

Composition of the Influenza vaccine to be used for coming season 2026.

WHO recommends composition of influenza virus vaccines twice a year during the months of February and September for Northern and Southern hemisphere, respectively. Recently, the Northern Hemisphere recommendation for trivalent vaccine has been released on February 26, 2026.

Northern Hemisphere (released in February, 2026)

Egg-based vaccines

- an A/Missouri/11/2025 (H1N1)pdm09-like virus;
- an A/Darwin/1454/2025 (H3N2)-like virus; and
- a B/Tokyo/EIS13-175/2025 (B/Victoria lineage)-like virus.

Cell culture-, recombinant protein- or nucleic acid-based vaccines

- an A/Missouri/11/2025 (H1N1)pdm09-like virus;
- an A/Darwin/1415/2025 (H3N2)-like virus; and
- a B/Pennsylvania/14/2025 (B/Victoria lineage)-like virus.

Southern Hemisphere (released in September, 2026)

Egg-based vaccines

- an A/Missouri/11/2025 (H1N1)pdm09-like virus,
- an A/Singapore/GP20238/2024 (H3N2)-like virus, and
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus.

Cell culture-, recombinant protein- or nucleic acid-based vaccines

- an A/Missouri/11/2025 (H1N1)pdm09-like virus;
- an A/Sydney/1359/2024 (H3N2)-like virus; and
- a B/Austria/1359417/2021 (B/Victoria lineage)-like virus.

In India, respiratory virus surveillance is systematically conducted through the DHR-ICMR Virus Research and Diagnostic Laboratory (VRDL) network, in collaboration with the WHO National Influenza Centre (NIC) at ICMR-NIV Pune, which also serves as a WHO Collaborating Centre under the Global Influenza Surveillance and Response System (GISRS). Currently, 73 sentinel sites across the country collect and report influenza testing data throughout the year.

Since 1 July 2025, a total of 73 influenza isolates were received /obtained at NIC. 49 isolates were processed for WGS with Illumina Nextera XT Library preparation Kit and Run on Mi seq

platform. Data analysis was done with CDC MIRA software. Out of 73 isolates 3 were Inf A (H1N1) pdm09, 52 Inf A (H3N2) and 18 Inf B (Victoria). Phylogenic analysis done with Nextclade analysis software.

- A. Inf A (H1N1) Pdm09 HA gene: All are from 6B.1A 5a2a .1 Clade, subclade D 3.1.1
- B. Inf A (H3N2) HA gene: All are from 3C.2a.1b.2a2a.3a and the newly emerged subclade K (J.2.4) Clade.
- C. Inf B Victoria strains belongs to V1A.3a.2 Clade

Antiviral susceptibility: All the 73 isolates (H1N1 /pdm09, H3N2 and Type B Victoria) tested for antiviral susceptibility by phenotypic assay and reported sensitive for oseltamivir drug.

Recommendation

1. Phylogenetic analysis of HA gene of A(H1N1) pdm09, A(H3N2) and Type B Victoria lineage showed that by an large the circulating strains matched with the WHO recommended Vaccinecomponent of **Northern hemisphere 2026-27**.
2. In conclusion, since the surveillance data indicates close resemblance of the circulating influenza strains in India with the Northern hemisphere recommendations of WHO, it would be ideal to administer the NH vaccine. However, in view of non-availability of Northern hemisphere vaccine, the available SH vaccine may be used and SH vaccine be replaced with NH vaccine as soon as it becomes available.