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Abstract

### Modeling Nucleoprotein Rabies Virus

Grecia C. Tovar-Rojas<sup>1</sup>, Fernando Bastida-González<sup>2</sup>, Paola B. Zárate-Segura<sup>1,2</sup>

<sup>1</sup>UPIBI-National Polytechnic Institute, Bioprocess department, Mexico Distrito Federal.

<sup>2</sup>ESM-National Polytechnic Institute, Molecular biology laboratory, Mexico Distrito Federal.

**Abstract:** Rabies virus (RABV) infects mammals causing acute encephalomyelitis (*Lyssavirus: Rhabdoviridae: Mononegavirales*). RABV genome consists of a single non segmented negative-strain RNA that encodes the five structural proteins: glycoprotein (G), the matrix protein (M), phosphoprotein (P), viral RNA-dependent RNA polymerase (L) and nucleoprotein (N). The N protein contains 450 amino acids highly conserved. In 2006 the crystal structure of nucleoprotein rabies virus (RABV N) was described, however this crystal lacks the description of loops. For construction RABV N model by homology and refinement loops was used MODELLER 9.12 program. The 3D model of RABV N obtained was evaluated stereochemical quality and reliability with Ramachandran PLOT and Errat server, showing 78% favorable residues and Z-score 58.6% respectively. Subsequently strongest interactions between aminoacids in nucleoprotein model were analyzed with PDBsum server, which were E20-R254, D4-R254, N11-E266, K417-E392 and E403-H369; these were compared with 2GTT interactions showing that E20-R254 and N11-E266 are importants due to these are present in both models. The interactions E20-R254 (polar-acid and polar-basic) and N11-E266 (polar-uncharged and polar-acid) is relevant due to that are the main contacts between neighboring protomers.

**Keywords:** Modeling, RABV, Nucleoprotein, interactions

**Corresponding author: Fernando Bastida**

[mijomeil@hotmail.com](mailto:mijomeil@hotmail.com)