Phylogenic analysis of the M genes of influenza viruses isolated from free-flying water birds from their Northern Territory to Hokkaido, Japan

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After the online publication of this article, two errors were found in the Abstract. The correct version is printed below:

Abstract During 2000–2007, 218 influenza viruses of 28 different combinations of HA (H1–H13) and NA (N1–N9) subtypes were isolated from fecal samples of free-flying water birds at two distant lakes in Hokkaido, Japan. Phylogenic analysis of the matrix (M) genes of 67 strains, selected on the basis of their subtype combinations,

revealed that A/duck/Hokkaido/W95/2006 (H10N8) was a reassortant whose M and NA genes belonged to North American non-gull-avian and the other six genes to Eurasian non-gull-avian lineages. The M genes of other 65 strains belonged to Eurasian non-gull-avian and the one to Eurasian-gull lineages. The M genes of 65 strains were grouped into three different sublineages, indicating that influenza viruses circulating in different populations of free-flying water birds have evolved independently in nature.

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