Molecular evolution and genetic variations of RNA edited products of Avian Paramyxoviruses

At DBT's National Institute of Animal Biotechnology (NIAB), Hyderabad, researchers analyzed by bioinformatic tools, the molecular evolution and genetic variations of V and W proteins of 55 viruses from 21 species of Avian Paramyxoviruses (APMVs). They predicted that the variations observed in the sequence and hexamer phase positions of the *P* gene editing sites are likely to influence the levels and relative proportions of P, V and W proteins' expressions, which in turn could explain the differences in the pathogenicity of APMVs.

Both the V and W proteins showed lower evolutionary rate. While the V proteins were conserved signifying their important role in immune evasion as previously known, the divergence in W proteins leads to speculation that W proteins may be contributing to the varied degree of pathogenesis in several hosts as exhibited by APMV species. This is the first comprehensive and comparative evolutionary study report on the *P* gene edited accessory viral proteins of APMVs. The information from this study will enable in understanding specific functions of conserved motifs/amino acids of V and W proteins and their evolutionary significance in causing infection. The knowledge thus gained can help in developing sensitive diagnostic tools and efficient vaccines to protect the bird species against APMVs. The work of Dr. Madhuri Subbaiah has been accepted for publication in the journal "*Scientific Reports*"

Avian paramyxoviruses (APMVs) are a group of 21 virus species isolated from a wide variety of bird species across the globe. The most well characterized of them, APMV-1, popularly known as Newcastle disease virus, causes severe disease in chickens causing huge economic loss to farmers. APMVs, similar to other paramyxoviruses such as Measles and Mumps viruses, are enveloped and carry a negative sense, non-segmented RNA genome. The viral genes are arranged in tandem as cassettes in the RNA genome, each coding for one protein. Additionally, in paramyxoviruses, 'co-transcriptional RNA editing' happens at a stretch of 'A' and 'G' nucleotides in the Phosphoprotein (P) gene, that enables maximizing the coding capacity of their smaller genome, i.e., from the *P* gene, three mRNAs are transcribed leading to expression of three proteins, P, V and W that share their N terminal sequences.

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