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Emergence of novel reassortant H6N2 avian influenza viruses in ducks in India Manoj Kumar<sup>#1</sup>, Shanmugasundaram Nagarajan<sup>#1</sup>, Harshad V. Murugkar<sup>1</sup>, Barnalee Saikia<sup>2</sup>, Bharati Singh<sup>1</sup>, Amit Mishra<sup>1</sup>, Sushil K. Tripathi<sup>1</sup>, Sonam Agarwal<sup>1</sup>, Shweta Shukla<sup>1</sup>, Diwakar D. Kulkarni<sup>1</sup>, Vijendra Pal Singh, Chakradhar Tosh<sup>1\*</sup>

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## **Abstract**

H6 subtype avian influenza viruses (AIV), established in terrestrial poultry, have jumped species barriers and caused human infection indicating pandemic potential of the virus. Here, we report isolation, and antigenic and genetic characterisation of two H6N2 viruses isolated from apparently healthy domestic ducks in Kerala and Assam, India during 2014 and 2015, respectively. Hemagglutination inhibition assay revealed antigenic divergence between the two isolates. This result was corroborated by amino acid differences at 55 positions (15.98%) between their hemagglutinin (HA) 1. The sequence analysis of the viruses indicated avian receptor specificity, avian origin, low pathogenicity to poultry and sensitivity to oseltamivir. However, Kerala 14 had V27I mutation marker for amantadine resistance in M2. The Assam15 virus had an additional N-linked glycosylation on HA2 (position 557) compared to Kerala 14 virus. Analysis of the HA gene re-

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