



Genetic Analysis of Powassan Virus Circulating in North America

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Introduction

Powassan virus (POWV), a tick-borne flavivirus, is the only member of the tick-borne encephalitis serogroup found in North America (1). It was first isolated in 1959 (1), and, since that time, two distinct lineages, Powassan virus (POWV, lineage I) and deer tick virus (DTV, lineage II) have been described (2) which are transmitted by different tick species based on geographical regions. In North America, *Ixodes cookei* (groundhog tick) acts as the primary vector of POWV throughout the Midwest and much of Canada (3), and *Ixodes scapularis* (deer tick) acts as the primary vector of DTV throughout the Northeast (4). Importantly, the incidence of human disease due to POWV has increased by 671% over the last 18 years; with DVT perhaps being the most worrisome genotype due to the wide spread range and prevalence of the vector species (5).

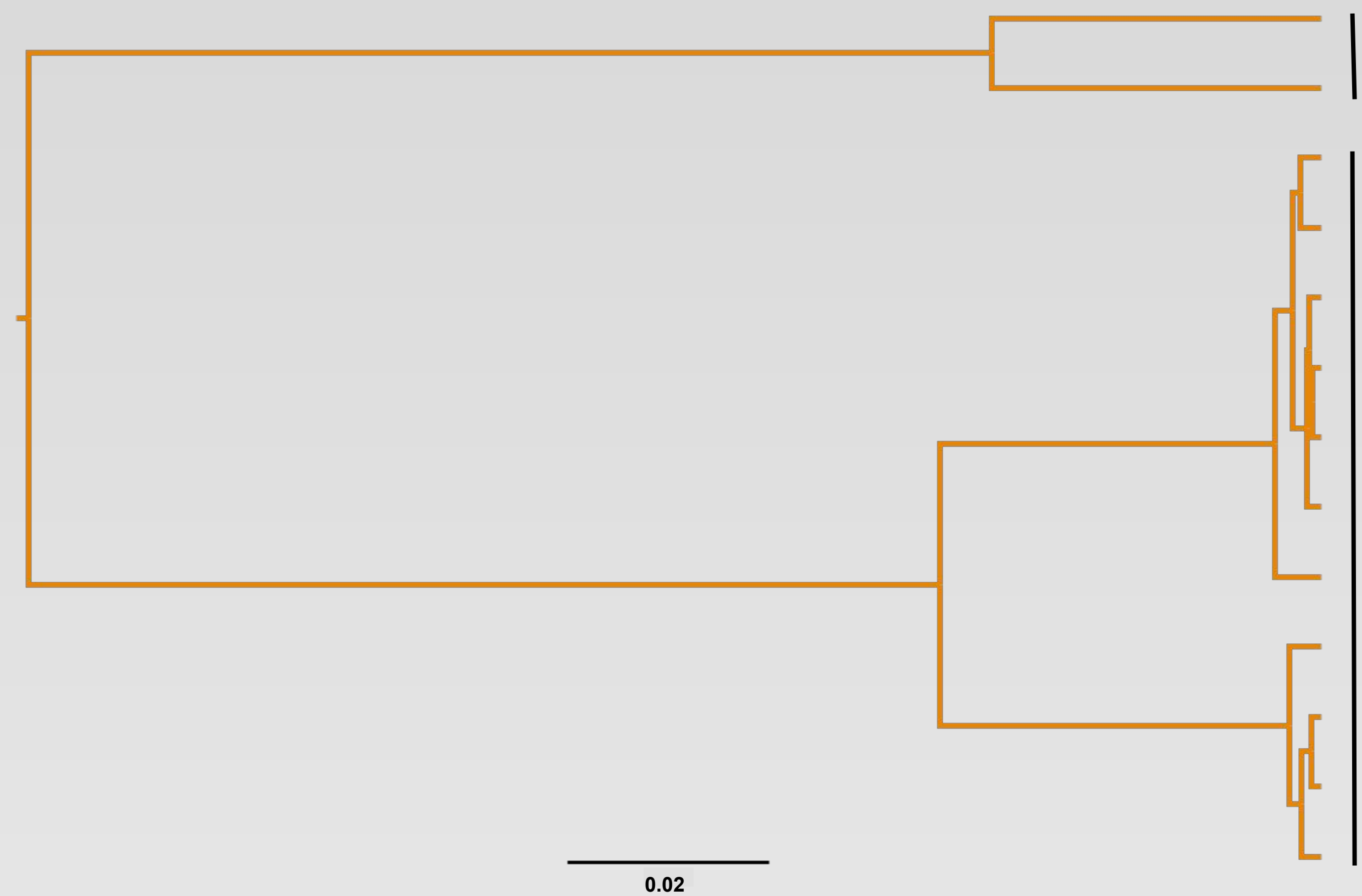


Figure 2: Phylogenetic analysis of POWV sequences of the complete genome (10635 nt). Sequence data were aligned using MEGA, version 7.0.26. Phylogenetic analysis was performed using the General Time Reversible model of nucleotide substitution. Programs from the BEAST package were used to produce phylogenetic trees. The statistical significance of the tree topology is represented by the posterior probability score. Lineages (I and II) are given on the right.

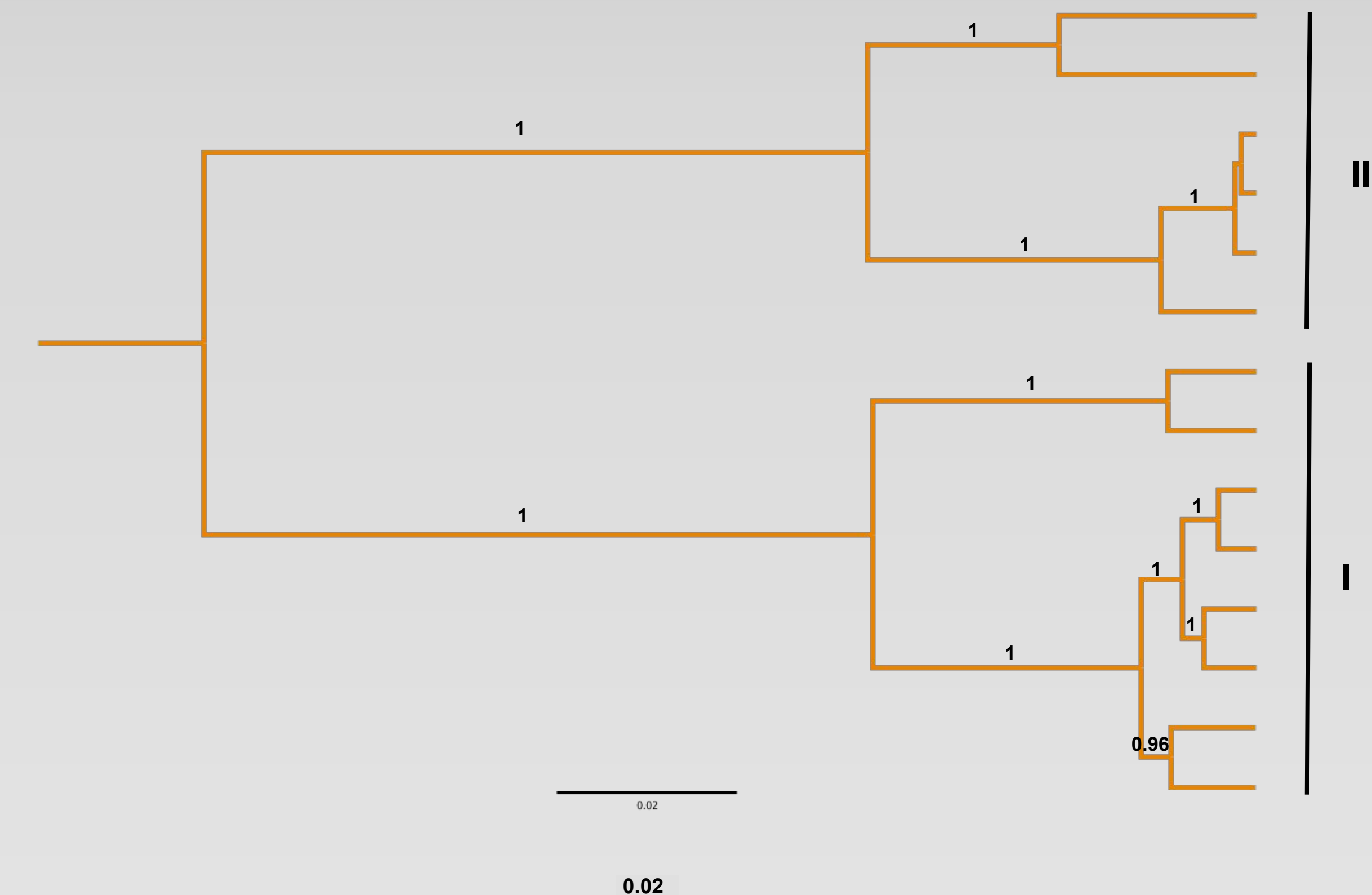


Figure 3: Phylogenetic analysis of POWV sequences of the non-structural protein NS5 region (2710 nt). Sequence data were aligned using MEGA, version 7.0.26. Phylogenetic analysis was performed using the General Time Reversible model of nucleotide substitution. Programs from the BEAST package were used to produce phylogenetic trees. The statistical significance of the tree topology is represented by the posterior probability score. Lineages (I and II) are given on the right.

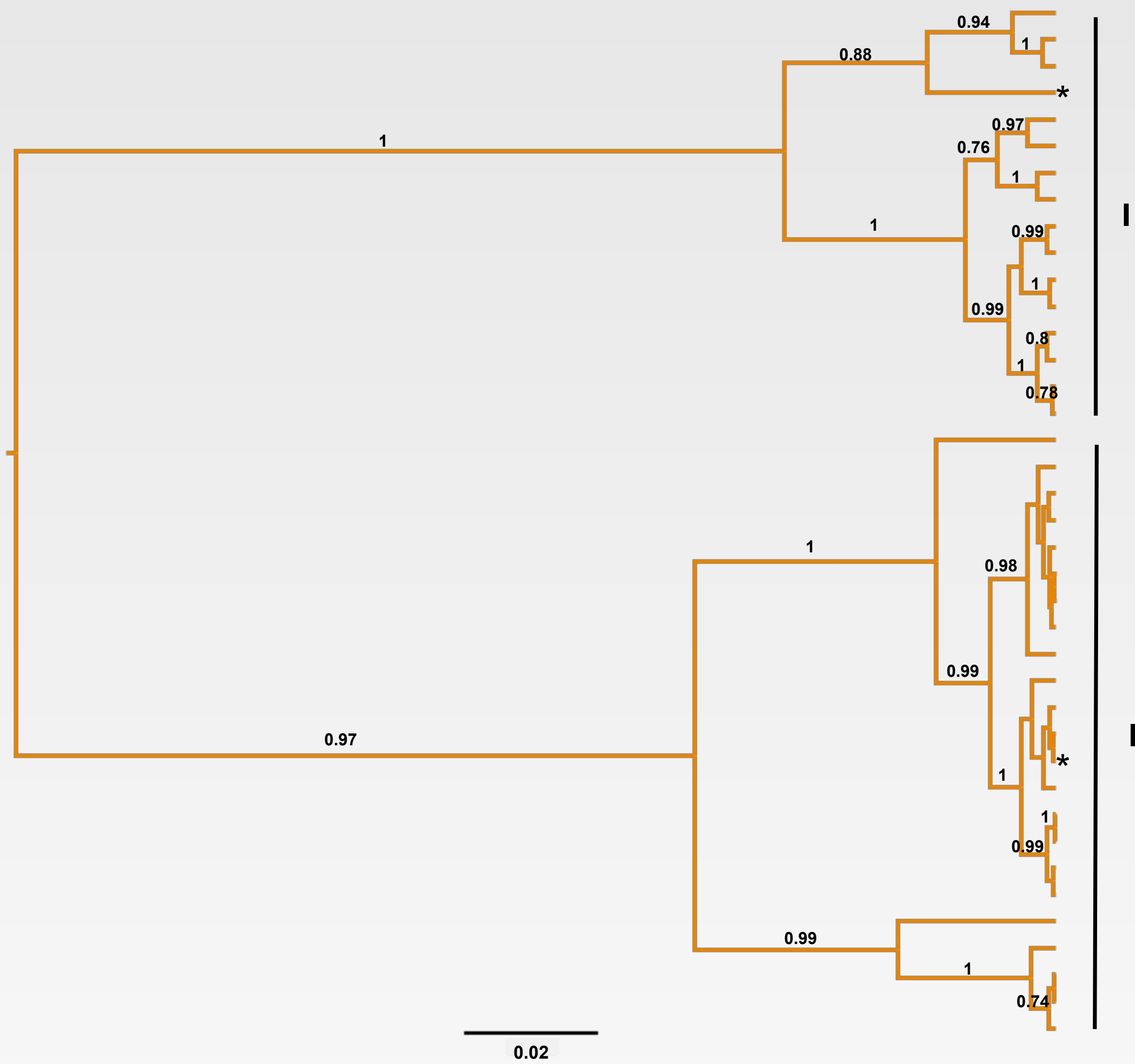


Figure 1: Phylogenetic analysis of POWV sequences of the envelope region (522 nt). Sequence data were aligned using MEGA, version 7.0.26. Phylogenetic analysis was performed using the General Time Reversible model of nucleotide substitution. Programs from the BEAST package were used to produce phylogenetic trees. The statistical significance of the tree topology is represented by the posterior probability score. Lineages (I and II) are given on the right.

Discussion

- Phylogenetic analyses using both partial and whole-genome sequences found support for two distinct lineages of POWV
- Isolates taken from overlapping geographic regions were placed in two separate lineages (See * samples in ENV tree)
- No recombination was detected in either gene region or whole-genome sequences
- Our results are concordant with previously published data

Future Directions

To better understand the Powassan virus and its effects on the tick community and human populations, more work needs to be done to investigate the presence and prevalence of this virus in natural populations. To this end, our lab at the University of Findlay works to survey the ticks of western Ohio for several viruses, including the Powassan virus, in the hopes of better understanding the viral population dynamics and increasing the body of knowledge for these under-studied viruses.

Table 1: Phylogeny-trait association tests of the structural region of DWV by geographic location and year of collection

	Index Ratio, observed to expected	Observed values (95% CI)	Expected values (95% CI)	P-value
<i>Association Index</i>				
Location	0.87	1.04 (0.96-1.12)	1.20 (0.83-1.53)	0.28
Year	0.74	1.04 (0.96-1.13)	1.40 (1.06-1.57)	0.04
<i>Parsimony Score (PS)</i>				
Location	0.90	7.00 (7.00-7.00)	7.76 (6.00-9.00)	0.34
Year	0.87	8.00 (8.00-8.00)	9.20 (8.00-10.00)	0.11

References

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