5, viruses included in all genotype groups except 1c group with 1/Lab/ZAF/98/OBP-116, whereas those in genotype group 1c group with the AHSV-4-LAV strain, 4/Lab/ZAF/98/OBP-116. For genes encoding NS3, viruses included in genotype groups 1a and 2 group with 1/Lab/ZAF/98/OBP-116, whereas those included in the remaining genotype groups group with 4/Lab/ZAF/98/OBP-116. Collectively, these data confirm that all 10 gene segments of

the viruses included in genotype groups 1a and 2 are probably derived from a most recent common ancestor closely resembling 1/Lab/ZAF/98/OBP-116; the viruses included in genotype groups 1b and 1c are probably reassortants derived from parental viruses very closely resembling 1/Lab/ZAF/98/OBP-116, 3/Lab/ZAF/98/OBP-116, and 4/Lab/ZAF/98/OBP-116; and viruses in genotype groups 3a and 3b are probably reassortants derived from parental viruses very closely resembling 1/Lab/ZAF/98/OBP-116 and 4/Lab/ZAF/98/OBP-116 (Figure 3).

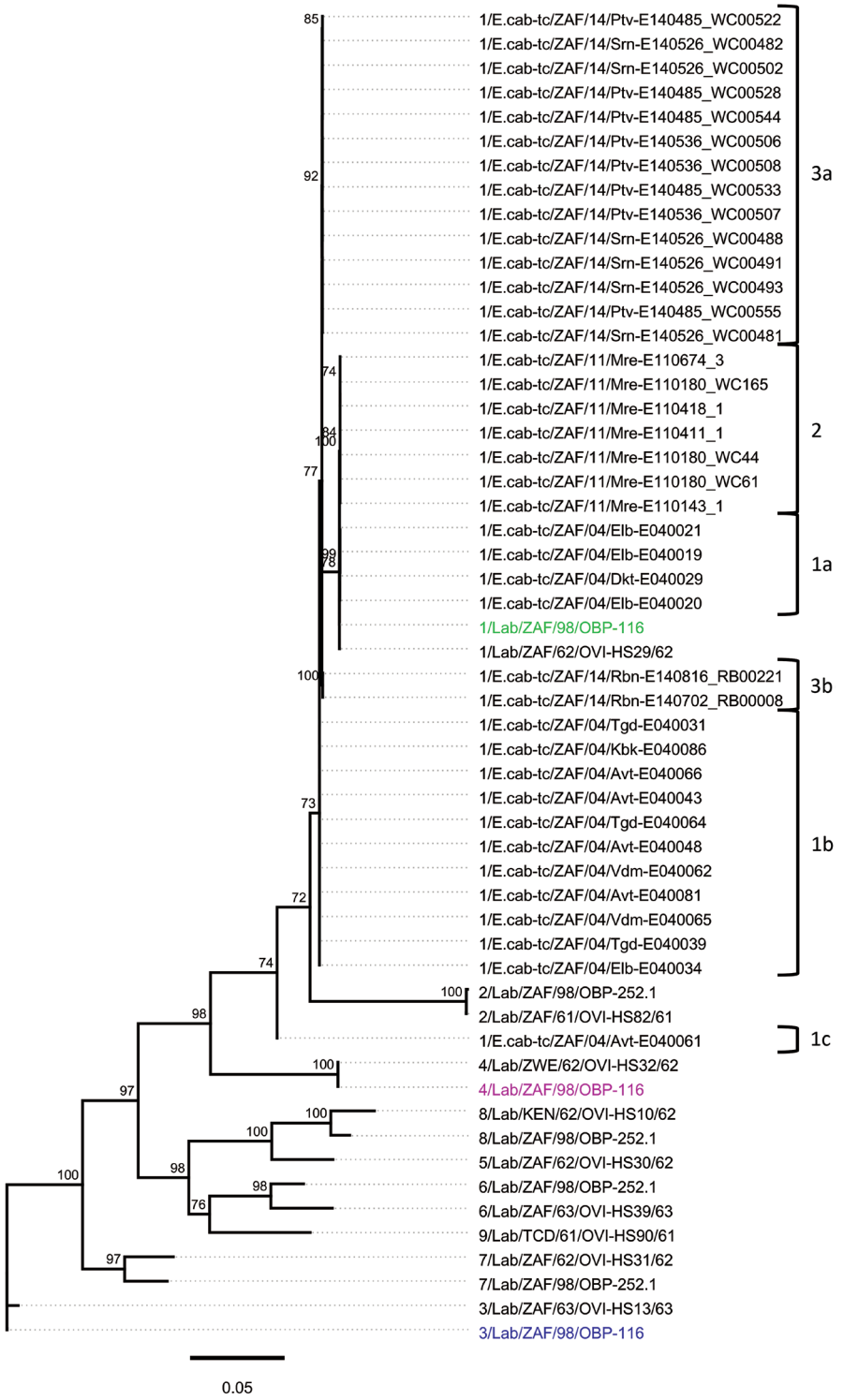

Figure 2. Whole-genome phylogeny of African horse sickness (AHS) viruses identified in AHS outbreaks in Western Cape Province, South Africa, 2004–2014. Maximum-likelihood phylogenetic tree indicating the genetic relationships of concatenated whole genome nucleotide sequences of AHS viruses from affected horses in the 2004, 2011, and 2014 outbreaks in the AHS controlled area in Western Cape Province to the AHS live, attenuated vaccine viruses and reference viruses. Green indicates vaccine-derived 1/Lab/ZAF/98/OBP-116, blue indicates vaccine-derived 3/Lab/ZAF/98/OBP-116, and red indicates vaccine-derived 4/Lab/ZAF/98/OBP-116. Branches are scaled to represent numbers of inferred nucleotide differences per site. Branches supported by full maximum-likelihood bootstrap values >70% are indicated. Genotype groups are indicated at right. Scale bar indicates genetic distance.

Table 2. Epidemiologic parameters for 4 outbreaks involving AHS virus type 1 in the AHS controlled area in Western Cape Province, South Africa, 2004–2014*

Parameter†	2004 Stellenbosch	2011 Mamre	2014 Porterville	2014 Robertson
No. confirmed cases	23 (16)‡	84 (73)§	89	22
No. deaths	18 (16)‡	64 (64)§	13	1
Case-fatality rate, %	78.3 (100)‡	76.2 (87.7)§	14.6	4.5
No. subclinical cases	0	15 (4)†	52	17
% Subclinical	0	17.9 (5.5)§	58.4	77.3
No. vaccinated cases	2/23	2/84	35/89	3/22
% Vaccinated	8.7	2.4	39.3	13.6
No. properties affected	10 (8)‡	47 (45)§	31	8

*AHS, African horse sickness.
†The parameters were calculated by using the current World Organization for Animal Health (OIE) case definition. Parameters calculated by using the case definitions when the outbreaks occurred are in parenthesis for the 2004 and 2011 outbreaks.
‡An additional 5 clinical cases and 2 deaths that met the criteria of the current OIE AHS case definition were not included based on the case definition in place at the time of this outbreak (*13*).
§An additional 11 subclinical cases that met the criteria of the current OIE AHS case definition were not included based on the case definition in place at the time of this outbreak (*15*).

Explicitly testing for intrasegment recombination and reassortment by using RDP4.63 (*29*) yielded no evidence of intracomponent recombination in any virus but strong evidence of reassortment in genotype group 1b, 1c, 3a, and 3b viruses (online Technical Appendix 2 Table 3). Genotype group 1b viruses have 6 genome segments (encoding VP2, VP3, VP5, VP6, NS1, and NS2) derived from a virus resembling 1/Lab/ZAF/98/OBP-116; 2 segments (encoding VP1 and VP7) derived from a virus resembling 3/Lab/ZAF/98/OBP-116 (multiple testing corrected $p = 2.27 \times 10^{-12}$ and 1.13×10^{-31}, respectively); 1 segment (encoding NS3) derived from a virus resembling 4/Lab/ZAF/98/OBP-116 ($p = 9.31 \times 10^{-240}$); and 1 segment (encoding VP4) that could plausibly have been derived from either 3/Lab/ZAF/98/OBP-116 or 1/Lab/ZAF/98/OBP-116 ($p = 7.66 \times 10^{-4}$) (Figure 4). Genotype group 1c viruses display a reassortant pattern resembling that of group 1b viruses except that the segment encoding VP5 is apparently derived from a virus resembling 4/Lab/ZAF/98/OBP-116 ($p = 1.96 \times 10^{-216}$). Genotype groups 3a and 3b viruses have 9 segments derived from a virus resembling 1/Lab/ZAF/98/OBP-116 and a single segment (NS3) derived from a virus resembling 4/Lab/ZAF/98/OBP-116 ($p = 9.31 \times 10^{-240}$) (Figure 4).

Several SNVs relative to the AHSV-LAV–derived viruses 1/Lab/ZAF/98/OBP-116 and 3/Lab/ZAF/98/OBP-116 are present in the NS1-encoding genes of viruses included in genotype groups 3a (2014 Porterville) and 3b (2014 Robertson) (online Technical Appendix 2 Table 4). Only a single nonsynonymous SNV exists between the NS1-encoding genes of 1/Lab/ZAF/98/OBP-116 and 3/Lab/ZAF/98/OBP-116 (NS1 I264T). All viruses included in genotype group 3a (2014 Porterville) have the I amino acid variant that is present in 1/Lab/ZAF/98/OBP-116, whereas viruses in genotype group 3b (2014 Robertson) include the T amino acid variant present in 3/Lab/ZAF/98/OBP-116. Viruses in the 3b genotype group (2014 Robertson) include ≥2 synonymous SNVs and ≥1 nonsynonymous SNV relative to 3/Lab/ZAF/98/OBP-116, which suggests that the NS1 gene of the virus strains in genotype group 3b are most probably derived from 3/Lab/ZAF/98/OBP-116, whereas those in genotype group 3a are more probably derived from 1/Lab/ZAF/98/OBP-116.

Seven nonsynonymous SNVs were identified between the whole genome sequences of the AHSV-1-LAV–derived virus, 1/Lab/ZAF/98/OBP-116, and its parental virus, 1/E.cab-tc/ZAF/62/OVI-HS29/62 (Table 1). SNVs are present at 4 of these 7 sites in the 4 viruses included in genotype group 1a. Intriguingly, 3 of these 4 changes are apparently reversions to the nonsynonymous SNV that is present in the virulent parental virus (I434T in VP5 and V81A and Q169R in VP6) and are therefore potentially reversion-to-virulence mutations. The 1 other SNV in the genotype group 1a viruses is site 201 in NS3, whereas in 1/Lab/ZAF/98/OBP-116 and 1/E.cab-tc/ZAF/62/OVI-HS29/62, a K and an M, respectively, are at this site, and in the group 1a viruses, an E is at this site. In 10 of the 11 field viruses in genotype group 1b, nonsynonymous SNVs were also detected at 4 of the 7 sites that differentiate the attenuated 1/Lab/ZAF/98/OBP-116 virus from its virulent parent, 1/E.cab-tc/ZAF/62/OVI-HS29/62. The remaining field virus in genotype group 1b, 1/E.cab-tc/ZAF/04/Vdm-E040065, includes 3 of these 4 SNVs. The I434T SNV in VP5 and the V81A and Q169R SNVs in VP6 of viruses in genotype group 1a are the same as those found in the genotype group 1b, 2, 3a, and 3b viruses. The K357N SNV in VP2 was detected only among viruses in genotype groups 1b and 1c. All the viruses included in genotype groups 1b, 1c, 3a, and 3b are also reassortants with an NS3-encoding segment derived from a virus resembling 4/Lab/ZAF/98/OBP-116; therefore, SNVs in this component of these viruses were not considered as genuine mutationally derived SNVs.

The 1/E.cab-tc/ZAF/04/Avt-E040061 strain in genotype group 1c has nonsynonymous SNVs at 3 of the 7 loci (K357N in VP2 and V81A and Q169R in VP6) but a

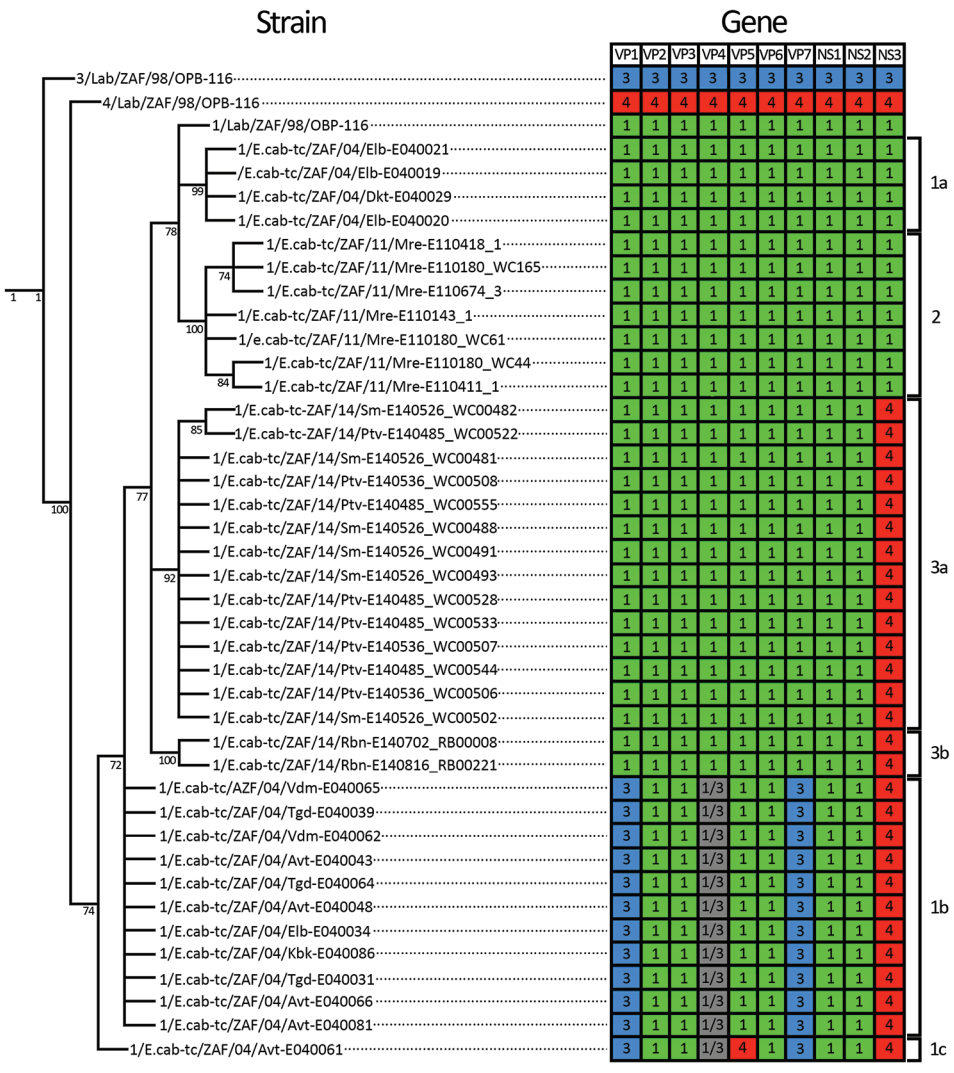

Figure 3. Cladogram and heat map of vaccine-derived African horse sickness (AHS) virus reassortants identified in AHS outbreaks in Western Cape Province, South Africa, 2004–2014. Cladogram indicates genetic relationships of concatenated AHS virus whole-genome nucleotide sequences from affected horses in the 2004, 2011, and 2014 outbreaks in the AHS controlled area in Western Cape Province. Heat map diagram summarizes the origin of the gene segments for each strain with 1/Lab/ZAF/98/OBP-116 (green blocks), 3/Lab/ZAF/98/OBP-116 (blue blocks), and 4/Lab/ZAF/98/OBP-116 (red blocks) vaccine-derived strains. Gray blocks indicate that the segment could be derived from either 1/Lab/ZAF/98/OBP-116 or 3/Lab/ZAF/98/OBP-116. Branches supported by full maximum-likelihood bootstrap values >70% are indicated. Genotype groups are indicated at right.

VP5-encoding gene apparently derived by reassortment from a virus resembling 4/Lab/ZAF/98/OBP-116, such that the SNVs in the VP5 of this strain were also not considered to be mutationally derived.

The 7 viruses included in genotype group 2 and the 16 viruses included in genotype groups 3a and 3b all exhibit potential reversion-to-virulence mutations at 3 of the 7 nonsynonymous SNV sites that differentiate the AHSV-1-LAV virus from its virulent parent (I434T in VP5 and V81A and Q169R in VP6). Additionally, a fourth SNV (K201N in NS3) at 1 of the 7 sites differentiating the AHSV-1 LAV from its parent (which had a K and an M, respectively, at this site) is also present in the genotype group 2 viruses.

Quantification of the Outbreaks

The epidemiologic parameters of the AHS outbreaks in the controlled area in 2004, 2011, and 2014 were inferred by using the current OIE case definition for AHS (*11*) (Table 2). Although the case-fatality rates (CFRs) were very high for the 2004 Stellenbosch (78.3%) and 2011 Mamre (76.2%) outbreaks, they were considerably lower for the 2014 Porterville (14.6%) and Robertson (4.5%) outbreaks. Additionally, the 2011 Mamre and 2004 Stellenbosch outbreaks were associated with the lowest vaccination rates among AHSV-infected horses (2.7% and 8.7%, respectively). Differences in the genetic constitution of the individual outbreak viruses could have been associated with the vastly different CFRs in each outbreak; however, whether these differences in CFRs are a consequence of lower virulence among the outbreak viruses or the result of existing vaccine-induced immunity in the exposed horses is unknown. Similarly, changes in the AHS case definition that only came into effect in 2008 (after the 2004 Stellenbosch outbreak) probably resulted in an underestimation of subclinical AHSV infections during that outbreak. Whereas during the Stellenbosch 2004 outbreak only clinically affected, deceased horses were classified

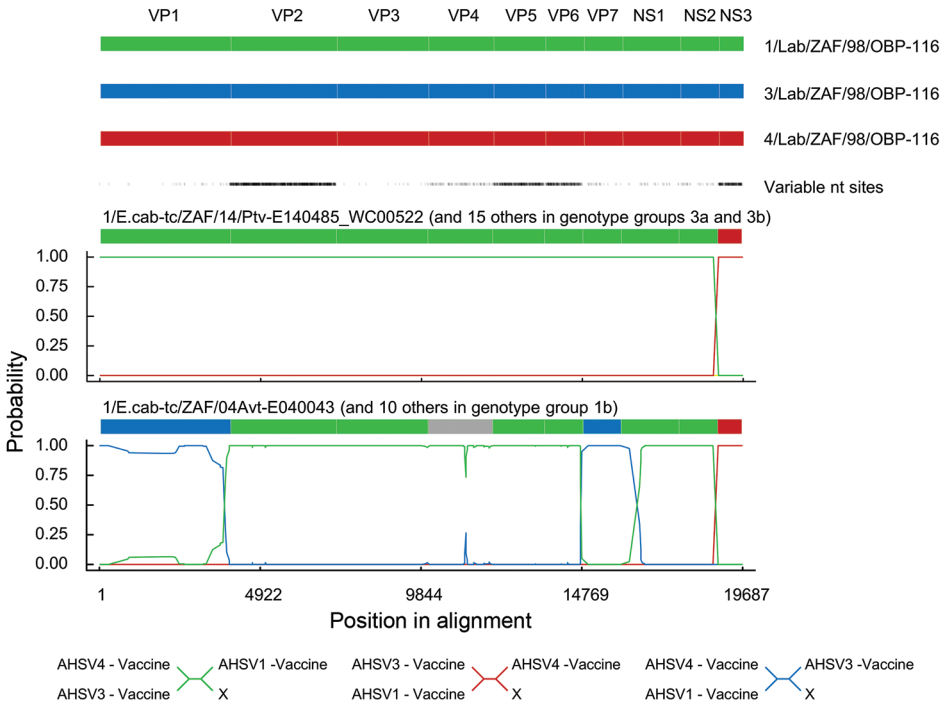

Figure 4. Statistical evidence of reassortment within the genomes of African horse sickness (AHS) virus field isolates identified in outbreaks in the AHS controlled area in Western Cape Province, South Africa, 2004–2014. A hidden Markov model–based approach (BURT-HMM) was used to classify individual nucleotides within each of the 10 segments of individual AHS virus isolates into 3 different categories: 1/Lab/ZAF/98/OBP-116-like (green), 3/Lab/ZAF/98/OBP-116-like (blue), and 4/Lab/ZAF/98/OBP-116-like (red). Probability supports for these classifications yielded by the BURT-HMM with the highest likelihood are plotted along the genome. Positions of segment boundaries are given in the diagram above the plots. The phylogenetic clusterings that are implied by differently colored segments in these plots are indicated below the plots. The segment indicated in gray could not be convincingly classified because it closely resembles both 1/Lab/ZAF/98/OBP-116 and 3/Lab/ZAF/98/OBP-116.

as having confirmed cases (*13*), major advances in AHS diagnostic testing (e.g., rRT-PCR–based methods) have occurred during the past 10 years that likely substantially increased the detection of subclinical infections by the time of the 2014 outbreaks (*15*,*32*).

Discussion

Whole-genome sequences were compared from 55 field, LAV, and laboratory strains of AHSV. The field viruses were obtained from horses during outbreaks of AHS of different clinical severity (CFRs ranging from 4.5% to 78.3%) in the AHS controlled area of South Africa during 2004, 2011, and 2014. Phylogenetic analyses confirmed that genetically distinct viruses were responsible for each outbreak and that these were all closely related to viruses contained in the trivalent AHSV-LAV (combination 1) used in South Africa. Evaluation of nonsynonymous SNVs confirmed some outbreak viruses to be revertants of the vaccine AHSV-1 strain toward the virulent parental type. Furthermore, some outbreak viruses were clearly reassortants with individual genome segments derived from multiple different virus types that are present in the trivalent vaccine preparation.

Potgieter et al. (*24*) hypothesized that changes in VP2 and VP5 can confer virulence or attenuation of individual AHSV strains, based upon comparisons of the consensus sequences of the genome of an attenuated AHSV-1 isolate (GenBank accession nos. FJ183364–FJ183373) and its virulent parent. Potgieter et al. (*24*) also proposed that virulence is related to tissue tropism because the outer capsid proteins are involved in cell entry and trigger apoptosis of host cells. Additionally, other studies have implicated NS3 as a determinant of AHSV virulence (*33*). The results of our study further confirm that changes in multiple VPs can affect the virulence of AHSV. Both reversion (to the virulent parental type) and novel SNVs were present in field-isolated viruses at various residue sites in VP2 (K357N in genotype group 1b viruses), VP5 (I434T in all field viruses evaluated except sample 1/E.cab-tc/ZAF/04/Avt- E040061), and VP6 (V81A in all field viruses and Q169R in all field viruses except sample 1/E.cab-tc/ZAF/04/Vdm-E040065) that differentiate the attenuated AHSV-1-LAV strain from its virulent parental strain. Furthermore, SNVs present at a site in NS3 (K201E in genotype group 1a viruses and K201N in genotype group 2) are potentially associated with reversion to virulence because of the effect of NS3 on virus release, membrane permeability, and viral yield (*34*). However, the determinants of AHSV virulence are probably complex and multigenic (*24*,*34*), which is consistent with the remarkable difference in CFRs between horses in the various outbreaks.

Given the genetic diversity of field strains of AHSV (*14*,*24*,*35*), our analyses overwhelmingly support the

premise that the potential reversion-to-virulence mutants and reassortants that we detected arose from viruses within the polyvalent AHSV-LAV formulation, and predominantly from AHSV-1-LAV. Although these mutants and reassortants most likely arose within vaccinated horses, the reason for the predominance of AHSV-1-LAV components in the emergent outbreak viruses is unknown. The data presented here also indicate that distinct founder events led to the expansion in Stellenbosch (2004) of viruses included in genotype groups 1a and 1b and, similarly, that the outbreaks in 2014 in Porterville (genotype group 3a) and Robertson (genotype group 3b) also probably originated independently from the LAV and were not from the spread of the same outbreak virus.

In summary, results of this study highlight the importance of genetic characterization of circulating strains of AHSV in epidemiologic investigations of AHS outbreaks. Although, the prevailing opinion in South Africa was that illegal movement of viremic equids into the AHS controlled area was responsible for the repeated occurrences of AHS in the controlled area, this is clearly not the only cause. Our data confirm that use of polyvalent AHSV-LAV can result in the emergence and spread of virulent viruses to adjacent susceptible horses, presumably by *Culicoides* midge vectors that are already resident within the AHS controlled area (*36*). Collectively, these findings have major implications for strategies to control AHS, both in AHS-endemic regions and during future incursions into currently AHSV-free areas. However, AHSV-LAV confers critical and effective protection for susceptible horses in AHS-endemic areas and, although potentially safer recombinant AHSV vaccines have proven effective in laboratory studies (*37*,*38*), these are not available commercially and they are yet to be evaluated in the field. Until alternative vaccines become commercially available, control of AHS will remain reliant on the use of AHSV-LAV coupled with the adoption of strategies to minimize the likelihood of natural dissemination of revertant and reassortant vaccine-derived viruses.

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Technical Appendix 1. Metadata for each of the 39 AHSV type 1 field isolates from the 2004 Stellenbosch, 2011 Mamre, 2014 Porterville and 2014 Robertson outbreaks of AHS in the AHS Controlled Area of the Western Cape Province of South Africa. Each record includes the Strain Name of the isolate as submitted to GenBank, the Abbreviated Strain Name, a hyperlink to the Biosample details for the isolate, a hyperlink to the GenBank accession numbers for the isolate, the average coverage per nucleotide for the consensus sequences, the animal name or laboratory name from which the sample or material was sourced, reference numbers for publications that have previously described these cases or isolates, the genotype group of the field isolate, the outcome of the case, the type off samples submitted for examination, the date that the samples were collected and the vaccination status of the donor horse.

Strain Name[a]	Abbreviated Strain Name[b]	BioSample Number	Assession Numbers	Coverage	Animal Name/Source	Reference	Genotype Group	Outcome	Sample	Sampled	Vaccination[c]
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2004/Elsenburg-E04001	1/E.cab-tc/ZAF/04/Elb-E040019	SAMN04038467	KT715641 - KT715650	101369	Laura	[23, 24, 25]	1a	Died	Organs	22/02/2004	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2004/Elsenburg-E04002	1/E.cab-tc/ZAF/04/Elb-E040020	SAMN03774773	KT186897 - KT186906	3823	Michelle	[23, 24, 25]	1a	Died	Organs	22/02/2004	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2004/Elsenburg-E04002	1/E.cab-tc/ZAF/04/Elb-E040021	SAMN03774774	KT186907 - KT186916	11093	Mara	[23, 24, 25]	1a	Died	Blood	24/02/2004	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2004/Daktari-E040029	1/E.cab-tc/ZAF/04/Dkt-E040029	SAMN03774771	KT186917 - KT186926	9984	Murphy Brown	[23, 24, 25]	1a	Died	Blood	28/02/2004	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2004/Troughend-E040031	1/E.cab-tc/ZAF/04/Tgd-E040031	SAMN03774781	KT186927 - KT186936	5223	SA Saddlehorse 1	[23, 24, 25]	1b	Died	Organs	26/02/2004	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2004/Elsenburg-E040034	1/E.cab-tc/ZAF/04/Elb-E040034	SAMN03774775	KT186937 - KT186946	13476	Mandy	[23, 25]	1b	Recovered	Blood	26/02/2004	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2004/Troughend-E040039	1/E.cab-tc/ZAF/04/Tgd-E040039	SAMN03774782	KT186947 - KT186956	9825	Melody Fire	[23, 25]	1b	Recovered	Blood	03/03/2004	Vaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2004/Avontuur-E040043	1/E.cab-tc/ZAF/04/Avt-E040043	SAMN03774767	KT186957 - KT186966	4683	Bow Street Bell	[23, 24, 25]	1b	Euthanased	Blood	04/03/2004	Vaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2004/Avontuur-E040048	1/E.cab-tc/ZAF/04/Avt-E040048	SAMN03774768	KT186967 - KT186976	10113	Bow Street Bell	[23, 24, 25]	1b	Euthanased	Organs	09/03/2004	Vaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2004/Vredenheim-E040062	1/E.cab-tc/ZAF/04/Vdm-E040062	SAMN03774784	KT186987 - KT186996	10978	Bruin Perd	[23, 24, 25]	1b	Died	Blood	15/03/2004	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2004/Troughend-E040064	1/E.cab-tc/ZAF/04/Tgd-E040064	SAMN03774783	KT186997 - KT187006	11652	SA Saddlehorse 2	[23, 24, 25]	1b	Died	Organs	17/03/2004	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2004/Vredenheim-E040065	1/E.cab-tc/ZAF/04/Vdm-E040065	SAMN03774785	KT187007 - KT187016	5823	Bruin Perd	[23, 24, 25]	1b	Died	Organs	17/03/2004	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2004/Avontuur-E040066	1/E.cab-tc/ZAF/04/Avt-E040066	SAMN03774769	KT187017 - KT187026	4128	Special Edition	[23, 24, 25]	1b	Died	Organs	18/03/2004	Vaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2004/Avontuur-E040081	1/E.cab-tc/ZAF/04/Avt-E040081	SAMN03774770	KT187037 - KT187046	15663	2003Stars and Stripes	[23, 24, 25]	1b	Died	Organs	24/03/2004	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2004/Kalbaskraal-E040086	1/E.cab-tc/ZAF/04/Kbk-E040086	SAMN03774776	KT187047 - KT187056	7654	Amber	[23, 24, 25]	1b	Died	Organs	29/03/2004	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2004/Avontuur-E040061	1/E.cab-tc/ZAF/04/Avt-E040061	SAMN03780052	KT186977 - KT186986	11336	Special Edition	[23, 24, 25]	1c	Died	Blood	16/03/2004	Vaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2011/Marme-E110143_1	1/E.cab-tc/ZAF/11/Mre-E110143_1	SAMN03765259	KT070447 - KT070456	3017	Ruben	[26]	2	Died	Organs	27/02/2011	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2011/Marme-E110180_WC165	1/E.cab-tc/ZAF/11/Mre-E110180_WC165	SAMN03765262	KT070477 - KT070486	3567	Trigger	[26]	2	Died	Organs	06/03/2011	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2011/Marme-E110180_WC61	1/E.cab-tc/ZAF/11/Mre-E110180_WC61	SAMN03765261	KT070507 - KT070516	5300	Jordan	[26]	2	Subclinical	Blood	06/03/2011	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2011/Marme-E110180_WC44	1/E.cab-tc/ZAF/11/Mre-E110180_WC44	SAMN03765260	KT070487 - KT070496	2970	Smokey	[26]	2	Recovered	Blood	06/03/2011	Vaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2011/Marme-E110418_1	1/E.cab-tc/ZAF/11/Mre-E110418_1	SAMN03765264	KT070497 - KT070506	6806	Moon	[26]	2	Died	Organs	22/03/2011	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2011/Marme-E110411_1	1/E.cab-tc/ZAF/11/Mre-E110411_1	SAMN03765263	KT070457 - KT070466	4566	Dusty	[26]	2	Died	Organs	26/03/2011	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2011/Marme-E110674_3	1/E.cab-tc/ZAF/11/Mre-E110674_3	SAMN03765265	KT070467 - KT070476	6847	Robin	[26]	2	Recovered	Blood	18/04/2011	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2014/Saron-E140526_WC00502	1/E.cab-tc/ZAF/14/Srn-E140526_WC00502	SAMN03769430	KT187187 - KT187196	10105	McGuiver	TS	3a	Subclinical	Blood	24/03/2014	Vaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2014/Saron-E140526_WC00493	1/E.cab-tc/ZAF/14/Srn-E140526_WC00493	SAMN03769429	KT187177 - KT187186	13406	Milky	TS	3a	Subclinical	Blood	24/03/2014	Vaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2014/Saron-E140526_WC00481	1/E.cab-tc/ZAF/14/Srn-E140526_WC00481	SAMN03769427	KT187137 - KT187146	7881	Ballaka	TS	3a	Subclinical	Blood	24/03/2014	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2014/Saron-E140526_WC00488	1/E.cab-tc/ZAF/14/Srn-E140526_WC00488	SAMN03769428	KT187157 - KT187166	18131	King	TS	3a	Subclinical	Blood	24/03/2014	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2014/Saron-E140526_WC00491	1/E.cab-tc/ZAF/14/Srn-E140526_WC00491	SAMN03774780	KT187167 - KT187176	8216	Fire	TS	3a	Recovered	Blood	24/03/2014	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2014/Saron-E140526_WC00482	1/E.cab-tc/ZAF/14/Srn-E140526_WC00482	SAMN03774779	KT187147 - KT187156	8624	Raily	TS	3a	Died	Blood	24/03/2014	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2014/Porterville-E140536_WC00507	1/E.cab-tc/ZAF/14/Ptv-E140536_WC00507	SAMN03769425	KT187207 - KT187216	12686	Jahan Zahmar	TS	3a	Recovered	Blood	27/03/2014	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2014/Porterville-E140536_WC00508	1/E.cab-tc/ZAF/14/Ptv-E140536_WC00508	SAMN03769426	KT187217 - KT187226	10474	Jahan Dajinah	TS	3a	Recovered	Blood	27/03/2014	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2014/Porterville-E140536_WC00506	1/E.cab-tc/ZAF/14/Ptv-E140536_WC00506	SAMN03769424	KT187197 - KT187206	14902	Jahan Nasibah	TS	3a	Recovered	Blood	27/03/2014	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2014/Porterville-E140485_WC00522	1/E.cab-tc/ZAF/14/Ptv-E140485_WC00522	SAMN03769419	KT187077 - KT187086	15126	Jahan Faraj	TS	3a	Recovered	Blood	31/03/2014	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2014/Porterville-E140485_WC00544	1/E.cab-tc/ZAF/14/Ptv-E140485_WC00544	SAMN03769422	KT187117 - KT187126	9638	Jahan Dhia	TS	3a	Subclinical	Blood	31/03/2014	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2014/Porterville-E140485_WC00528	1/E.cab-tc/ZAF/14/Ptv-E140485_WC00528	SAMN03769420	KT187097 - KT187106	10108	Jahan Jihad	TS	3a	Recovered	Blood	31/03/2014	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2014/Porterville-E140485_WC00533	1/E.cab-tc/ZAF/14/Ptv-E140485_WC00533	SAMN03769421	KT187107 - KT187116	8122	Jahan Al Rabiah	TS	3a	Recovered	Blood	31/03/2014	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2014/Porterville-E140485_WC00555	1/E.cab-tc/ZAF/14/Ptv-E140485_WC00555	SAMN03769423	KT187127 - KT187136	5588	el-Jahrousse Mia	TS	3a	Recovered	Blood	31/03/2014	Vaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2014/Robertson-E140702_RB00008	1/E.cab-tc/ZAF/14/Rbn-E140702_RB00008	SAMN03774777	KT187087 - KT187096	6356	2013Hersonet	TS	3b	Recovered	Blood	25/04/2014	Unvaccinated
African horse sickness virus 1 strain 1/E.caballus-tc/ZAF/2014/Robertson-E140816_RB00221	1/E.cab-tc/ZAF/14/Rbn-E140816_RB00221	SAMN03774778	KT187227 - KT187236	6721	2013Tale Of The Glacier	TS	3b	Subclinical	Blood	08/05/2014	Unvaccinated
African horse sickness virus 1 strain 1/Labstr/ZAF/1998/OBP-116	1/Lab/ZAF/98/OBP-116	SAMN03764401	KT030330 - KT030339	7547	OBP AHSV1 LAV, Batch 116	[41]					
African horse sickness virus 2 strain 2/Labstr/ZAF/1998/OBP-252.1	2/Lab/ZAF/98/OBP-252.1	SAMN04038462	KT715601 - KT715610	29050	OBP AHSV2 LAV, Batch 252.1	[42]					
African horse sickness virus 3 strain 3/Labstr/ZAF/1998/OBP-116	3/Lab/ZAF/98/OBP-116	SAMN03764402	KT030340 - KT030349	11756	OBP AHSV3 LAV, Batch 116	[41]					
African horse sickness virus 4 strain 4/Labstr/ZAF/1998/OBP-116	4/Lab/ZAF/98/OBP-116	SAMN03764403	KT030350 - KT030359	6977	OBP AHSV4 LAV, Batch 116	[41]					
African horse sickness virus 6 strain 6/Labstr/ZAF/1998/OBP-252.1	6/Lab/ZAF/98/OBP-252.1	SAMN04038463	KT715611 - KT715620	35724	OBP AHSV6 LAV, Batch 252.1	[42]					
African horse sickness virus 7 strain 7/Labstr/ZAF/1998/OBP-252.1	7/Lab/ZAF/98/OBP-252.1	SAMN04038464	KT715621 - KT715630	137497	OBP AHSV7 LAV, Batch 252.1	[42]					
African horse sickness virus 8 strain 8/Labstr/ZAF/1998/OBP-252.1	8/Lab/ZAF/98/OBP-252.1	SAMN04038465	KT715631 - KT715640	120396	OBP AHSV8 LAV, Batch 252.1	[42]					
African horse sickness virus 1 strain 1/Labstr/ZAF/1962/OVI-HS29/62	1/Lab/ZAF/62/OVI-HS29/62	SAMN03765190	KT030570 - KT030579	8401	ARC-OVI OIE Laboratory Reference Strain AHSV1	[44], TS					
African horse sickness virus 2 strain 2/Labstr/ZAF/1961/OVI-HS82/61	2/Lab/ZAF/61/OVI-HS82/61	SAMN03765191	KT030580 - KT030589	7698	ARC-OVI OIE Laboratory Reference Strain AHSV2	[44], TS					
African horse sickness virus 3 strain 3/Labstr/ZAF/1963/OVI-HS13/63	3/Lab/ZAF/63/OVI-HS13/63	SAMN03765192	KT030590 - KT030599	5281	ARC-OVI OIE Laboratory Reference Strain AHSV3	[44], TS					
African horse sickness virus 4 strain 4/Labstr/ZWE/1962/OVI-HS32/62	4/Lab/ZWE/62/OVI-HS32/62	SAMN03765193	KT030600 - KT030609	11579	ARC-OVI OIE Laboratory Reference Strain AHSV4	[44], TS					
African horse sickness virus 5 strain 5/Labstr/ZAF/1962/OVI-HS30/62	5/Lab/ZAF/62/OVI-HS30/62	SAMN03765194	KT030610 - KT030619	8637	ARC-OVI OIE Laboratory Reference Strain AHSV5	[44], TS					
African horse sickness virus 6 strain 6/Labstr/ZAF/1963/OVI-HS39/63	6/Lab/ZAF/63/OVI-HS39/63	SAMN03765195	KT030620 - KT030629	12422	ARC-OVI OIE Laboratory Reference Strain AHSV6	[44], TS					
African horse sickness virus 7 strain 7/Labstr/ZAF/1962/OVI-HS31/62	7/Lab/ZAF/62/OVI-HS31/62	SAMN03765197	KT030640 - KT030649	9632	ARC-OVI OIE Laboratory Reference Strain AHSV7	[44], TS					
African horse sickness virus 8 strain 8/Labstr/KEN/1962/OVI-HS10/62	8/Lab/KEN/62/OVI-HS10/62	SAMN03765198	KT030650 - KT030659	9208	ARC-OVI OIE Laboratory Reference Strain AHSV8	[44], TS					
African horse sickness virus 9 strain 9/Labstr/TCD/1961/OVI-HS90/61	9/Lab/TCD/61/OVI-HS90/61	SAMN03765199	KT030660 - KT030669	4957	ARC-OVI OIE Laboratory Reference Strain AHSV9	[44], TS					

[a] Strain Name is formatted as follows: <virus name> strain <type>/<isolation host-suffix>/<country of sampling>/<year of sampling>/<variant designation>-<isolate designation> where <virus name> is the taxonomic name of the virus, <type> is the type of the virus strain, <isolation host-suffix> the first letter of genus name.full name of species from which the samples were collected and the suffix -tc indicates the strain was propagated on tissue culture, <country of sampling> is the ISO 3166-1 alpha-3 code for the country of sampling, <year of sampling> is the 4 digit year in which the sample was collected, <variant designation> is the name of the region in which the sample was collected and <isolate designation> is the laboratory code given to the specific sample.

[b] Abbreviated Strain Name is formatted as follows: <type>/<isolation host-suffix>/<country of sampling>/<year of sampling>/<variant designation>-<isolate designation> where <type> is the type of the virus strain, <isolation host-suffix> four-letter format comprising first letter of genus name.first three letters of species from which the samples were collected and the suffix -tc indicated that the strain was propagated on tissue culture, <country of sampling> is the ISO 3166-1 alpha-3 code for the country of sampling, <year of sampling> is the 2 digit year in which the sample was collected and <variant designation> 3 letter code for the name of the region in which the sample was collected and <isolate designation> is the laboratory code given to the specific sample.

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African Horse Sickness Caused by Genome Reassortment and Reversion to Virulence of Live, Attenuated Vaccine Viruses, South Africa, 2004–2014

Technical Appendix 2

Technical Appendix Table 1. Summary of results of best-fit substitution models obtained using PhyML-SMS (Smart Model Selection) with the Akaike information criterion for the concatenated alignments of the complete AHSV genomes and individual AHSV gene segments of the strains included in this study

Gene	Model	Proportion invariable	Rate category	Gamma shape
Genome	GTR +G6	0	6	0.136
VP1	GTR +G6	0	6	0.261
VP2	GTR +G6 +I	0.186	6	1.196
VP3	GTR +G6	0	6	0.157
VP4	GTR +G6 +I	0.44	6	0.874
VP5	GTR +G6 +I	0.356	6	0.599
VP6	GTR +G6	0	6	0.459
VP7	GTR +G6 +I	0.616	6	1.379
NS1	GTR +G6 +I	0.606	6	1.184
NS2	GTR	0	1	
NS3	GTR +G6	0	6	0.652

Technical Appendix Table 2. RAMI indices describing the microdiverse genotype groups identified in AHSV-1 isolates from the 2004, 2011, and 2014 outbreaks of AHS in the Western Cape Province of South Africa

Cluster	Abundance	$X_{distance}$	$X_{depth,\ nearest}$	$X_{depth,\ deepest}$	$Y_{distance}$	$Y_{depth,\ nearest}$	$Y_{depth,\ deepest}$
1a	4	0.00011	0.000055	0.000055	0.120843	0.000274	0.17623
1b	11	0.000067	0.000034	0.000034	0.113798	0.004972	0.165405
1c	1	0	0	0			
2	7	0.00033	0.000102	0.000187	0.120925	0.00036	0.176316
3a	14	0.000121	0.000041	0.000062	0.114587	0.000173	0.166889
3b	2	0.000459	0.000229	0.000229	0.114779	0.000375	0.167091
Other	1	0	0	0			
Average	6.5	0.0002174	0.0000922	0.0001134	0.1169864	0.0012308	0.1703862

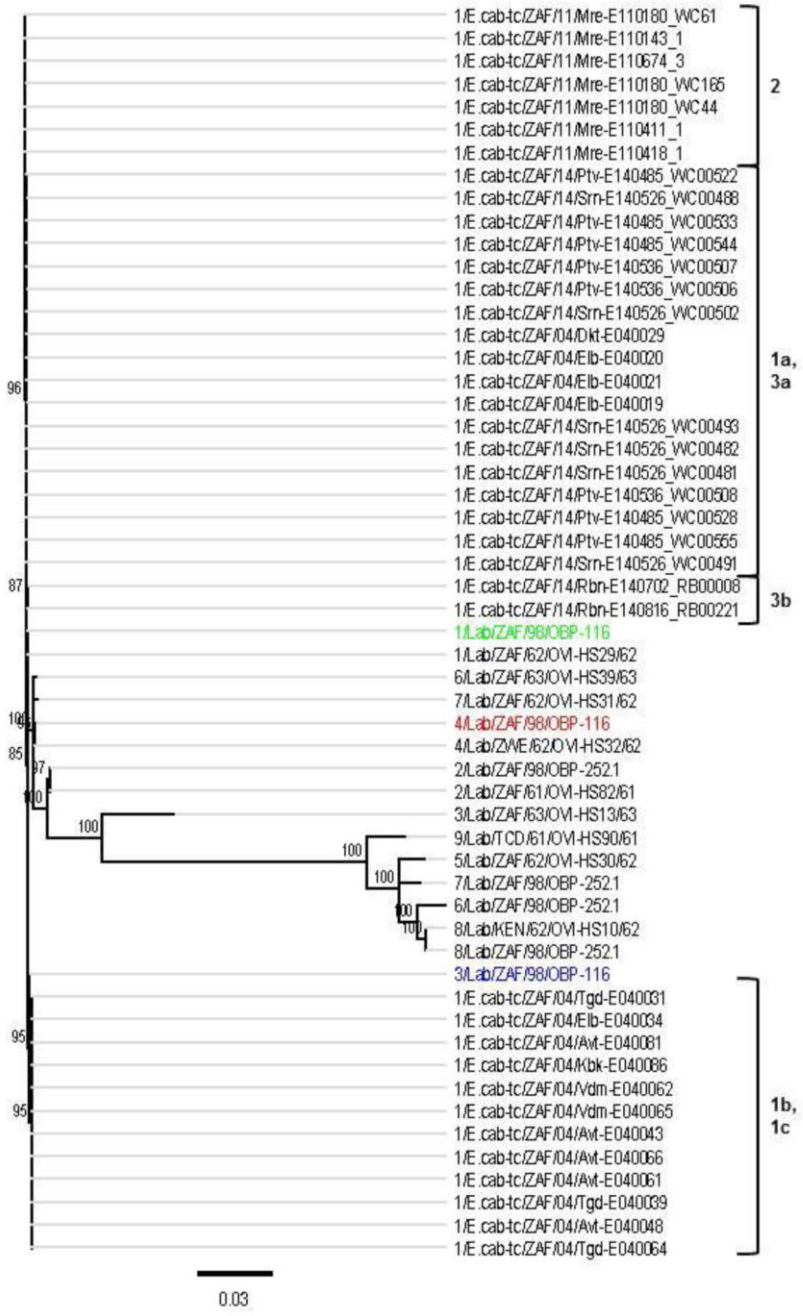
Technical Appendix Table 3. Summary statistics (p values) of tests for reassortment of gene segments of AHSV using 7 methods incorporated within RDP4

	Gene				
Method	VP1	VP4	VP5	VP7	NS3
RDP	NS	NS	3.60×10^{-298}	1.22×10^{-31}	6.17×10^{-238}
GENECONV	NS	5.83×10^{-2}	1.87×10^{-293}	1.13×10^{-31}	9.31×10^{-240}
Bootscan	NS	7.66×10^{-4}	2.95×10^{-298}	1.22×10^{-31}	5.55×10^{-238}
Maxchi	NS	NS	3.55×10^{-46}	1.39×10^{-5}	1.25×10^{-37}
Chimaera	NS	NS	8.97×10^{-48}	5.93×10^{-5}	9.88×10^{-38}
SiSscan	NS	NS	1.29×10^{-63}	6.38×10^{-6}	2.30×10^{-45}
3Seq	$2.\ 27 \times 10^{-12}$	NS	1.22×10^{-13}	NS	2.20×10^{-182}

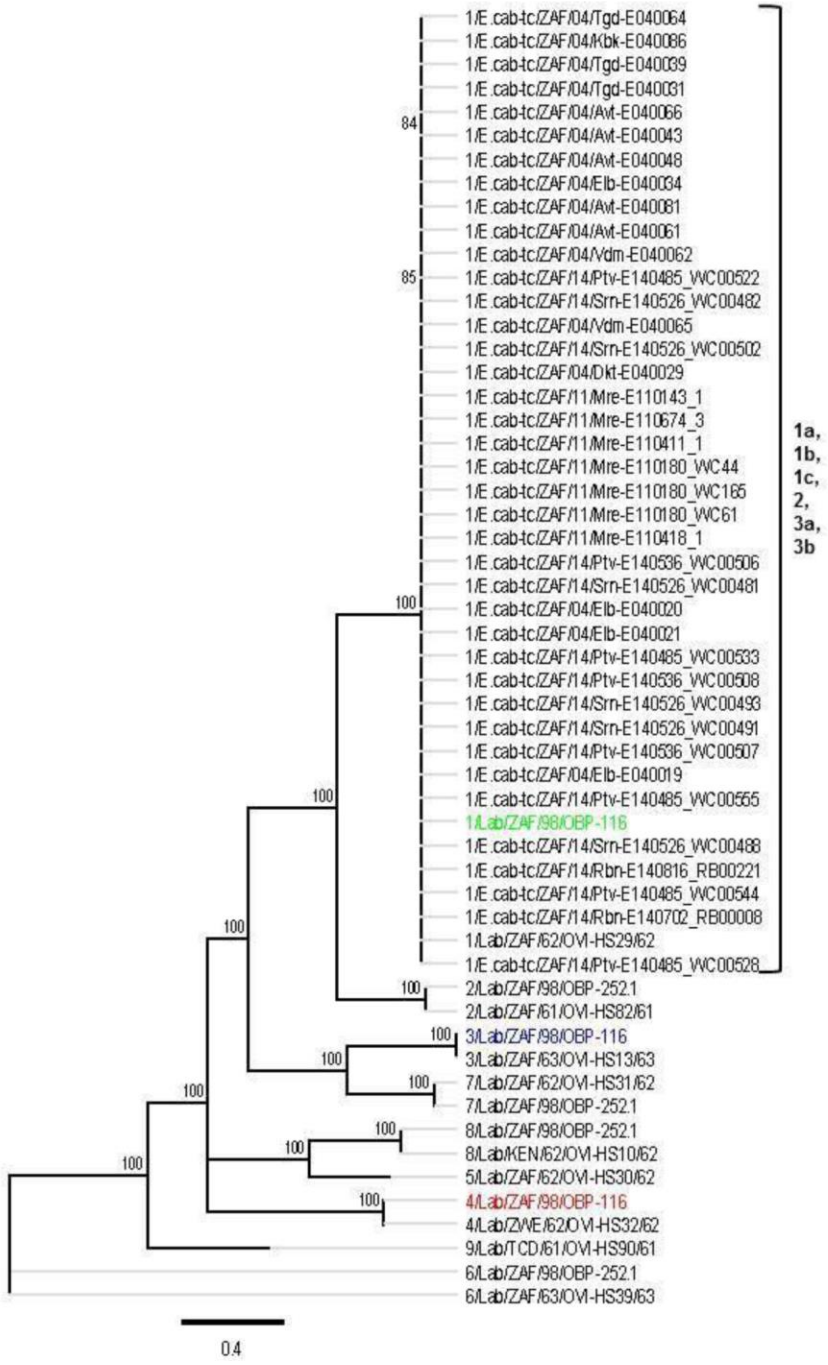
Technical Appendix Table 4. Summary of single nucleotide variants (SNVs) observed in NS1 of 1/Lab/ZAF/98/OBP-116 and 3/Lab/ZAF/98/OBP-116 vaccine derived strains and strains isolated during 2014 AHS outbreaks in Porterville and Robertson

	Virus strains				
Position	1/OBP-116 (+11)	3/OBP-116	1/Srn-WC00481	1/RB00008	1/RB00221
839 (268)*	U (A)†	U (A)	U (A)	A (A)	A (A)
884 (283)	U (Y)	U (Y)	C (Y)	U (Y)	U (Y)
1126 (264)	U (I)	C (T)	U (I)	C (T)	C (T)
1191 (386)	U (L)	U (L)	U (L)	C (L)	C (L)
1382 (449)	G (T)	G (T)	G (T)	G (T)	A (T)
1392 (453)	G (E)	G (E)	G (E)	C (Q)	C (Q)

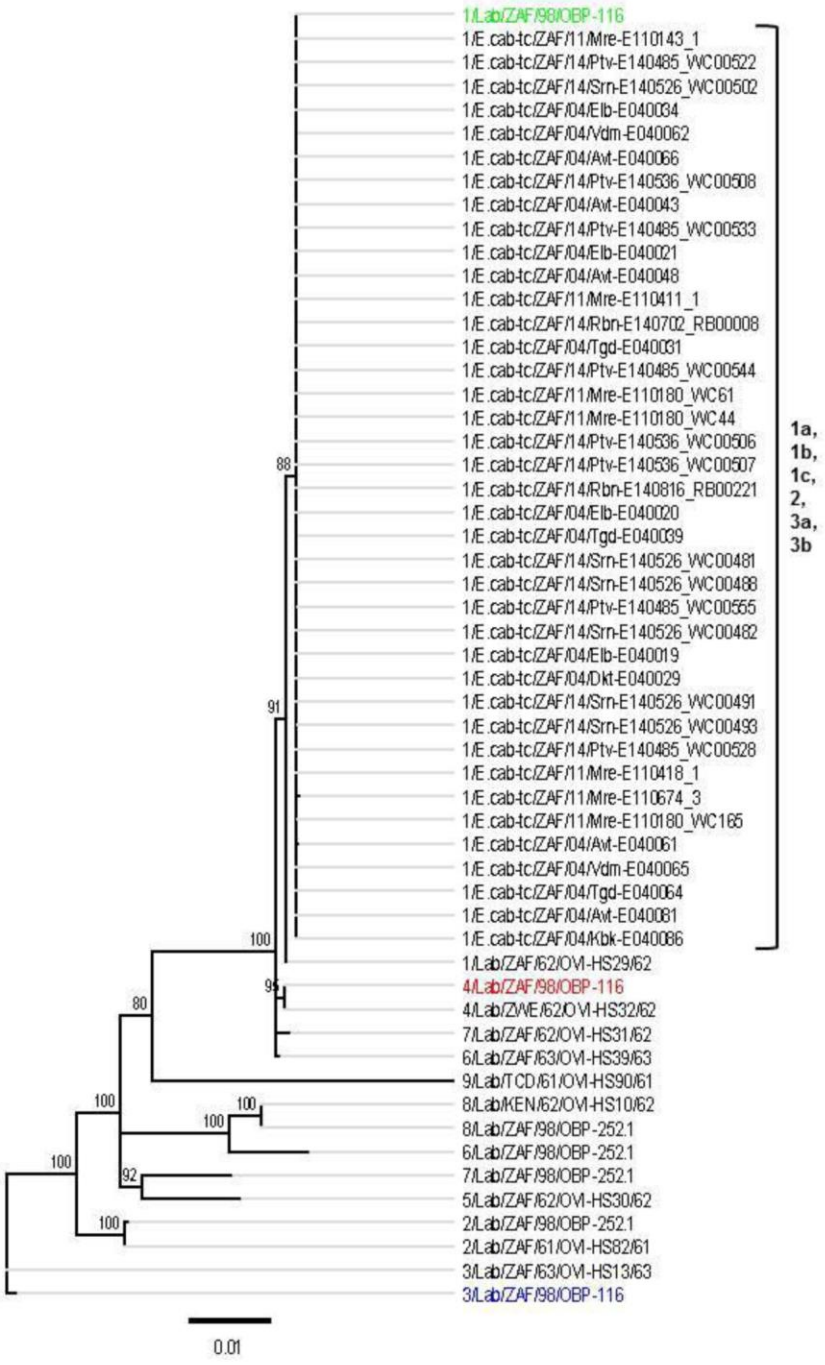
*Position given as nucleotide and (amino acid).
†SNVs given as nucleotide and (amino acid).



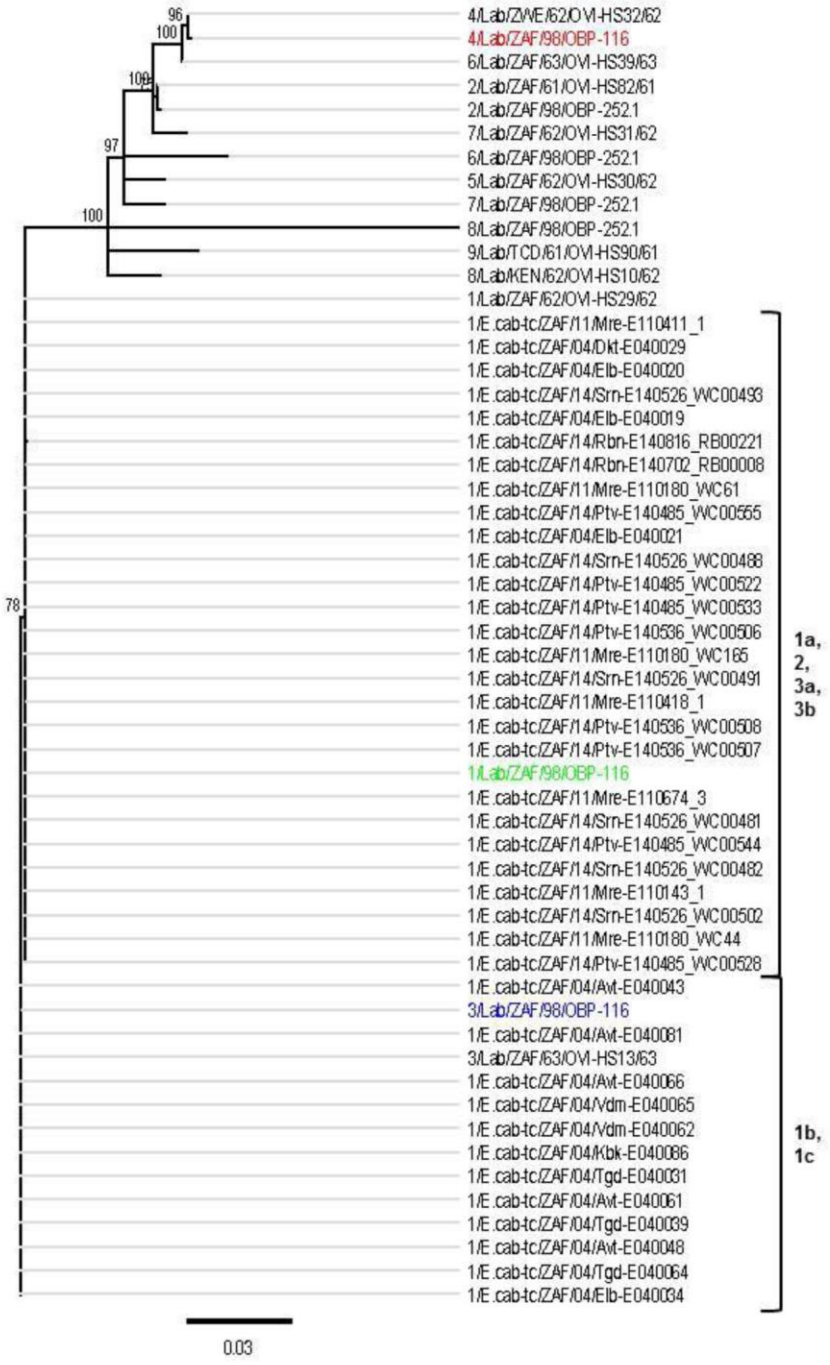
Technical Appendix Figure 1. Maximum-likelihood phylogenetic tree indicating the genetic relationships of concatenated VP1 nucleotide sequences from affected horses in the 2004, 2011 and 2014 outbreaks in the AHS controlled area to the AHSV live, attenuated vaccine and reference viruses. Branches are scaled to represent numbers of inferred nucleotide differences per site with the scale bar at the bottom of the tree indicating genetic distance. Branches supported by full maximum-likelihood bootstrap values >70% are indicated. Genotype groups are indicated with brackets and group names to the right of the tree.



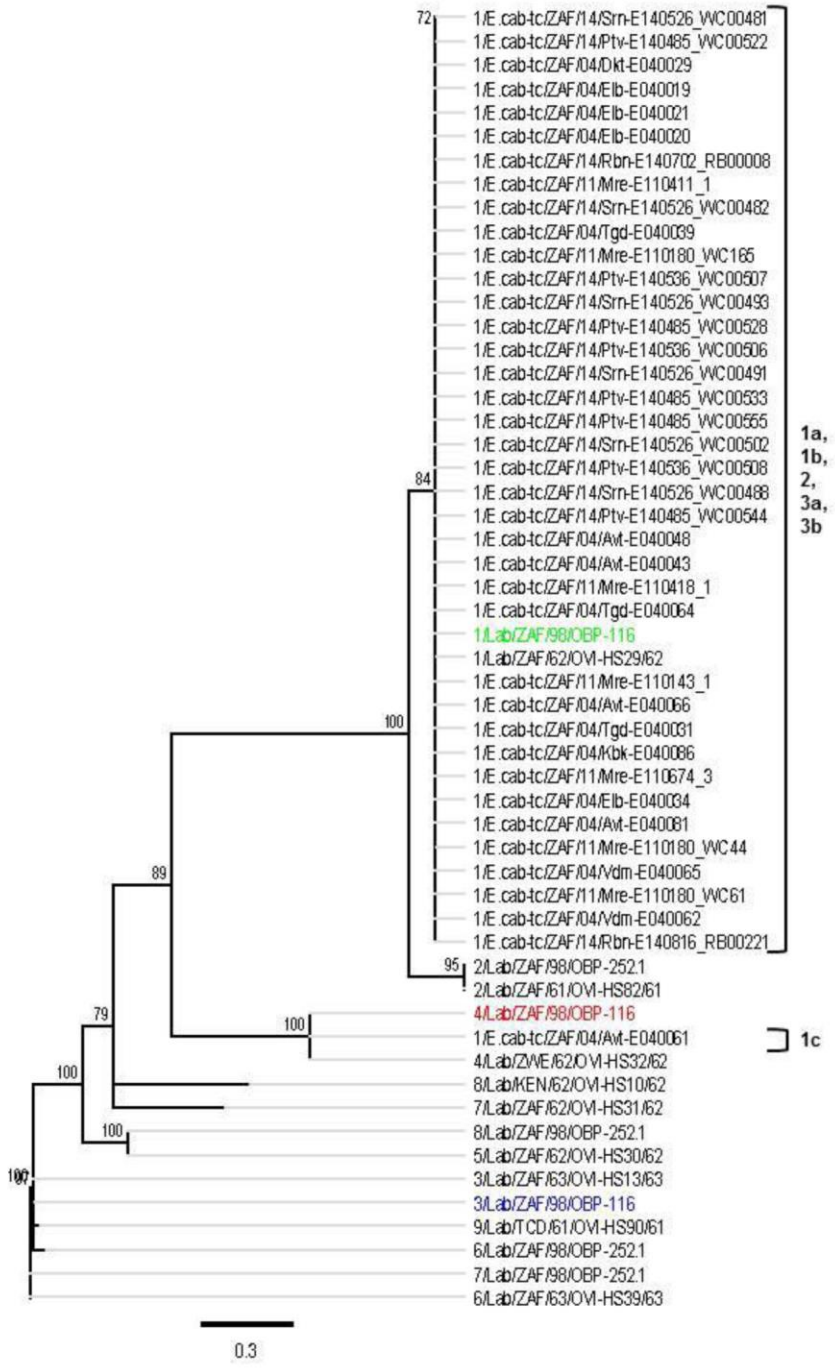
Technical Appendix Figure 2. Maximum-likelihood phylogenetic tree indicating the genetic relationships of concatenated VP2 nucleotide sequences from affected horses in the 2004, 2011 and 2014 outbreaks in the AHS controlled area to the AHSV live, attenuated vaccine and reference viruses.



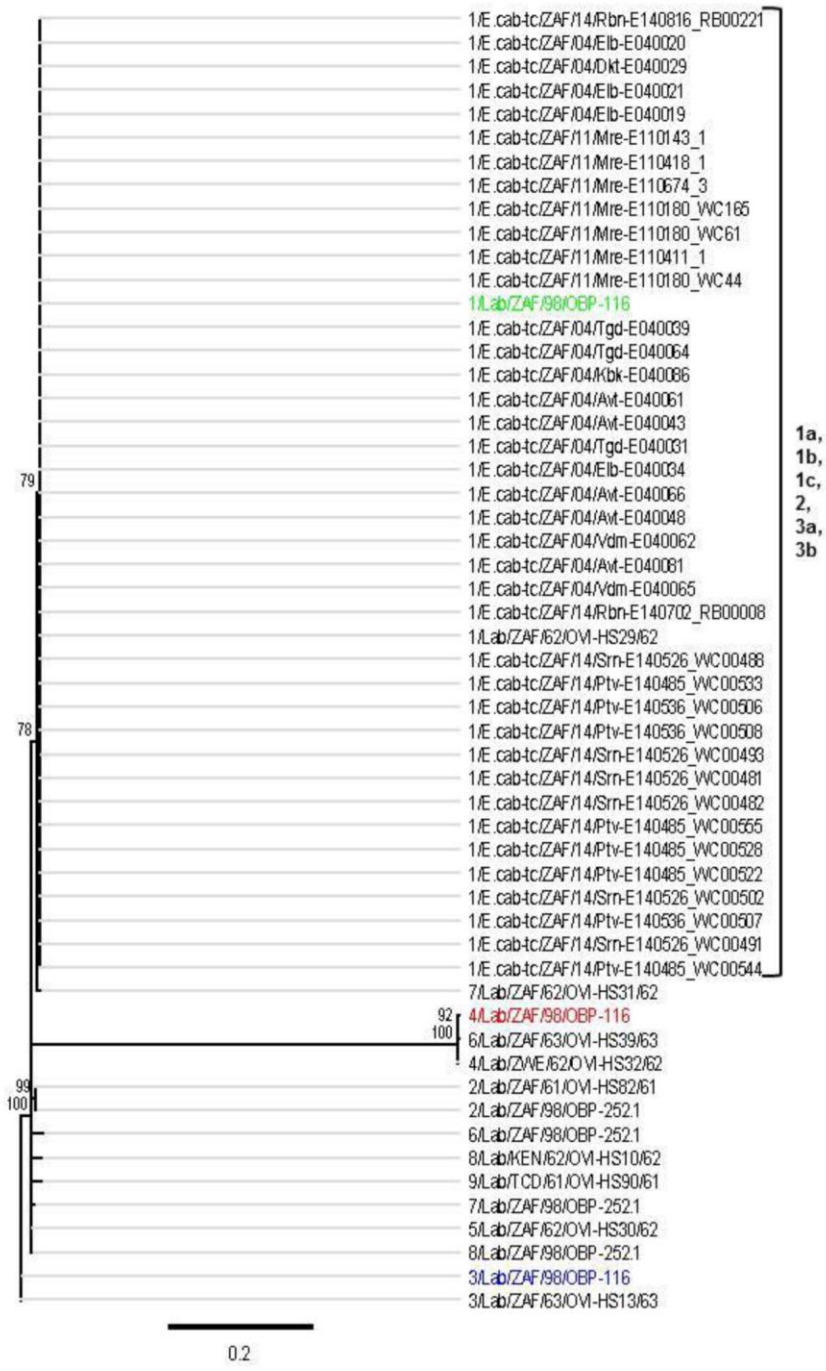
Technical Appendix Figure 3. Maximum-likelihood phylogenetic tree indicating the genetic relationships of concatenated VP3 nucleotide sequences from affected horses in the 2004, 2011 and 2014 outbreaks in the AHS controlled area to the AHSV live, attenuated vaccine and reference viruses.



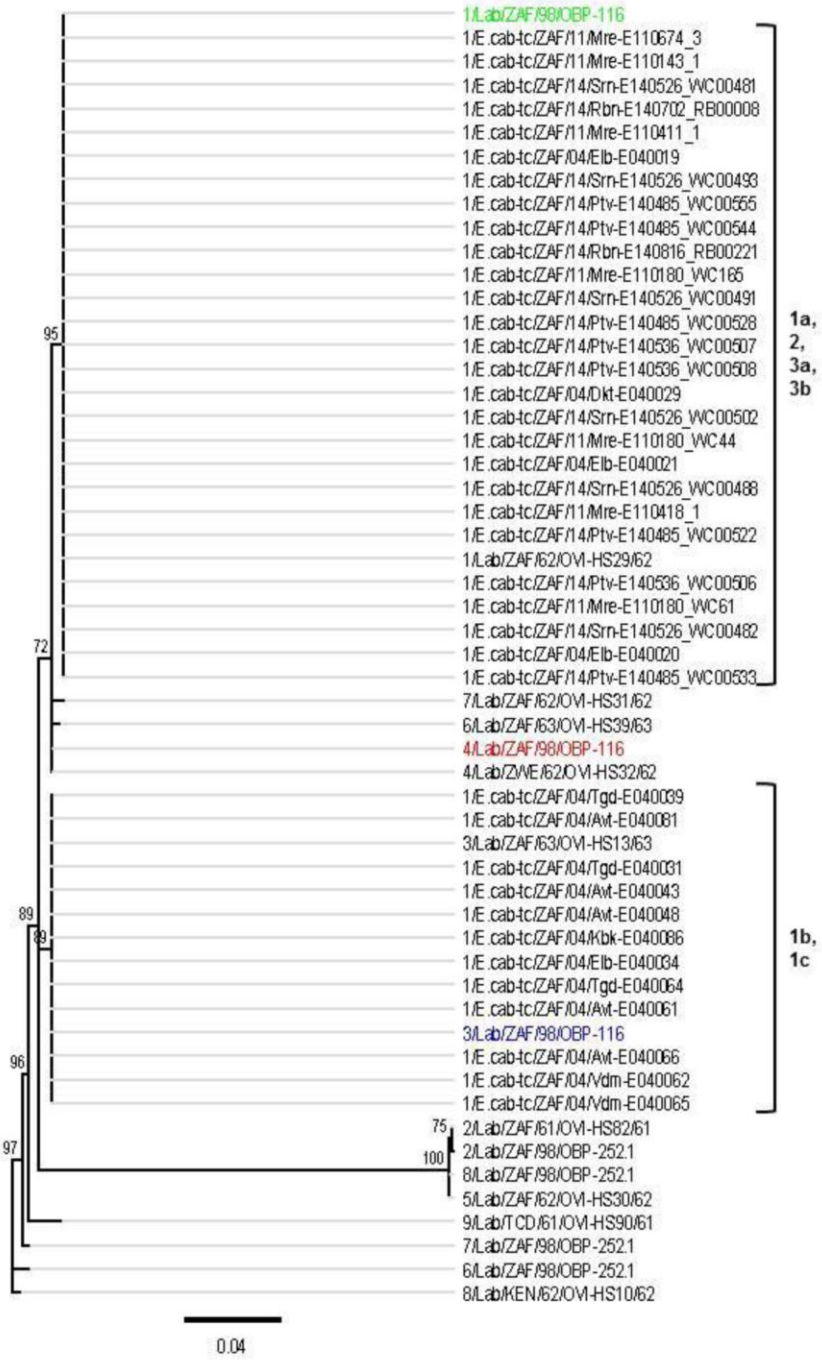
Technical Appendix Figure 4. Maximum-likelihood phylogenetic tree indicating the genetic relationships of concatenated VP4 nucleotide sequences from affected horses in the 2004, 2011 and 2014 outbreaks in the AHS controlled area to the AHSV live, attenuated vaccine and reference viruses.



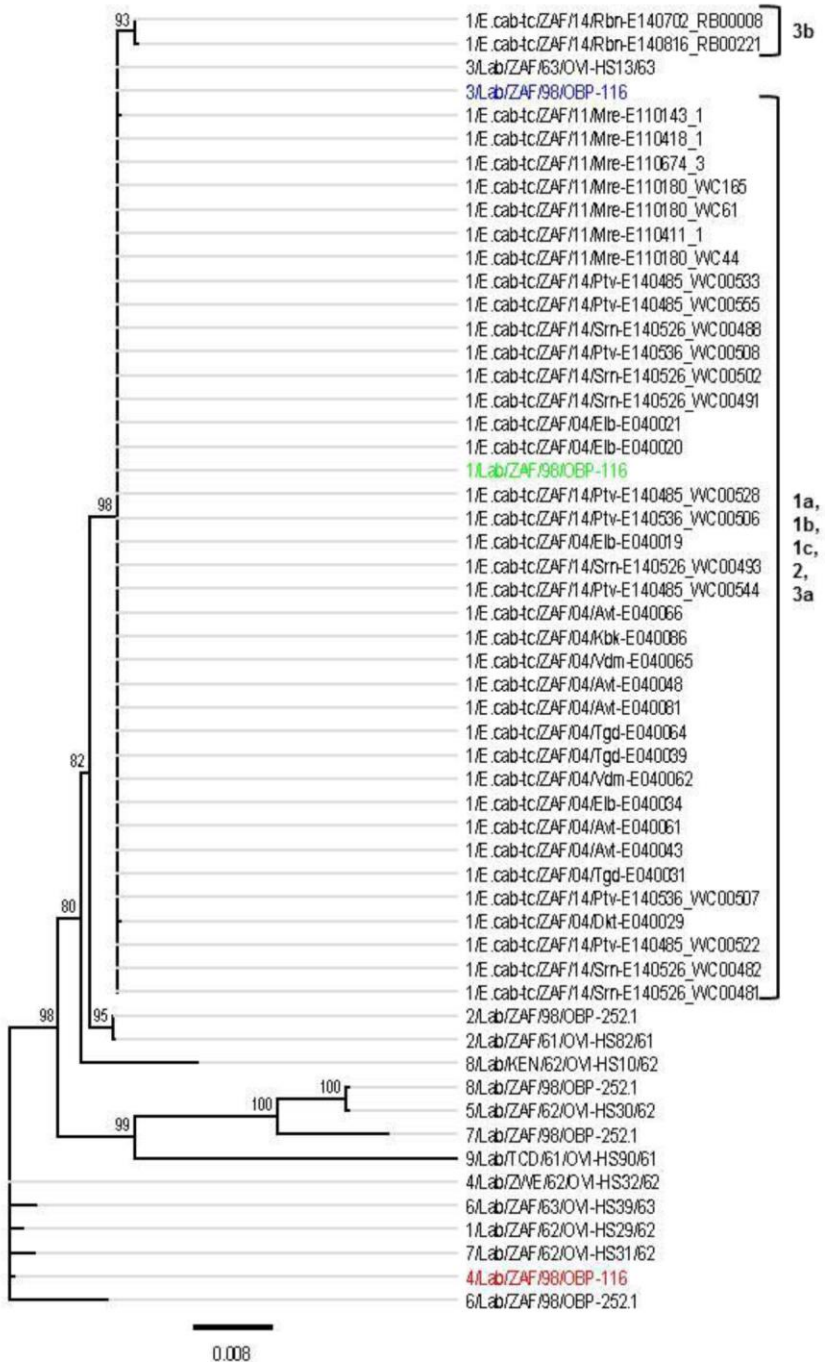
Technical Appendix Figure 5. Maximum-likelihood phylogenetic tree indicating the genetic relationships of concatenated VP5 nucleotide sequences from affected horses in the 2004, 2011 and 2014 outbreaks in the AHS controlled area to the AHSV live, attenuated vaccine and reference viruses.



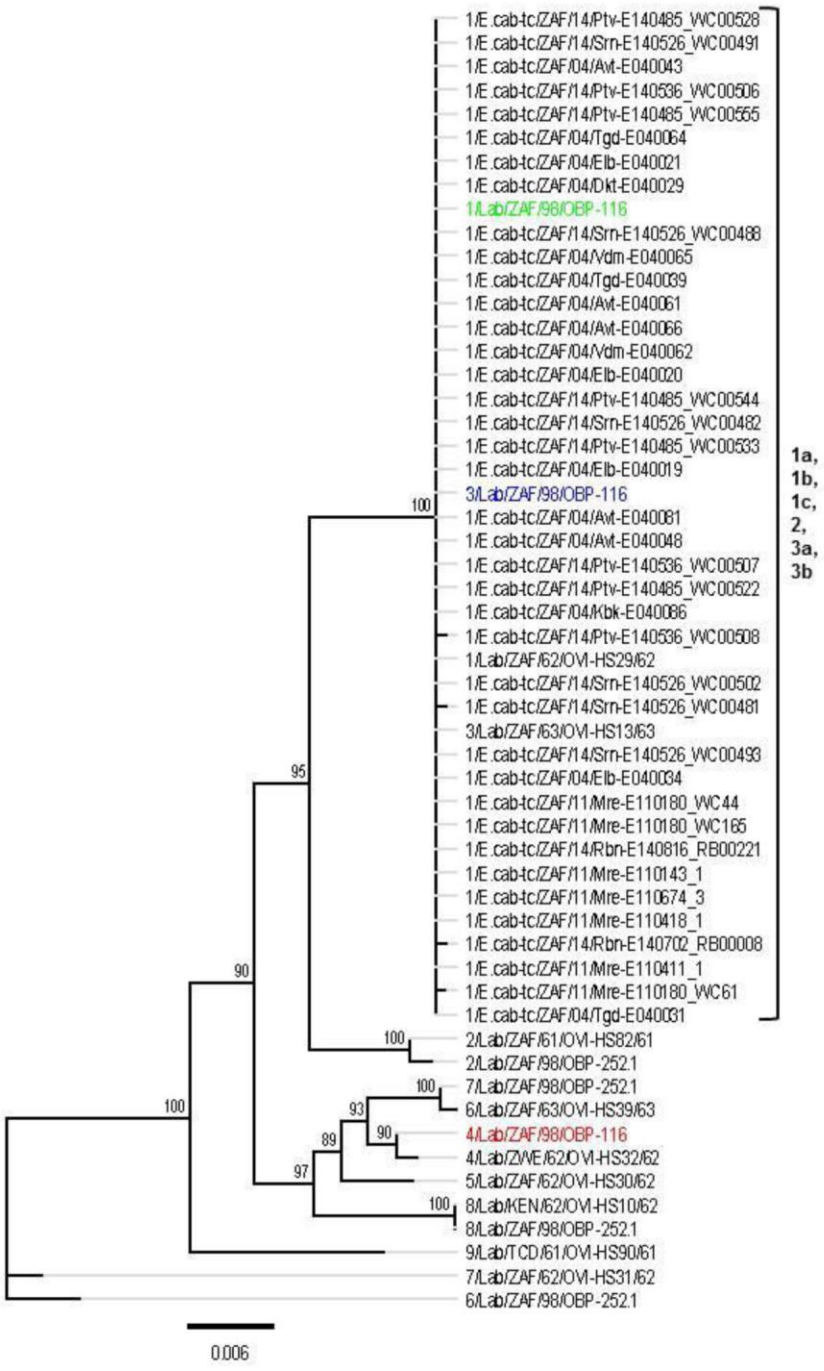
Technical Appendix Figure 6. Maximum-likelihood phylogenetic tree indicating the genetic relationships of concatenated VP6 nucleotide sequences from affected horses in the 2004, 2011 and 2014 outbreaks in the AHS Controlled Area to the AHSV live, attenuated vaccine and reference viruses.



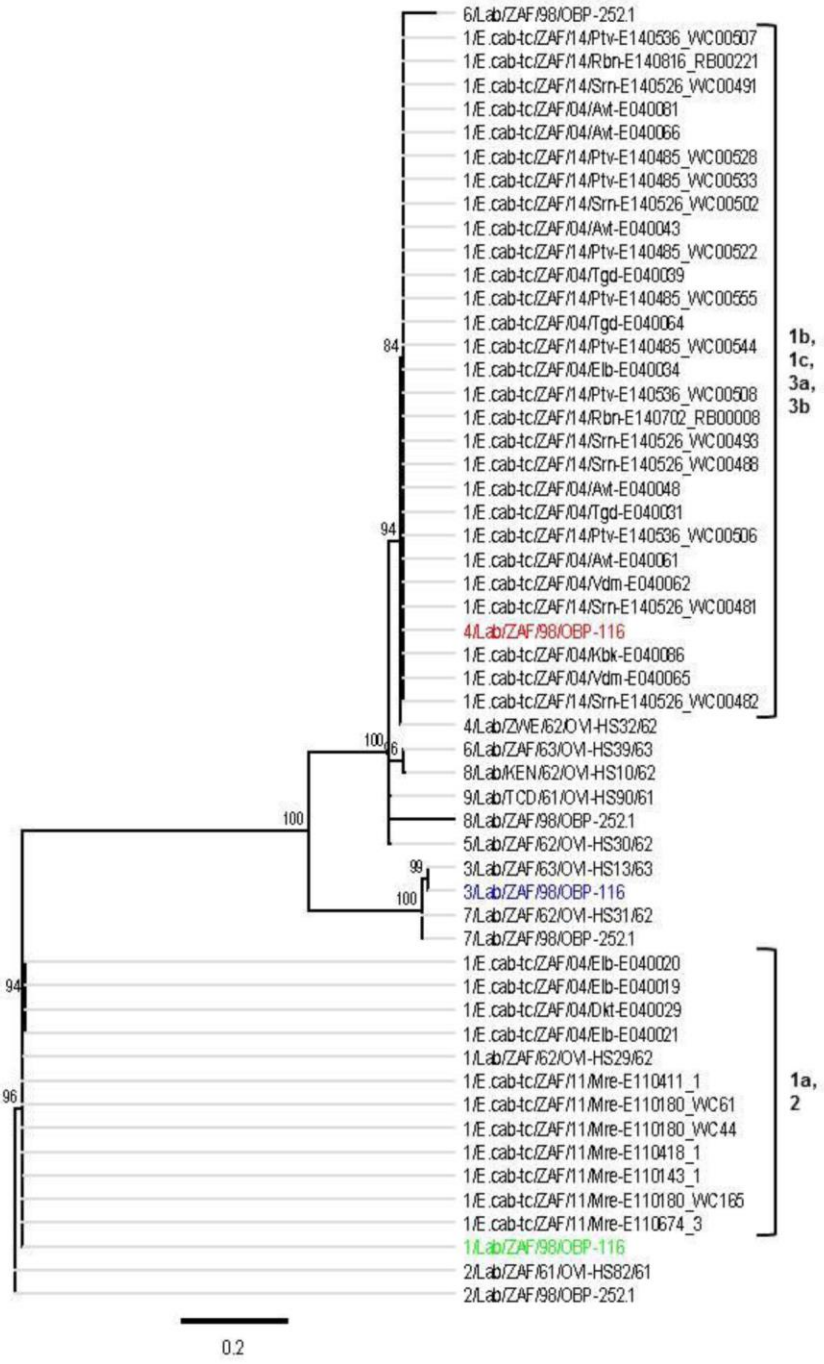
Technical Appendix Figure 7. Maximum-likelihood phylogenetic tree indicating the genetic relationships of concatenated VP7 nucleotide sequences from affected horses in the 2004, 2011 and 2014 outbreaks in the AHS Controlled Area to the AHSV live, attenuated vaccine and reference viruses.



Technical Appendix Figure 8. Maximum-likelihood phylogenetic tree indicating the genetic relationships of concatenated NS1 nucleotide sequences from affected horses in the 2004, 2011 and 2014 outbreaks in the AHS Controlled Area to the AHSV live, attenuated vaccine and reference viruses.



Technical Appendix Figure 9. Maximum-likelihood phylogenetic tree indicating the genetic relationships of concatenated NS2 nucleotide sequences from affected horses in the 2004, 2011 and 2014 outbreaks in the AHS Controlled Area to the AHSV live, attenuated vaccine and reference viruses.



Technical Appendix Figure 10. Maximum-likelihood phylogenetic tree indicating the genetic relationships of concatenated NS3 nucleotide sequences from affected horses in the 2004, 2011 and 2014 outbreaks in the AHS Controlled Area to the AHSV live, attenuated vaccine and reference viruses.