TAbic® IBVAR206

Technical Bulletin

Information from Phibro Technical Services

Phibro Molecular Analysis of IBV GI-23 and TAbic® IBVAR206 Protection

Dana Goldenberg, PhD
Research & Development Team Leader

The GI-23 lineage of Infectious Bronchitis Virus (IBV) has been globally detected. The combination of an RNA polymerase that lacks proofreading and the virus's natural tendency to undergo recombination allows IBV to gradually accumulate genetic changes as part of its normal evolutionary process. For this reason, Phibro maintains routine molecular surveillance to monitor these developments and verify that TAbic IBVAR206 continues to match circulating strains. References: https://www.pahc.com/vaccines/ibvar206-map/

Although GI-23 remains one of the predominant lineages detected globally, sequence analyses show predictable diversification into several sub-lineages. Molecular analyses indicate that recent GI-23 isolates cluster into several sub-lineages, however, these classifications are not based on a unified set of criteria. As different groups apply distinct thresholds and reference sequences, the same isolate may be assigned to different sub-lineages.

IBV GI-23 Sub-lineage Classification Reported in Selected Regions

Although the GI-23 lineage of IBV has been detected in approximately 44 countries worldwide, sub-lineage–level classification is not consistently performed or reported across all regions.

Accordingly, this overview focuses on selected regions where GI-23 sub-lineages have been described, based on available molecular sequence analyses reported in the scientific literature and Phibro surveillance activities.

Country	GI-23 Lineage / Sub-lineage	Notes	Reference
Israel	GI-23.2, GI-23.2.3 (dominant)	Clear separation of sub-lineages; 23.2.3 dominant since 2023	Israel Veterinary Services; Poultry Council
Egypt	GI-23 (Egy/var I & II → GI-23.1, GI-23.2)	High diversity: sub-lineage assignment varies	Shosha et al., 2024
Jordan	GI-23.1, GI-23.2	Historical origin of VAR2	Houta et al., 2021
Turkey	GI-23.1, GI-23.2	Circulating for many years	Houta et al., 2021
Iran	GI-23.2 (VAR2-like)	Related to Israeli/Jordanian strains	Houta et al., 2021
Iraq	GI-23.1, GI-23.2	Sub-lineage definitions are not standardized	Houta et al., 2021
Poland	GI-23.2, GI-23.2.3	Reported 2018–2022	Lisowska et al., 2021
South Africa	GI-23.2	Several outbreaks 2022–2023	Local surveillance
Brazil	GI-23 (SA.1 / SA.2) GI-23.1	2023-2025	Trevisol 2023; Ikuta 2023 Dos Santos et al., 2025

To resolve these inconsistencies, we are assembling a broad global dataset and constructing a standardized phylogenetic framework to enable consistent GI-23 sub-lineage nomenclature worldwide.

A targeted RT PCR approach has been developed to support differentiation between the TAbic® IBVAR206 vaccine and circulating field isolates, and to facilitate ongoing molecular characterization of GI-23 related viruses.

Recent data indicate a predominance of the GI-23.2.3 cluster, alongside detection of GI-23.1 field isolates and GI-23.1–related vaccine–derived sequences.

Accurate GI-23 sub-lineage assignment requires sequence based analysis, as reliable discrimination cannot be achieved using partial sequence data alone.

Within this context, expanded sequence datasets and refined phylogenetic analyses are supporting improved confidence in GI-23 sub-lineage assignment.

Our ongoing efforts to define a genetic signature for reliable differentiation of the IBVAR206 vaccine strain from GI-23 field viruses indicate that sequence data alone may not always allow differentiation between a closely related field isolate and a live attenuated vaccine-derived virus. Interpretation should therefore also consider the relevant vaccination, clinical, and epidemiological context, including timing of sampling relative to vaccination, sampling context, flock clinical status, concurrent respiratory or immunosuppressive conditions, and, where available, RT-qPCR Ct values. These findings emphasize the importance of assessing GI-23 detections within an integrated molecular, clinical, and epidemiological framework.

Vaccine Efficacy Following Challenge with a GI-23.2.3 Field Isolate

To evaluate the TAbic IBVAR206 performance, we conducted a challenge study using a GI-23.2.3 field isolate.

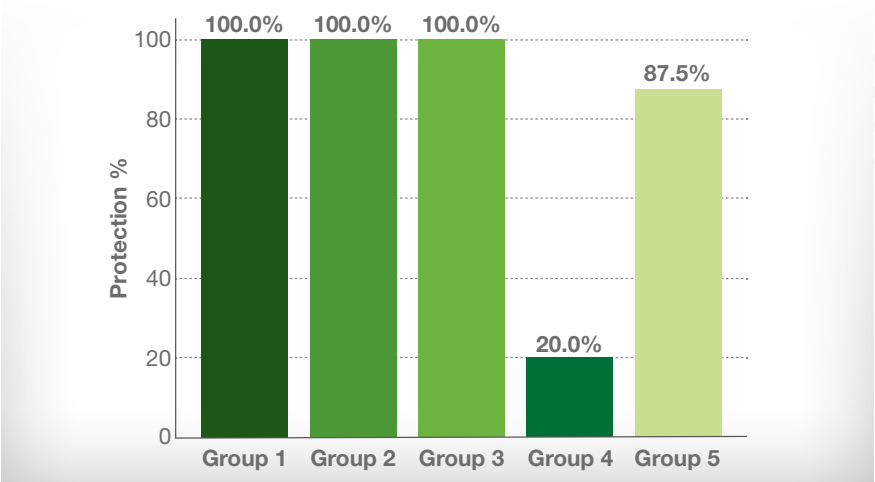
Despite the natural genetic evolution of this sub-lineage, the TAbic IBVAR206 vaccine provided effective protection, as demonstrated by the ciliostasis test.

In summary, all vaccinated groups were fully protected following challenge with the virulent GI-23.2.3 field strain. Because GI-23 continues to evolve and sub-lineages and clades can vary by region, vaccination programs should be guided by local, sequence-based surveillance. Continued IBV genotyping/phylogeny can be of help to confirm what serotypes, lineages, sub-lineages and clades are circulating in your area and support timely program adjustments. Refer to the product information approved in your country.

Group	Vaccine Day 1	Vaccine Day 14	Challenge Day 28
1	IBVAR206	-	Yes
2	IBVAR206	IBVAR206	Yes
3	IBVAR206	Inactivated IBVAR206	Yes
4	-	-	Yes
5	-	-	-

Protection rate following challenge with the virulent field strain GI-23.2.3

TAbic IBVAR206 challenge study using a GI-23.2.3 field isolate



This information has been prepared for industry technical professionals.