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Hemagglutinin receptor binding specificity of H10N7 avian influenza

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Influenza is a constant global burden to human health. In order to evolve from its avian form and gain the pandemic potential for increased transmissibility between humans, the hemagglutinin (HA) of avian influenza viruses will need to undergo mutations in its receptor binding site (RBS) that bring about an avian to human receptor preference switch. In order to understand the major determinants of virus transmissibility and the pandemic potential of the novel avian influenza viruses we have determined the crystallographic structure of the novel avian influenza H10N7 A/Turkey/MN/3/79 to 1.96Å and mapped the RBS. The amino acid residues responsible for conferring receptor selectivity were identified by site direct mutagenesis of recombinant H10 HA proteins. The receptor binding selectivity of the HAs was determined using sialyl glycan binding assays. Docking models were constructed of the H10 HA in complex with α2,6-sialic acid (human) and α2,3-sialic acid (avian) pentasaccharide receptor analogs to ascertain the correlation between the binding assay data and the interactions within the receptor binding pocket. The presented findings provide a structure recognition perspective for the receptor binding properties of the novel avian H10 influenza HA.

Biography

Tony Velkov has completed his PhD from Monash University, Australia in 2000. His research focus is in the field of anti-infective discovery. He was awarded a National Health and Medical Research Council (NHMRC) Research Fellowships in 2006, 2011 and 2015. The quality and impact of his independent research was recognized by the NHMRC with an Excellence Awards in 2011 and 2015. He has published over 70 papers in high caliber journals and 5 book chapters.

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