**Table S3.** **Selection pressure acting upon codons (individual genes) of WNV strains collected in the US (1999-2011).**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Genea** | **Codon** | **Methodsc** | | | |
|  |  | **FEL** | **IFEL** | **SLAC** | **MEME** |
|  |  | ***P* value** | | | |
|  |  |  |  |  |  |
| NS1 (n=224), codons: 352 , ωb: 0.153  75 negatively selected sites |  |  |  |  |  |
| 1 | S9N/T | 0.04 | 1 | 0.34 | 0.04 |
| 2 | **L111F** | **0.09** | **0.07** | *0.16* | **0.09** |
| 3 | **N147D/S** | **0.07** | **0.05** | 0.48 | **0.07** |
| 4 | D240N/E | 0.04 | 1 | 0.34 | 0.04 |
| 5 | **Q324R/K** | **0.08** | **0.10** | 0.20 | **0.08** |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
| NS2A (n=201), codons: 231 , ωb: 0.095  67 negatively selected sites |  |  |  |  |  |
| 1 | H119Y | 0.04 | *0.11* | 0.23 | 0.04 |
| 2 | R188K | 0.08 | *0.19* | *0.18* | 0.08 |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
| NS3 (n=294), codons: 619, ωb: 0.077  185 negatively selected sites |  |  |  |  |  |
| 1 | L336S | 0.09 | 1 | *0.14* | 0.09 |
|  |  |  |  |  |  |
|  |  |  |  |  |  |
| NS4A (n=134), codons: 149 , ωb: 0.109  33 negatively selected sites |  |  |  |  |  |
| 1 | **A85T/V/I** | **0.04** | **0.01** | **0.06** | **0.04** |
|  |  |  |  |  |  |
| NS4B (n=223), codons: 255, ωb: 0.127  80 negatively selected sites |  |  |  |  |  |
| 1 | G104E | 0.10 | 1 | 0.29 | 0.10 |
|  |  |  |  |  |  |
| NS5 (n=320), codons: 905, ω: 0.104  231 negatively selected sites |  |  |  |  |  |
| 1 | **K314R** | **0.05** | **0.01** | **0.09** | **0.05** |
| 2 | S604R | 0.06 | 1 | 0.48 | 0.06 |
| 3 | Y706C/H | 0.09 | 1 | 0.47 | 0.09 |

Table represent the analysis of the individual genes of WNV for the ALL dataset (n=363), detected by the methods employed in HyPhy (Datamonkey server).   
a number of sequences differ from the input (n=363), after removal of identical sequences by the server  
b ω = dN/dS ratio

c FEL = Fixed effects likelihood, IFEL = Internal Fixed effects likelihood, SLAC = Single-likelihood ancestor counting, MEME = Mixed Effects Model of Evolution. All codons present in the table are recognized by at least two methods. In bold, codons recognized by three or four methods, with statistical significance. *p* values in italics represent codons detected to be under positive selection, not significantly, but close to *p* threshold (0.1).