The pandemic influenza A(H1N1)pdm09 virus has been reported in Peru since 2009. We report the whole-genome sequence analysis of a viral isolate from an infection case that occurred during an influenza outbreak in 2013. This strain shows novel hemagglutinin (HA) mutations that may cause an antigenic drift that diminishes the protective effect of the vaccine.

The whole-genome sequence of the Peruvian A(H1N1)pdm09 isolate from 2013 has been deposited in DDBJ/ENA/GenBank under accession no. KJ147484 to KJ147491. The sequence accession numbers.

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