**Table S6.** Assessing substitution saturation of ranavirus core genes with DAMBE.

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Cluster1 | Cluster2 | Cluster3 | Cluster4 | Cluster5a | Cluster6 | Cluster8b | Cluster9 | Cluster10 | Cluster11 | Cluster12 | Cluster13b |
| *Iss* | 0.18 | 0.23 | 0.39 | 0.13 | 1.15 | 0.13 | 0.32 | 0.17 | 0.07 | 0.13 | 0.29 | 0.33 |
| *Iss.c* (symmetrical tree) | 0.73 | 0.76 | 0.79 | 0.76 | 0.73 | 0.76 | 0.73 | 0.71 | 0.77 | 0.78 | 0.75 | 0.73 |
| Prob (symmetrical tree) | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| *Iss.c* (asymmetrical tree) | 0.41 | 0.47 | 0.52 | 0.47 | 0.41 | 0.46 | 0.41 | 0.39 | 0.48 | 0.51 | 0.45 | 0.41 |
| Prob (asymmetrical tree) | 0 | 0 | 0 | 0 | 0 | 0 | 0.04 | 0 | 0 | 0 | 0 | 0.1 |
|  | Cluster14 | Cluster15b | Cluster16 | Cluster20a | Cluster21 | Cluster22b | Cluster26 | Cluster37 | Cluster38a | Cluster39 | Cluster44 |  |
| *Iss* | 0.24 | 0.27 | 0.16 | 0.75 | 0.22 | 0.28 | 0.19 | 0.21 | 0.57 | 0.15 | 0.11 |  |
| *Iss.c* (symmetrical tree) | 0.72 | 0.7 | 0.73 | 0.79 | 0.77 | 0.71 | 0.68 | 0.69 | 0.7 | 0.72 | 0.72 |  |
| Prob (symmetrical tree) | 0 | 0 | 0 | 0.36 | 0 | 0 | 0 | 0 | 0.1 | 0 | 0 |  |
| *Iss.c* (asymmetrical tree) | 0.39 | 0.38 | 0.42 | 0.52 | 0.48 | 0.38 | 0.35 | 0.37 | 0.38 | 0.4 | 0.4 |  |
| Prob (asymmetrical tree) | 0 | 0.04 | 0 | 0 | 0 | 0.07 | 0 | 0 | 0.02 | 0 | 0 |  |

If *Iss* value is significantly smaller than Iss.c, substitution saturation is not serious.

Red font represents lower-quality sequence

a: *Iss* > *Iss.c*, which indicated that the sequences have experienced severe substitution saturation.

b: *Iss* < *Iss.c*, P value > 0.01.