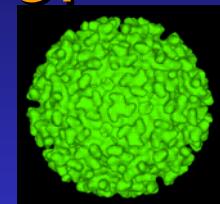




Epiornitic determinants of West Nile virus in North America: a murder of crows

CDC WNV annual meeting
February 23, 2006, San Francisco, CA

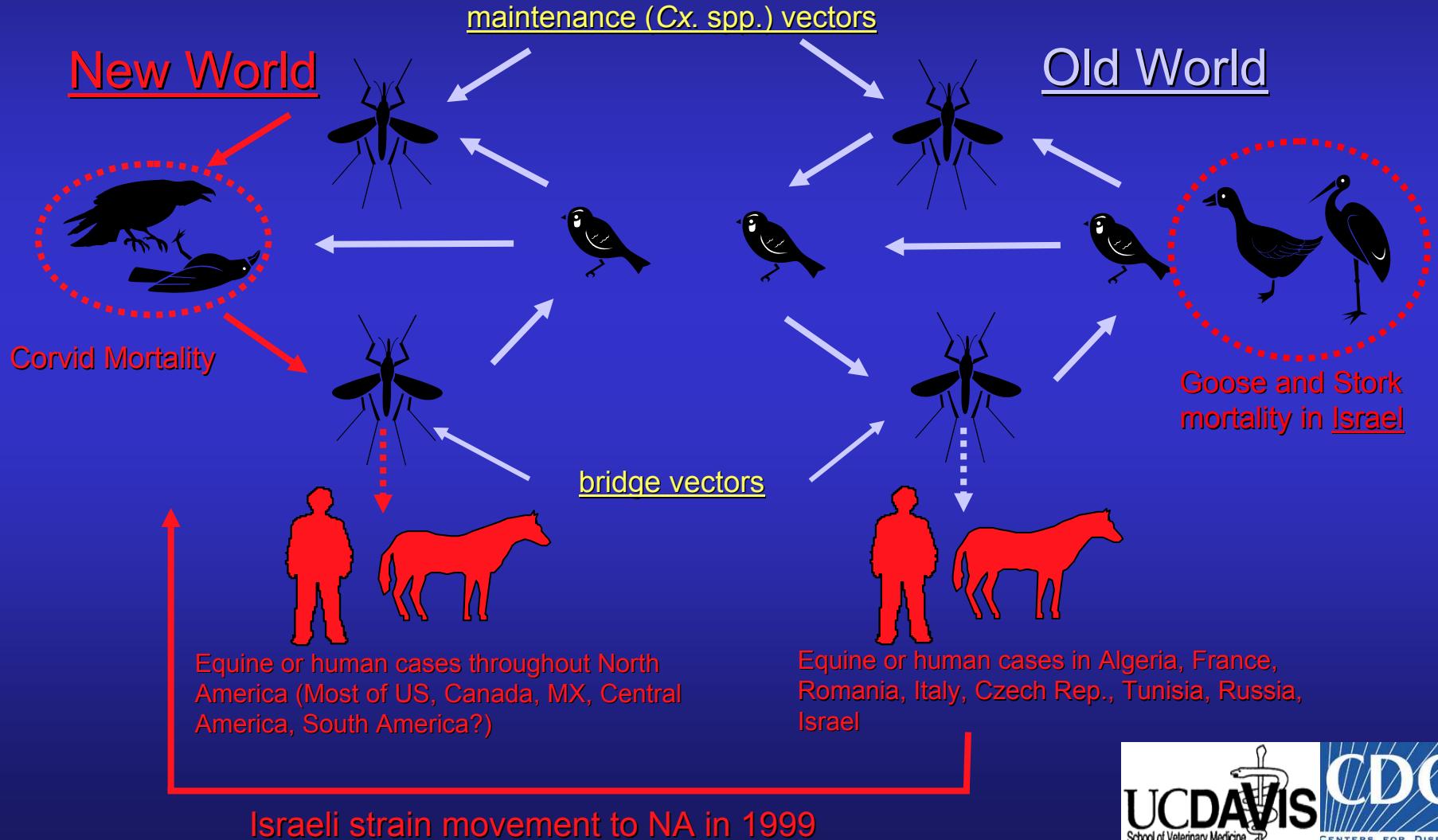


Aaron C. Brault^{1,2,3}, Stanley A. Langevin^{1,3}, Richard A. Bowen⁴,
Leslie Woods^{2,5}, Nicholas A. Panella³, Claire Y.-H. Huang³,
Nicholas Komar³, Ann M. Powers³, Barry R. Miller³, Richard M.
Kinney³, David W.C. Beasley⁶ and Alan D.T. Barrett⁶

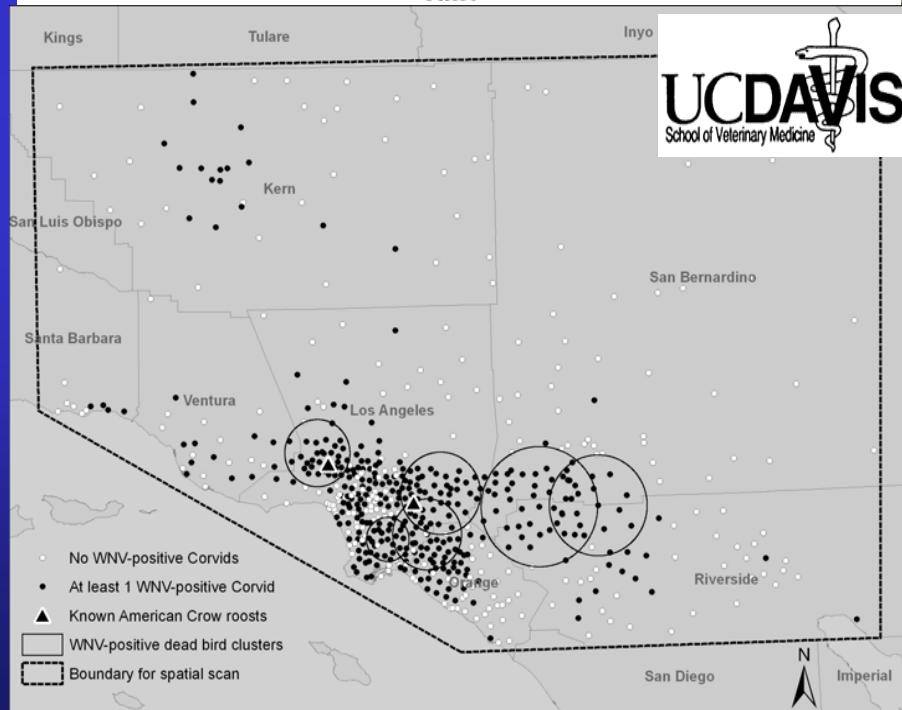
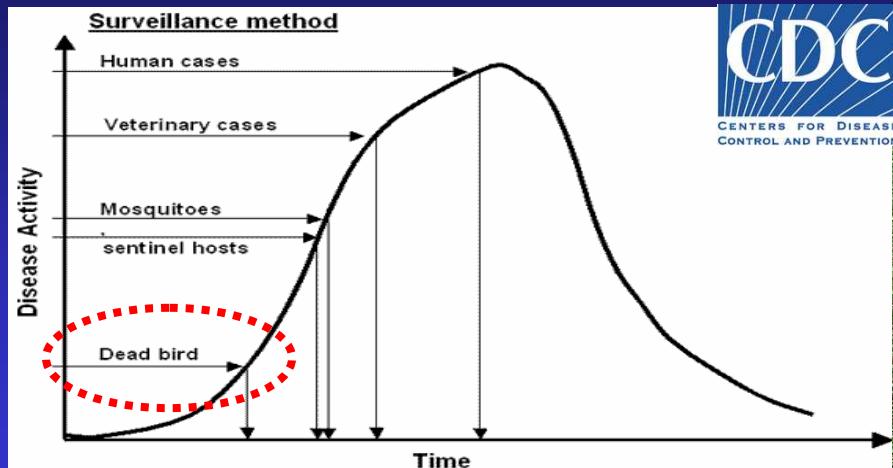
¹Center for Vector-borne Diseases, ²Department of Pathology, Microbiology and Immunology, School of Veterinary Medicine, University of California, Davis, CA; ³Division of Vector-Borne Infectious Diseases, National Center for Infectious Diseases, Centers for Disease Control and Prevention, U.S. Department of Health and Human Services, Fort Collins, CO; ⁴Department of Biomedical Sciences, Colorado State University, Fort Collins, CO; ⁵California Animal Health and Food Safety Laboratory, Davis, CA.; Center for Tropical Diseases and Department of Pathology, University of Texas Medical Branch, Galveston, TX



West Nile viral transmission cycles

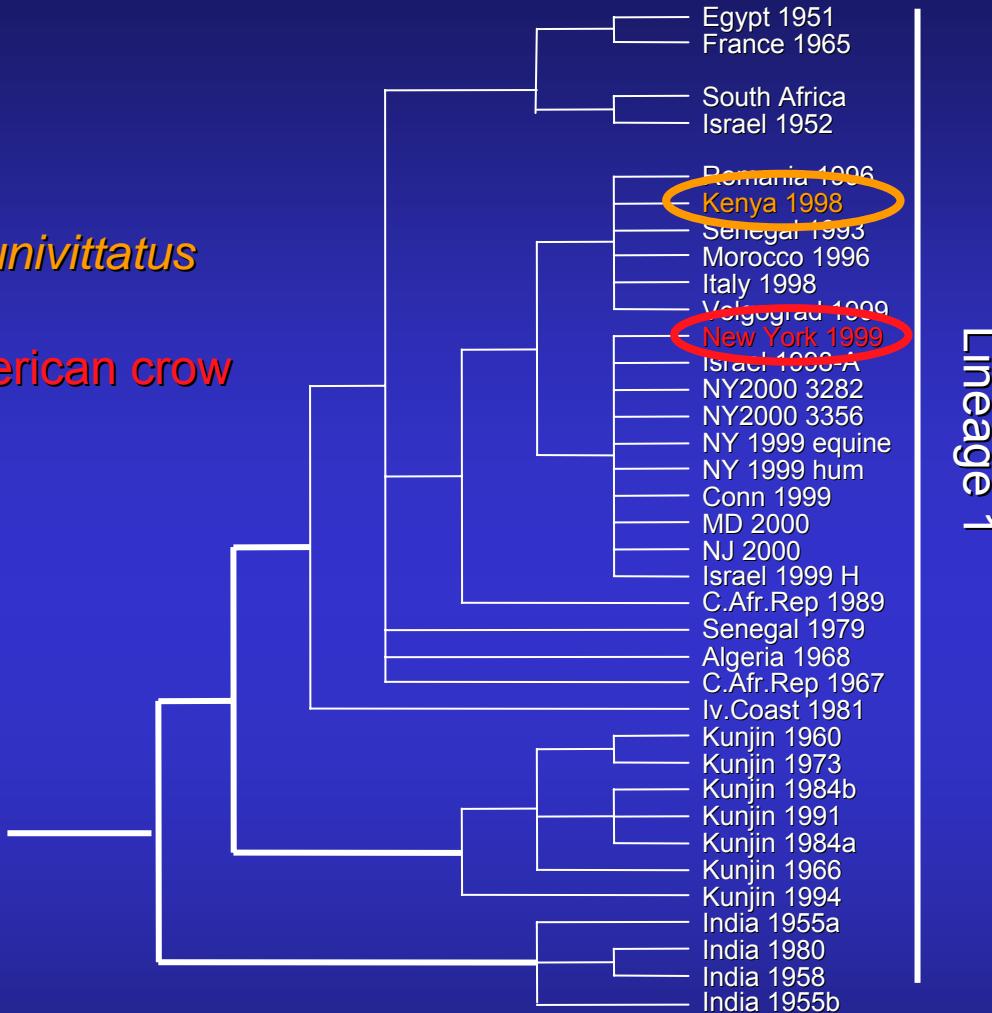


American crow mortality as a sentinel for WN viral activity



Phylogenetic Relationships among West Nile Viruses

Kenya-98- *Culex univittatus*
(V1, BHK1)
New York-99- American crow
(V1)

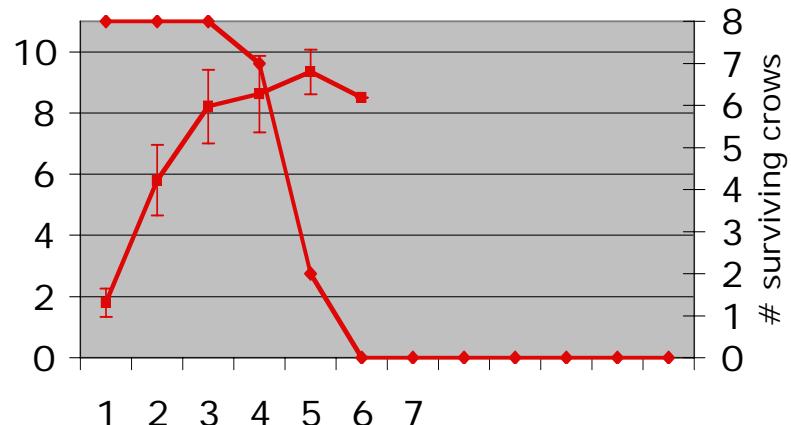


Lineage 1

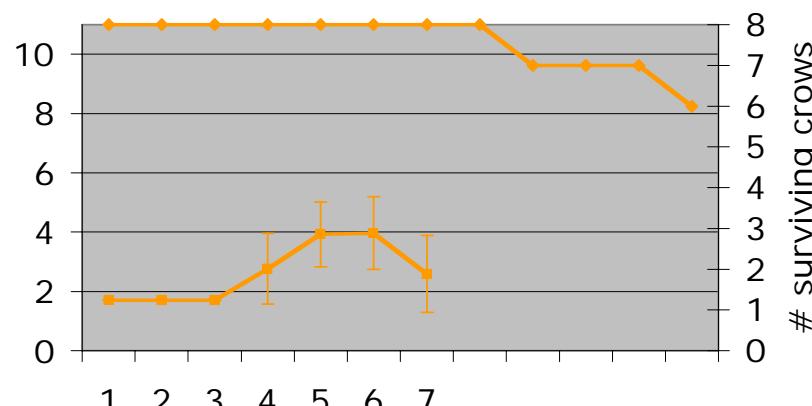
Lanciotti, R. S., J. T. Roehrig, V. Deubel, J. Smith, M. Parker, K. Steele, B. Crise, K. E. Volpe, M. B. Crabtree, J. H. Scherret, R. A. Hall, J. S. MacKenzie, C. B. Cropp, B. Panigrahy, E. Ostlund, B. Schmitt, M. Malkinson, C. Banet, J. Weissman, N. Komar, H. M. Savage, W. Stone, T. McNamara, and D. J. Gubler. 1999. Origin of the West Nile virus responsible for an outbreak of encephalitis in the northeastern United States. *Science* 286:2333-7.

Viremia and survival data for crows inoculated with WNVs

NY-99 survival vs viral product

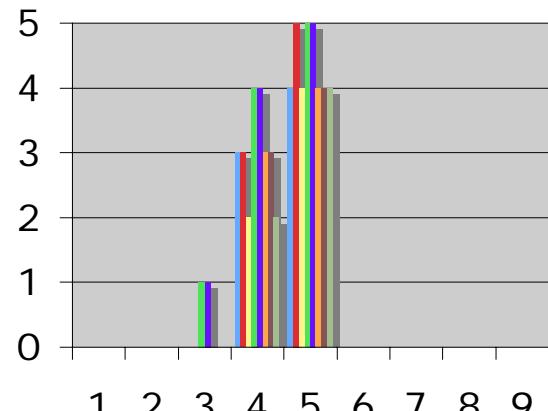


KEN survival vs. viremia



heart
liver
lung
spleen
kidney
intestine
muscle
brain

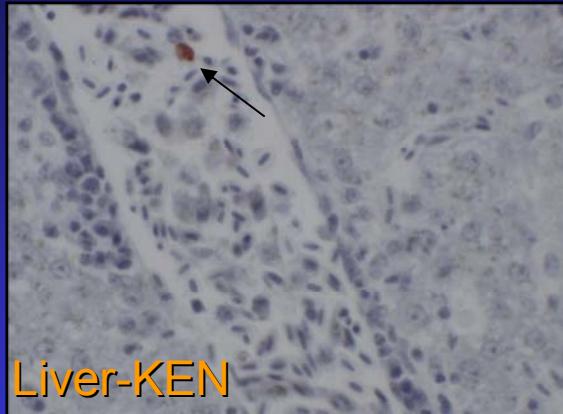
days post-infection



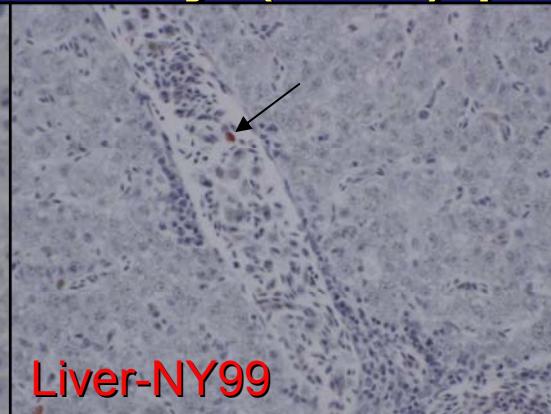
heart
liver
lung
spleen
kidney
intestine
muscle
brain

days post-infe

Immunohistochemistry (IHC) positive leukocytes



Liver-KEN

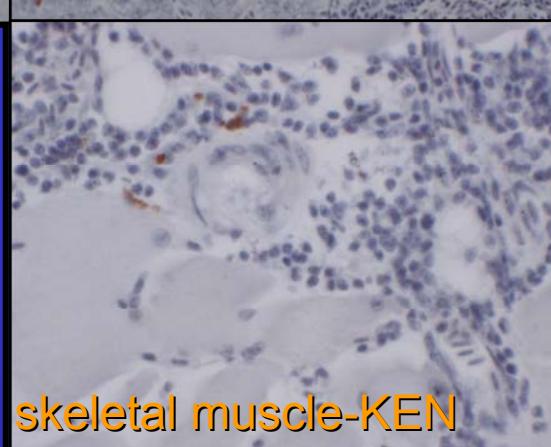


Liver-NY99

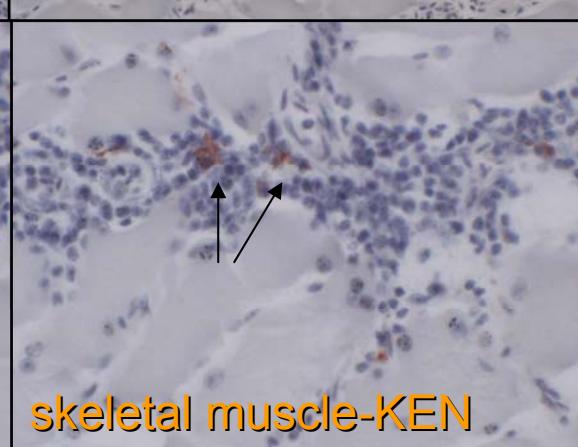


skeletal muscle-NY99

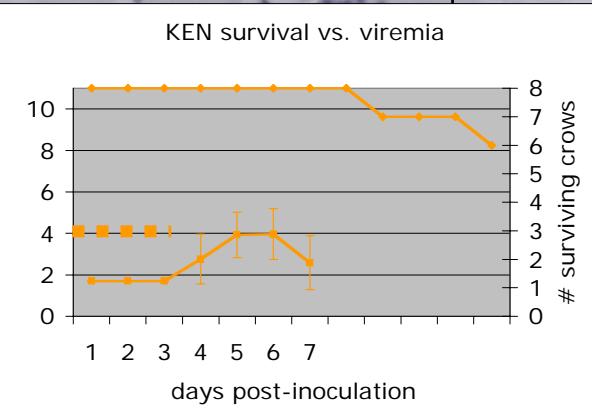
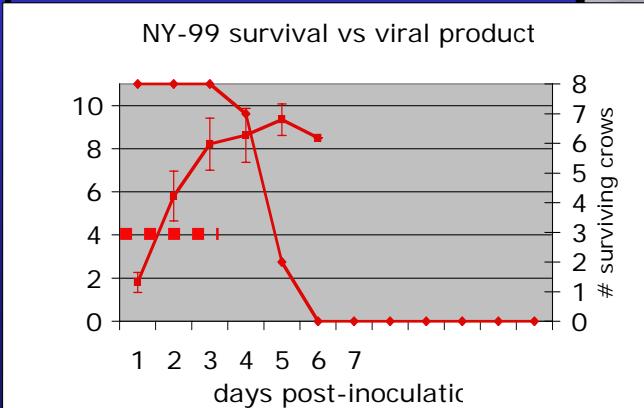
Crows were sacrificed at dpi 1-5. Birds were necropsied and tissues stored in 10% buffered formalin, paraffin embedded, sectioned and IHC was performed using WNV polyclonal antiserum.



skeletal muscle-KEN



skeletal muscle-KEN

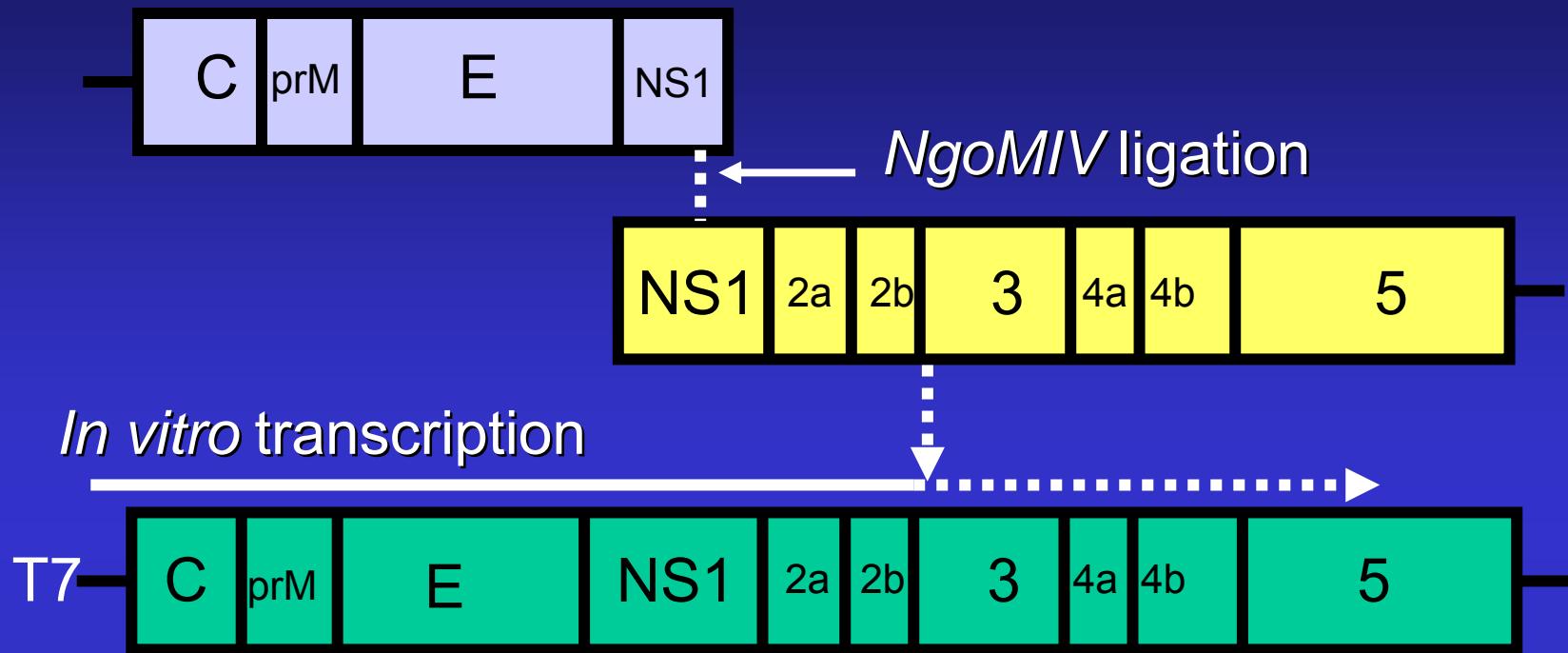


Amino acid differences between NY99 and KEN genomes

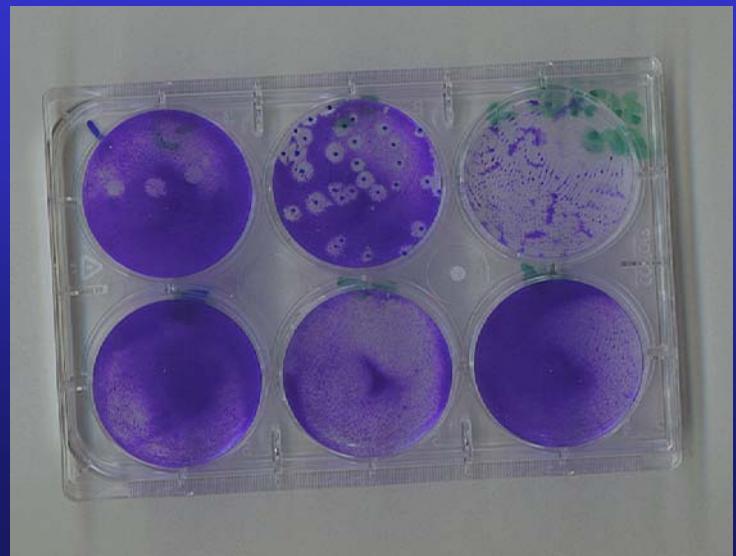
Gene region	aa position	NY99	KN-3829	
Capsid	108	Lys	Asn	Charrel, R. N., A. C. Brault, P. Gallian, J. J. Lemasson, B. Murgue, S. Murri, B. Pastorino, H. Zeller, R. de Chesse, P. de Micco, and X. de Lamballerie. 2003. Evolutionary relationship between Old World West Nile virus strains. Evidence for viral gene flow between Africa, the Middle East, and Europe. <i>Virology</i> 315:381-8.
Capsid	113	Val	Ala	
Envelope	126	Val	Ala	Charrel, R. N., A. C. Brault, P. Gallian, J. J. Lemasson, B. Murgue, S. Murri, B. Pastorino, H. Zeller, R. de Chesse, P. de Micco, and X. de Lamballerie. 2003. Evolutionary relationship between Old World West Nile virus strains. Evidence for viral gene flow between Africa, the Middle East, and Europe. <i>Virology</i> 315:381-8.
Envelope	159	Val	Ile	
NS1	70	Ala	Ser	Non-conservative substitution within the helicase domain of NS3.
NS2a	52	Thr	Ala	
NS2b	103	Val	Ala	
NS3	249	Pro	Thr	Non-conservative substitution within the helicase domain of NS3.
NS3	356	Thr	Ile	
NS4a	85	Ala	Val	
NS4b	249	Glu	Asp	

In addition to the coding amino acid differences, 22 nucleotide differences were identified in the 3'NCR. The 5'NCR regions from both genomes were identical.

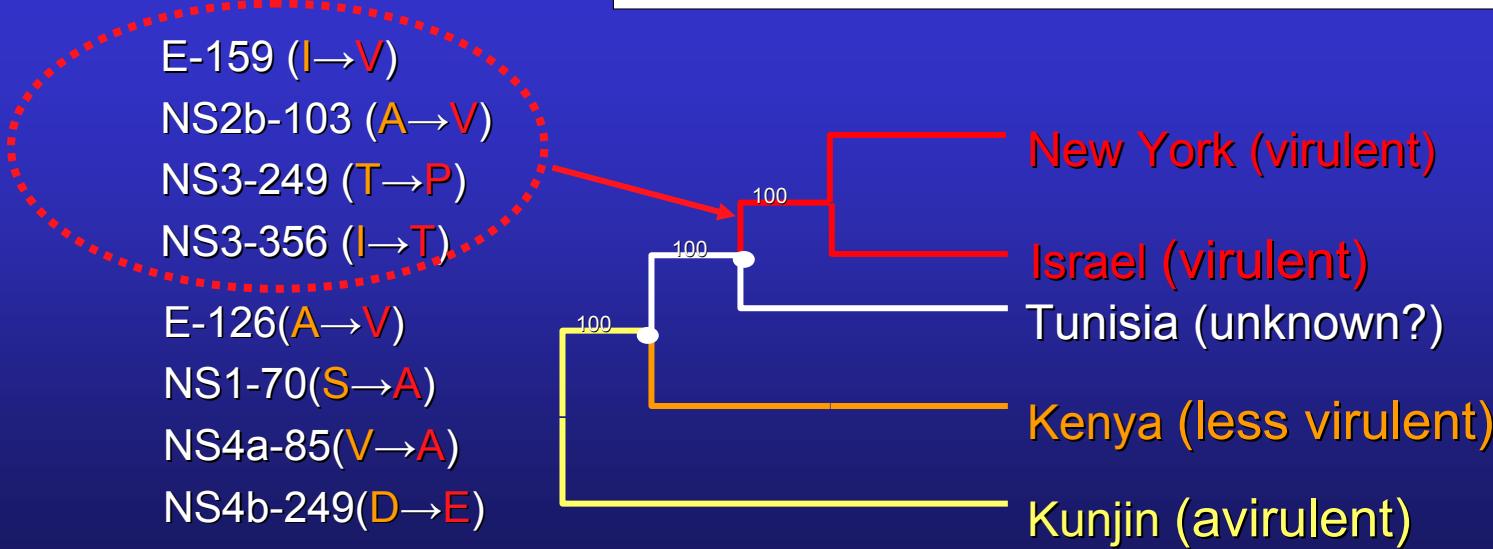
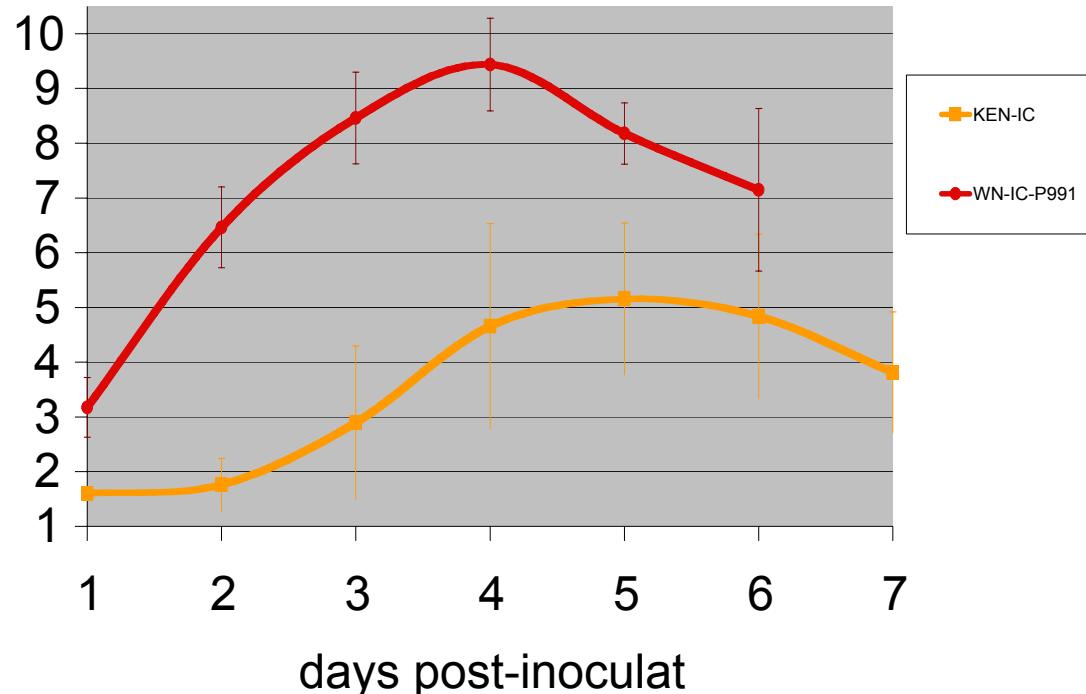
Generation of recombinant WNV



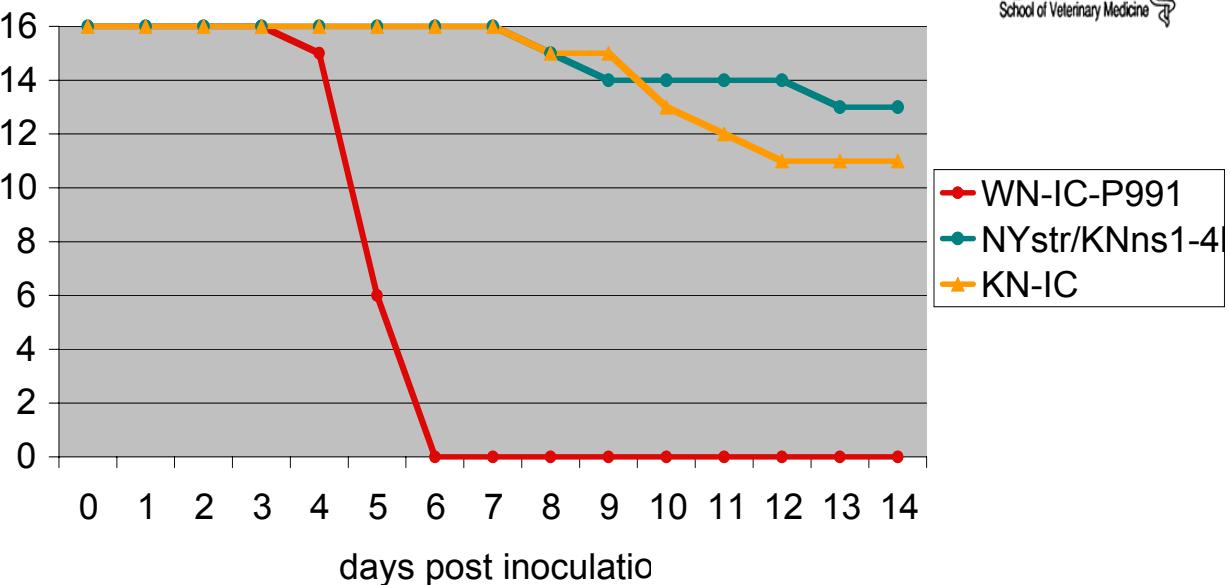
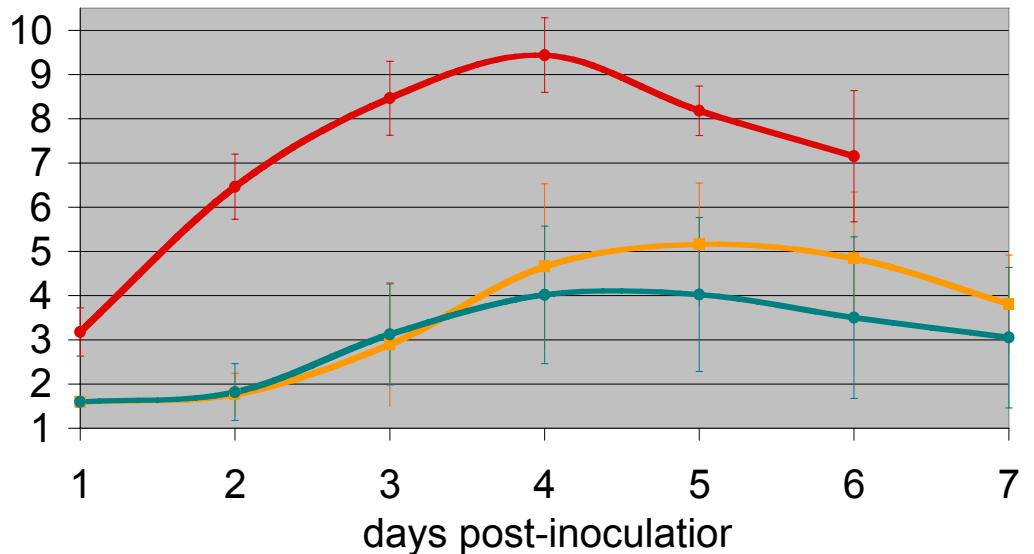
Plasmid DNAs were ligated at a common *NgoMIV* site and ligation product was used as template for *in vitro* transcription



Gene region	aa position	P991	KN-IC
Capsid	108	Lys	Asn
Capsid	113	Val	Ala
Envelope	126	Val	Ala
Envelope	159	Val	Ile
NS1	70	Ala	Ser
NS2a	52	Thr	Ala
NS2b	103	Val	Ala
NS3	249	Pro	Thr
NS3	356	Thr	Ile
NS4a	85	Ala	Val
NS4b	249	Glu	Asp



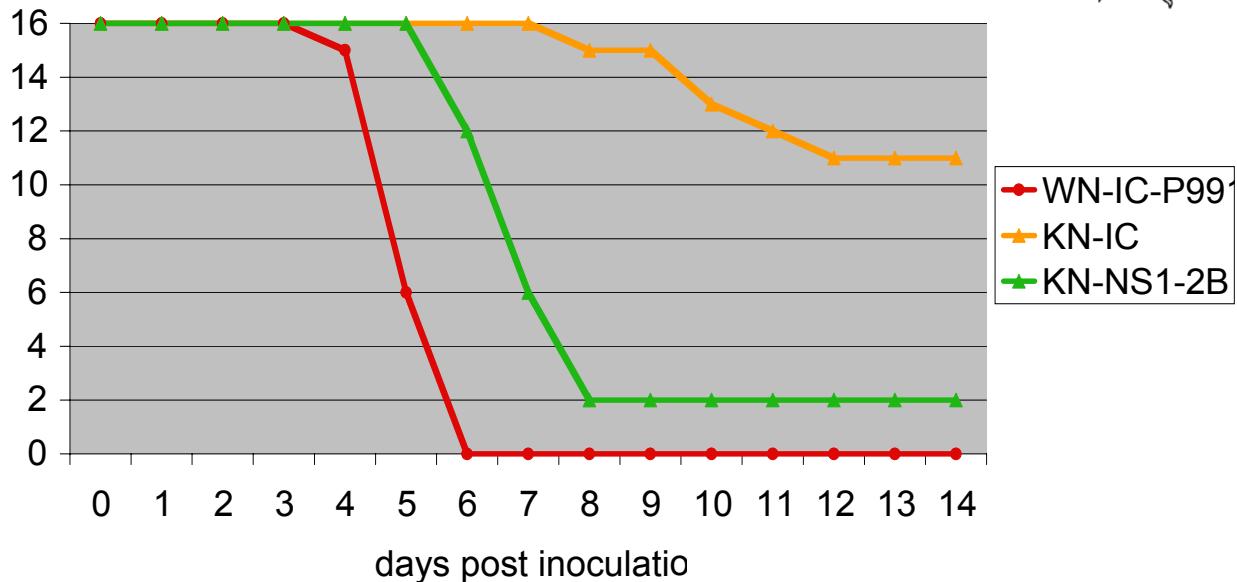
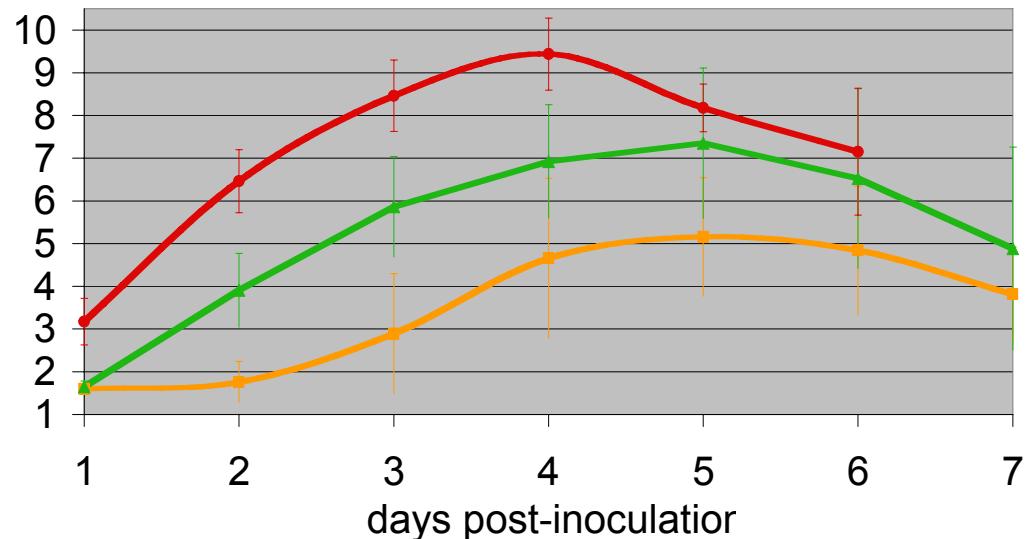
Role of structural amino acid substitutions



Generation of chimera with the structural aa of NY99 does not increase virulence or viremia in the KEN genetic backbone.

Gene	aa position	P991	KN-IC
Capsid	108	Lys	Asn
Capsid	113	Val	Ala
Envelope	126	Val	Ala
Envelope	159	Val	Ile
NS1	70	Ala	Ser
NS2a	52	Thr	Ala
NS2b	103	Val	Ala
NS3	249	Pro	Thr
NS3	356	Thr	Ile
NS4a	85	Ala	Val
NS4b	249	Glu	Asp

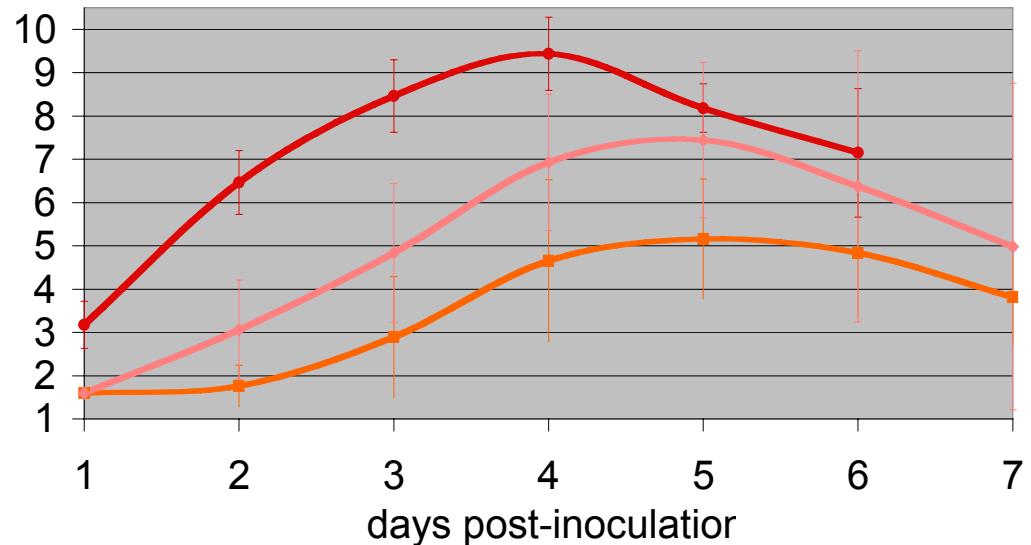
Role of NS3-4b substitutions



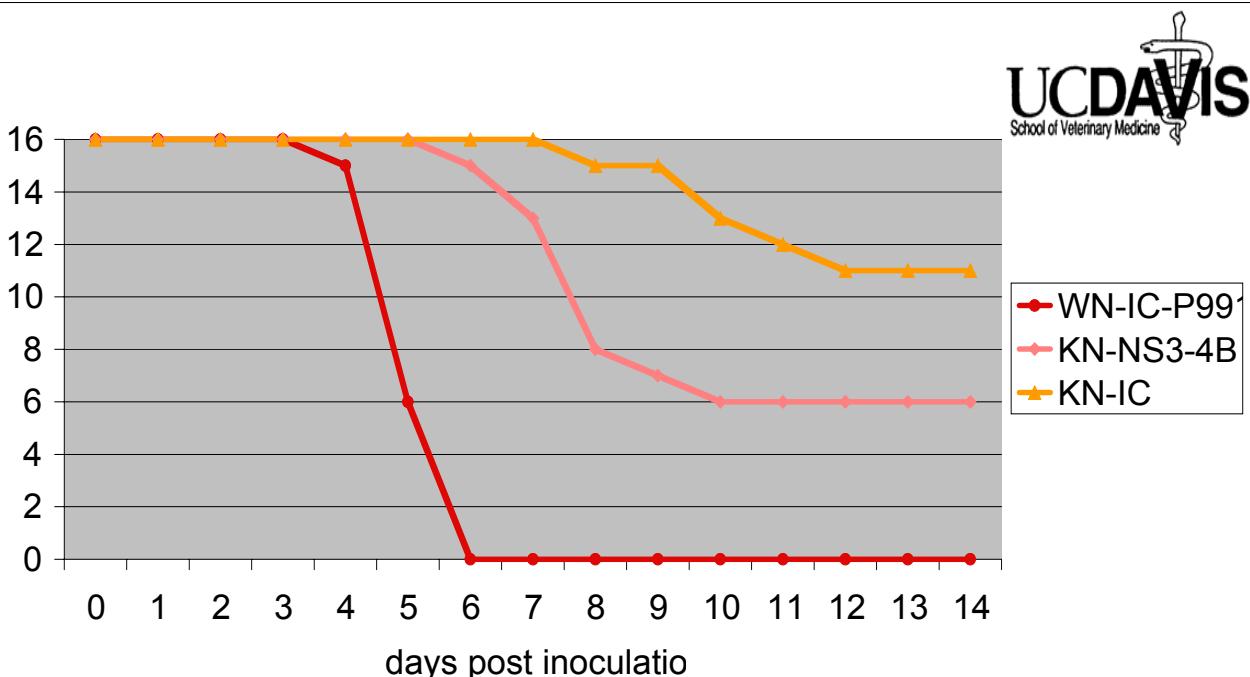
Generation of chimera with the NS3-4b of NY99 increases virulence from 30% to 90% with an increase in mean viremia of >300-fold.

Gene	aa position	P991	KN-IC
NS1	70	Ala	Ser
NS2a	52	Thr	Ala
NS2b	103	Val	Ala
NS3	249	Pro	Thr
NS3	356	Thr	Ile
NS4a	85	Ala	Val
NS4b	249	Glu	Asp

Role of NS1-2b substitutions

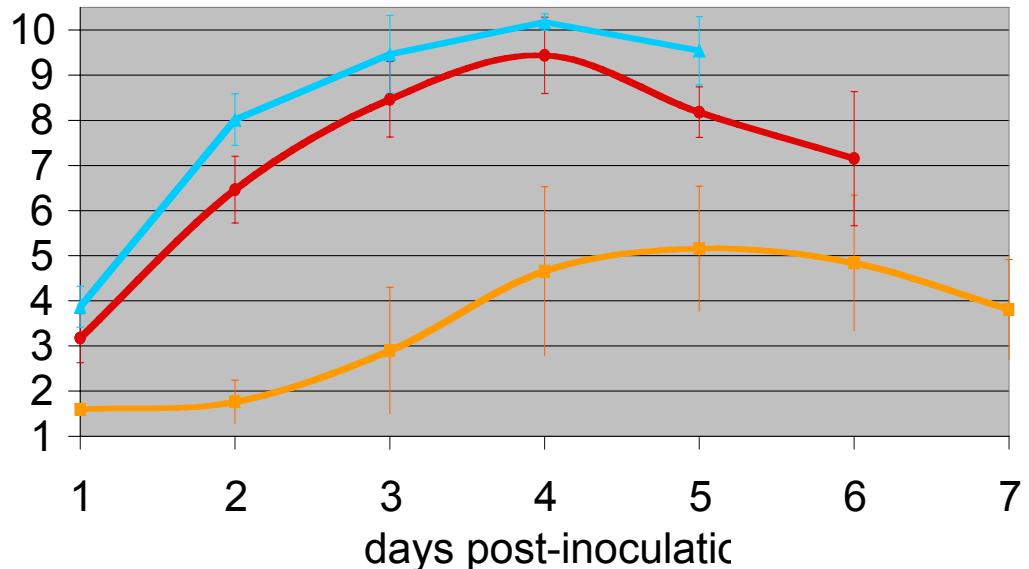


Gene	aa position	P991	KN-IC
NS1	70	Ala	Ser
NS2a	52	Thr	Ala
NS2b	103	Val	Ala
NS3	249	Pro	Thr
NS3	356	Thr	Ile
NS4a	85	Ala	Val
NS4b	249	Glu	Asp

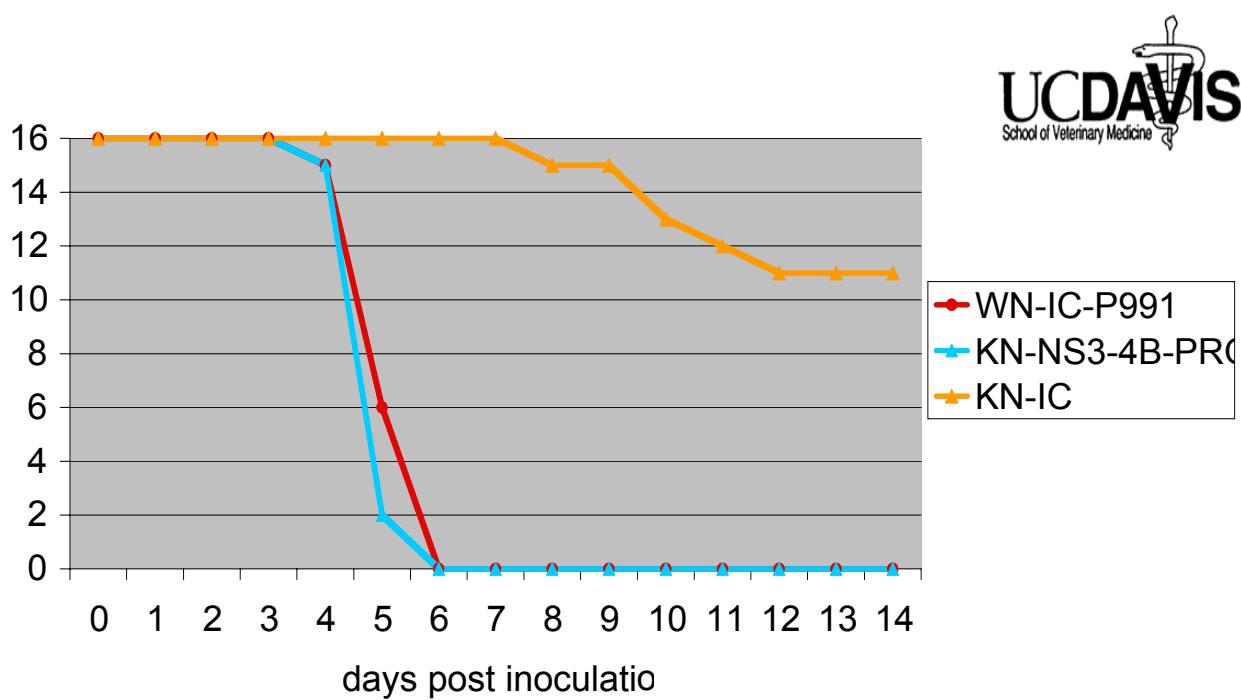


Generation of chimera with the NS1-2b of NY99 increases virulence from 30% to 60% with an increase in mean viremia of >300-fold.

Role of NS1-2b and NS3-249^{Pro}

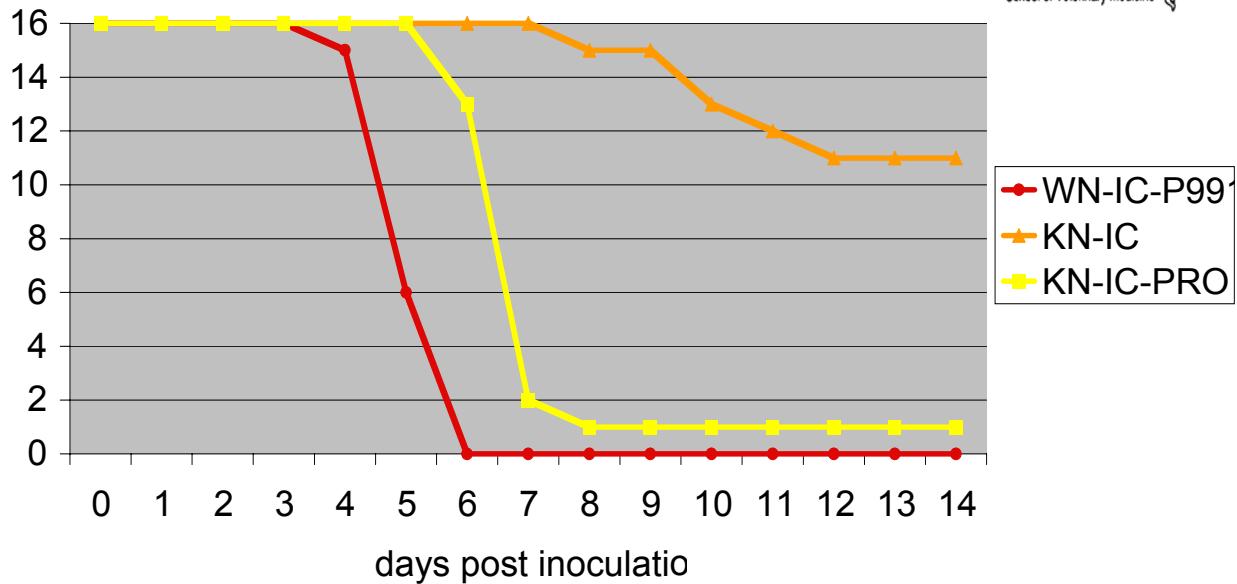
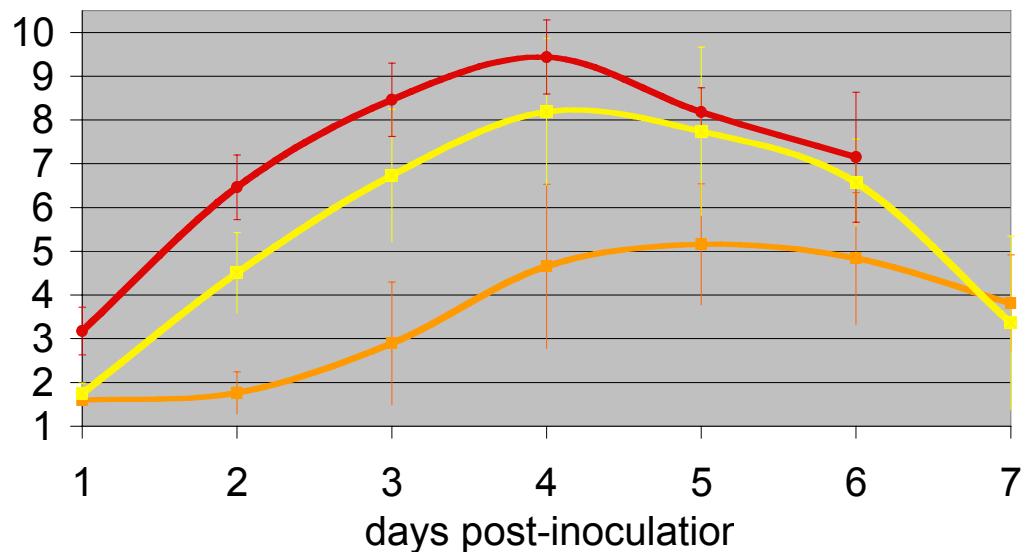


Gene	aa position	P991	KN-IC
NS1	70	Ala	Ser
NS2a	52	Thr	Ala
NS2b	103	Val	Ala
NS3	249	Pro	Thr
NS3	356	Thr	Ile
NS4a	85	Ala	Val
NS4b	249	Glu	Asp



Reconstitution of the NS3-249^{Pro} in the NS1-2b backbone generates a wild-type virulence and viremia phenotype

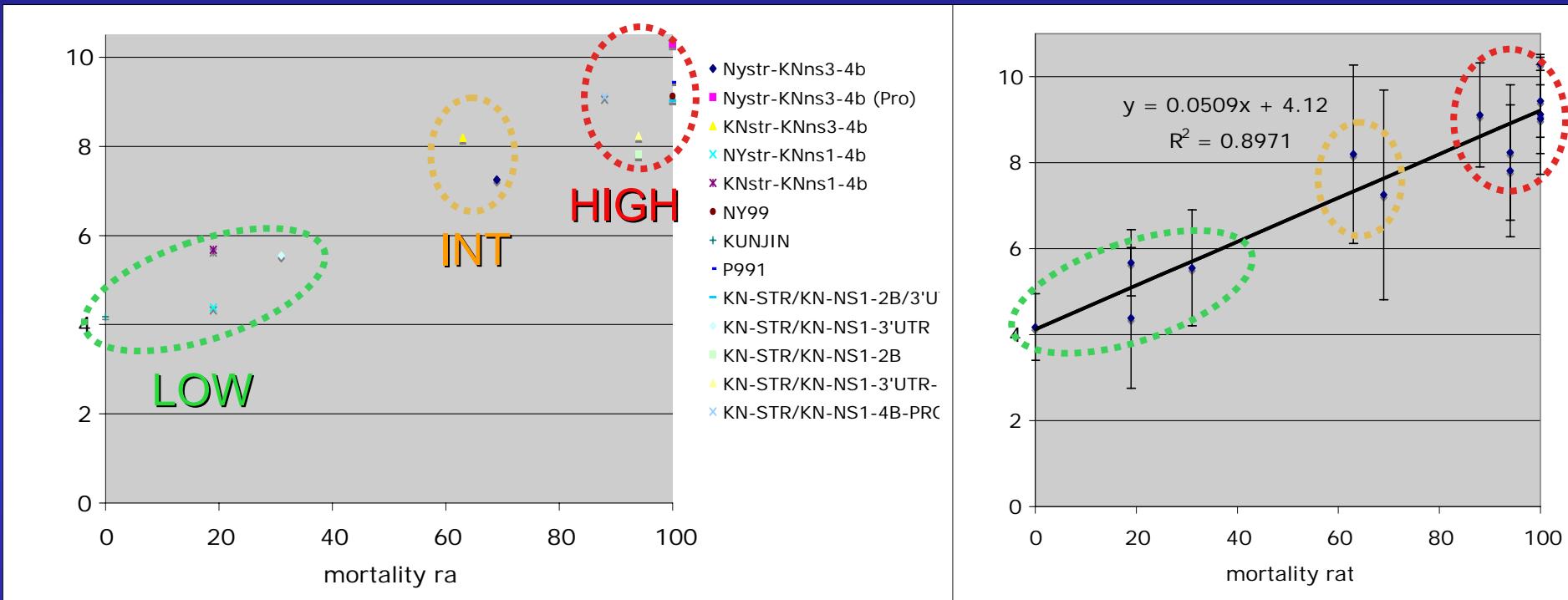
Role of NS3-249-Pro



Insertion of the 249-Pro increases viremia >1,000-fold and increases virulence from 30% to 94%.

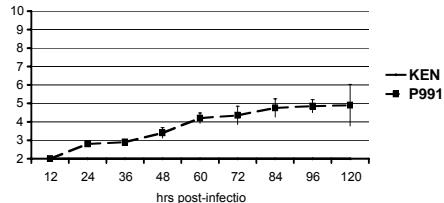
Gene	aa position	P991	KN-IC
NS1	70	Ala	Ser
NS2a	52	Thr	Ala
NS2b	103	Val	Ala
NS3	249	Pro	Thr
NS3	356	Thr	Ile
NS4a	85	Ala	Val
NS4b	249	Glu	Asp

Positive correlation between viremia and mortality

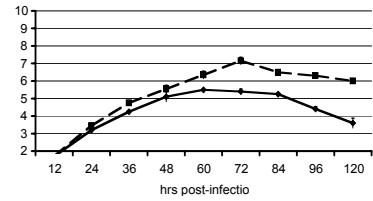


Lack both the NY99 NS1-2B as well as the NS3-249^{Pro}
Contain the NY99 NS1-2B; Lack the NS3-249^{Pro}
Contain the NS3-249^{Pro} with or without the NY99 NS1-2B

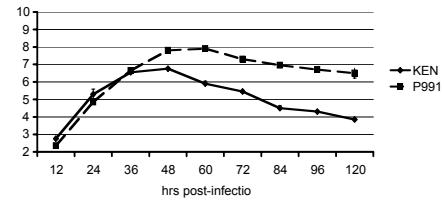
DEF-45C



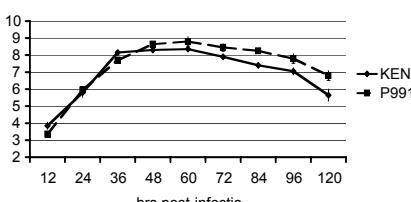
DEF-44.5C



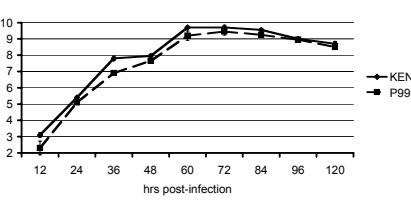
DEF-44C



DEF-43C

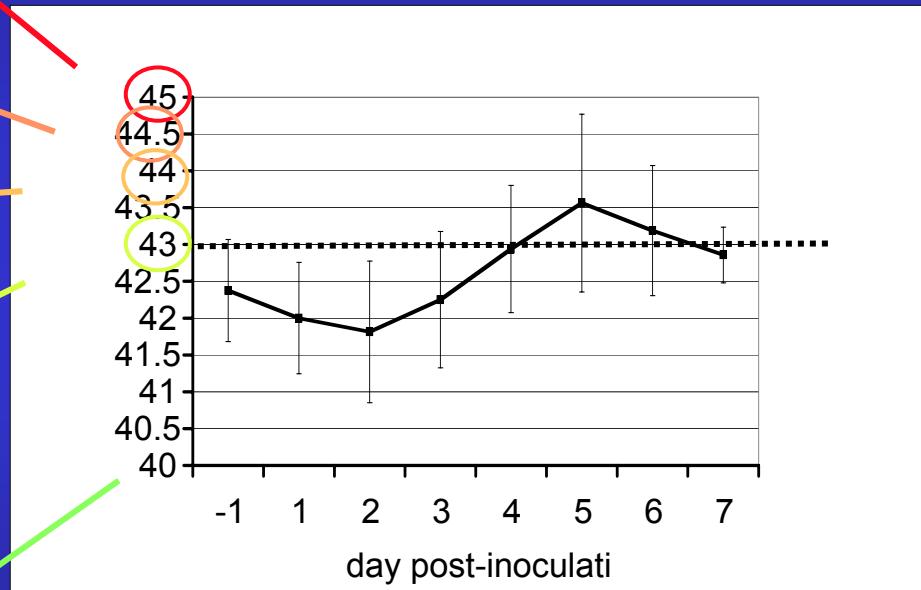


DEF-37°C



Differential *in vitro* temperature replication

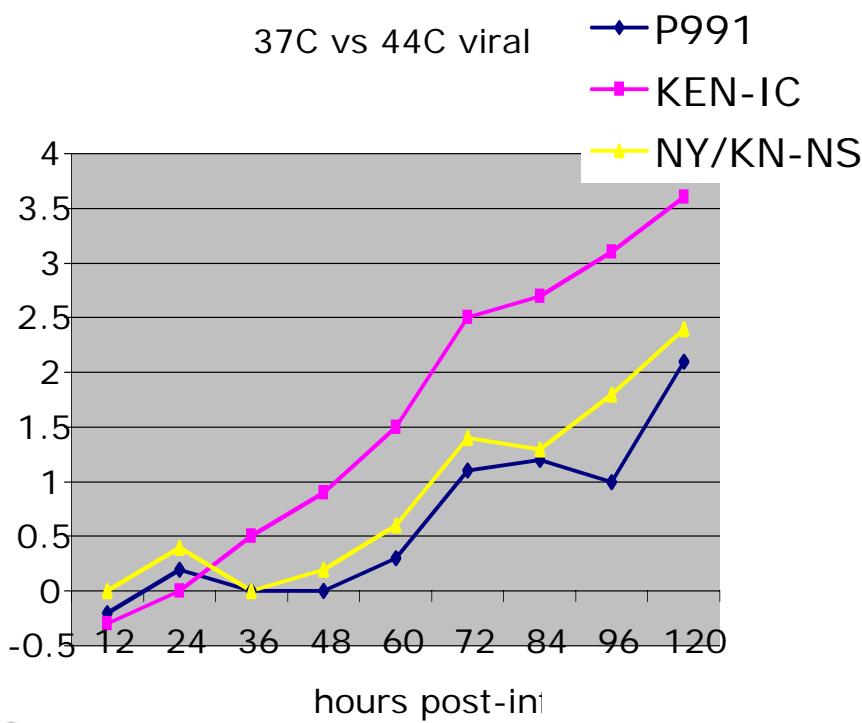
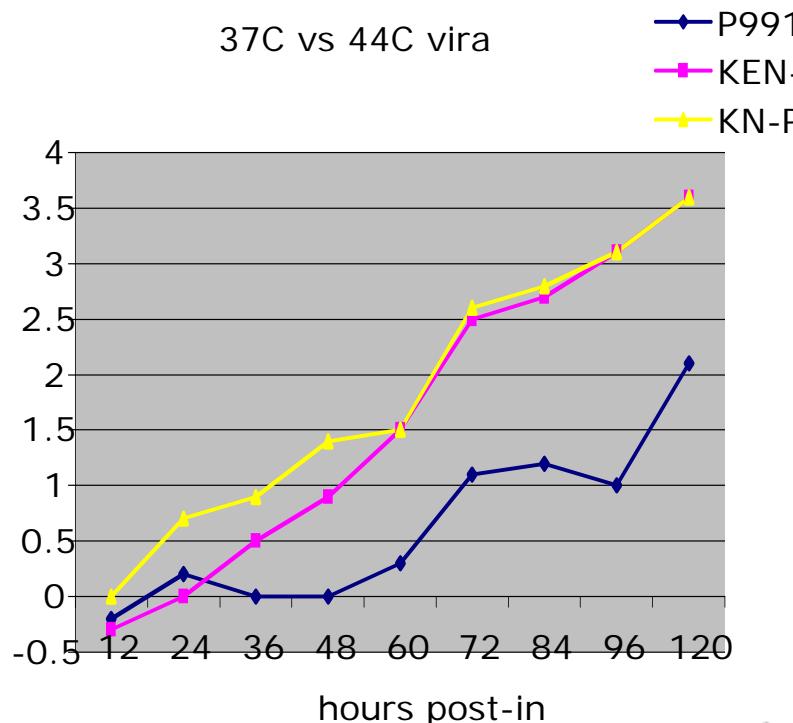
Mean body temperatures in infected AMCRs



Replication in duck embryonic fibroblast cells

(DEF). Monolayers of DEF cells were infected at an moi of 0.01 of P991 and KEN-IC viruses. Culture supernatants were sampled at 12 hr time-points (12 hpi-120 hpi). Titers were determined by plaque assay on Vero cells.

NS3-249^{Pro} not temperature sensitivity determinant

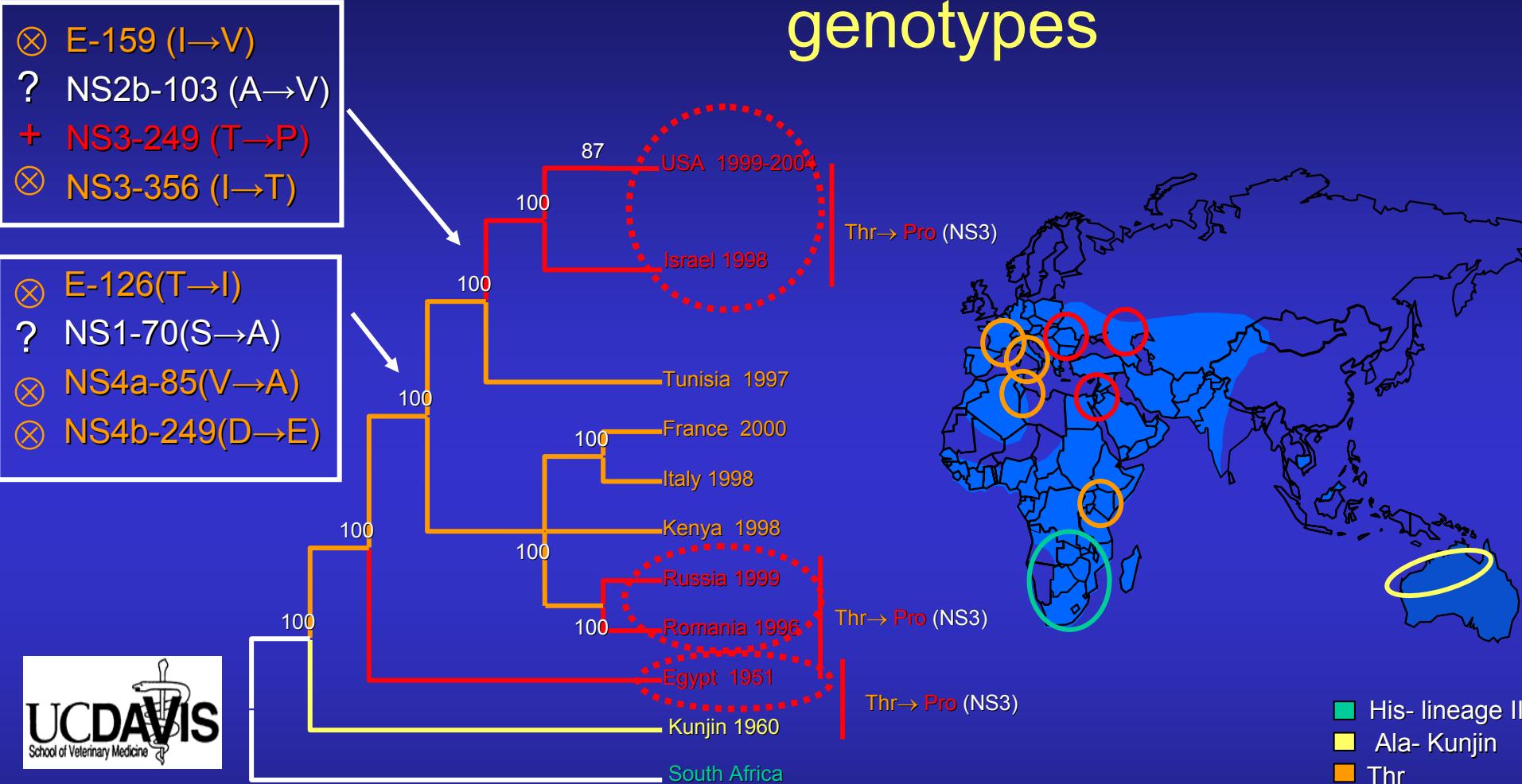


*DEN-2 (PDK-53) vaccine candidate indicate that an NS3-250 substitution involved in a *ts* phenotype

Butrapet, S., C. Y. Huang, D. J. Pierro, N. Bhamaraprabhati, D. J. Gubler, and R. M. Kinney. 2000. Attenuation markers of a candidate dengue type 2 vaccine virus, strain 16681 (PDK-53), are defined by mutations in the 5' noncoding region and nonstructural proteins 1 and 3. *J Virol* 74:3011-9.

Monolayers of DEF cells were infected at an moi of 0.01 of P991, KEN-IC and recombinant WNVs. Culture supernatants were sampled at 12 hr time-points (12 hpi-120 hpi). Titers were determined by plaque assay on Vero cells. Viral titers calculated between culture supernatants drawn from 37°C were compared to those from 44°C cultures and are represented as GMT log differentials.

Distribution of West Nile viral NS3 genotypes



NS3-249^{Pro} substitution is involved in the avian virulence phenotype
 Synergistic effect of NS1-2B mutations? Mechanism? Selection for Virulence?

Genomic sequence of TM-171 Mex03 isolate



Isolate from dead raven at
wildlife reserve in Villahermosa,
Tabasco.

RNA and, subsequently, Vero
cell passaged virus sent to
UTMB.

46 nucleotide differences (0.42%) from NY99; 4 amino acid
differences:

prM/M-141

Ile \otimes Thr

E-156

Ser \otimes Pro* (loss of glycosylation motif)

NS4B-245

Ile \otimes Val*

NS5-898

Thr \otimes Ile*



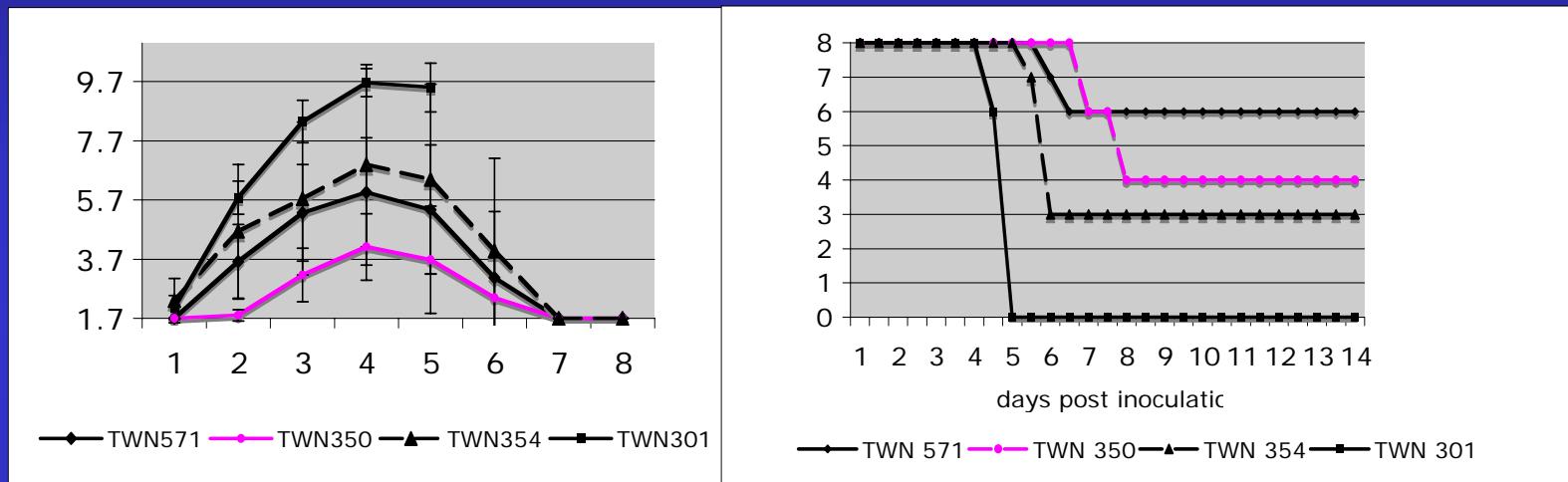


Strains used for Avian Virulence Testing



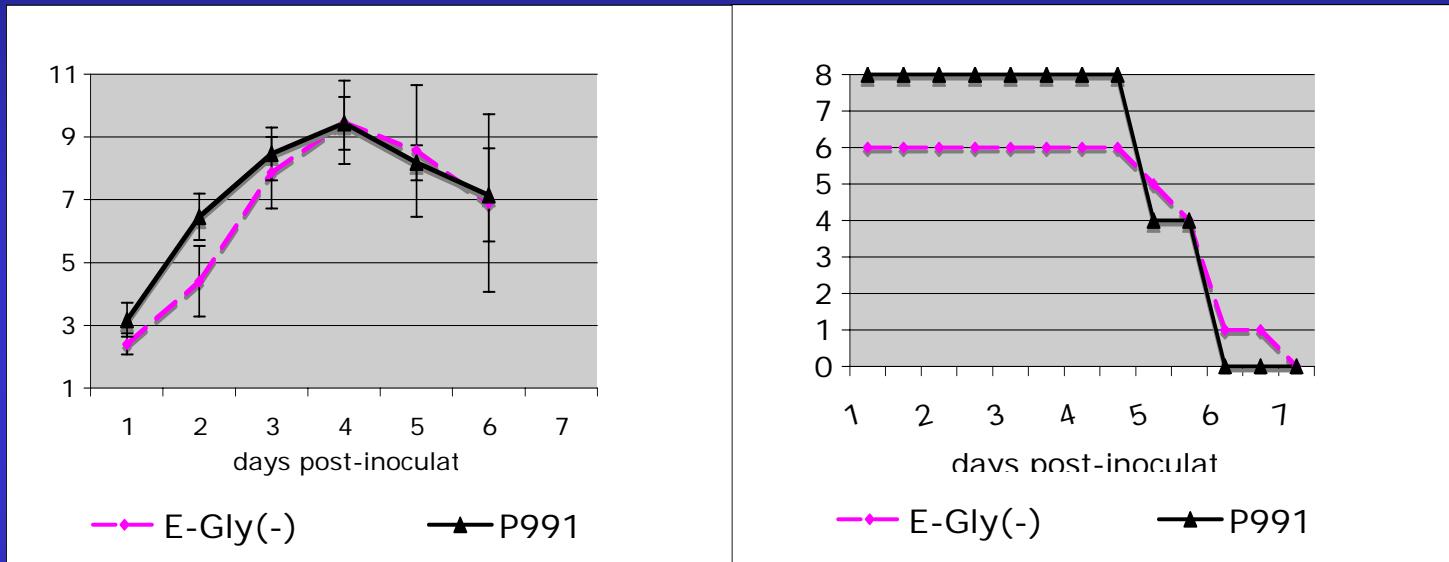
Virus Strain	Sequence	Glycosylation	Source	Location	Accession number
TWN 301	N-Y-S	Yes	Bird 1461	Texas	AY712947
TWN 571	N-Y-S	Yes	Pigeon 1153	Texas	AY712945
TWN 350	N-Y-P	No	TM171-03/Raven-small plaque variant	Mexico	AY660002
TWN 354	N-Y-S	Yes	TM171-03/Raven-large plaque variant	Mexico	AY660002

Infection of AMCRs with WNV strains with Differential Mouse neurovirulence phenotypes



Eight AMCRS were inoculated subcutaneously with 1500 PFU of the respective WNV strains. TWN 350, 354 (MX) and TWN 301, 571 (TX).

Role of E glycosylation for virulence modulation in AMCR?



NYS
↓
NYP



Site-directed Mutagenesis was utilized for the single site ablation of the E glycosylation motif; the resulting virus [E-gly(-)] was utilized for the inoculation of 6 AMCRs.

Conclusions

- Differences in replication of KEN vs NY99 WNVs appears to be the result of alternative viral production in circulating leukocytes
- The NS3-249 helicase mutation is the dominant virulence determinant which is modulated by NS1-2B determinants
- AMCR virulence is modulated by peak viremia; the NS3-249 substitution has been associated with WNV emergence over the past 50 years.
- Some mouse attenuated strains of WNV have reduced virulence potential in AMCRs as well (not a complete correlation-KEN and gly(-) viruses)

Acknowledgements



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- Stan Langevin
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- Payal Maharaj

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- Leslie Woods

University of QLSD

- Alex Khromykh

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CDC UO1 CI000235



CDC-Fort Collins, CO

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- Stan Langevin
- Nick Panella
- Barry R. Miller
- Mike Bunning (USAF)
- Richard Kinney
- Claire Huang
- Ann M. Powers
- Janae Raetz
- Tiffany Whitehurst

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- Bob McLean

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- Shawn Silliman (Chaplin Nature Preserve)

Colorado Dept. of Wildlife

- Todd Sanders

Colorado State University

- Richard Bowen
- Paul Gordy
- Max Teehee
- Laura Austgen

UTMB-Galveston

- Alan D.T. Barrett
- David W.C. Beasley

