

**Recommendations for a Standardized Avian Coronavirus (AvCoV) Nomenclature:
Outcome from Discussions Within the Framework of the European Union COST
Action FA1207: “Towards Control of Avian Coronaviruses: Strategies for
Vaccination, Diagnosis and Surveillance”**

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Letter to the Editor—

Recommendations for a Standardized Avian Coronavirus (AvCoV) Nomenclature: Outcome from Discussions Within the Framework of the European Union COST Action FA1207: “Towards Control of Avian Coronaviruses: Strategies for Vaccination, Diagnosis and Surveillance”

SUMMARY. Viruses within the *Coronaviridae* family show variations within their genome sequences, especially within the major structural protein, the Spike (S) glycoprotein gene. Therefore, many different antigenic forms, serotypes, or variant strains of avian coronaviruses (AvCoV) exist worldwide. Only a few of them, the so called protectotypes, cross protect against different serotypes. New serotypes arise by recombination or spontaneous mutations. From time to time, antigenic virus variants appear which differ significantly from known serotypes. The result of this variability is an inconsistent nomenclature and classification of virus strains. Furthermore, there are currently no standard classification methods defined.

Within the framework of the COST Action FA1207 “Towards control of avian coronaviruses: strategies for diagnosis, surveillance, and vaccination” (working groups “Molecular virology” and “Epidemiology”), we aimed at defining and developing a unified and internationally standardized nomenclature and classification of AvCoVs. We recommend the use of “CoV Genus/AvCov/host/country/specimen id/year” to refer to AvCoV strains.

We launched a European Union “COST Action” (network centered around nationally funded research projects in fields that are of interest to at least five COST countries) in 2013 and created a network between scientists with expertise in AvCoV. The Action stimulates cooperation between researchers, fosters harmonization of nomenclature and classification, and facilitates surveillance. In order to achieve this and to cover all important aspects, five interlinked Working Groups were established which deal with Molecular Virology, Serology and Immunology, Host pathogen and receptor interactions, Epidemiology, and Conceptualizing an infrastructure for collaborative research, respectively. Furthermore, a joint website was created where general information on AvCoV, notifications of outbreaks and research results are shared between the COST members: <http://cost-controllingaviancoronaviruses.org/>. We present here the outcome from discussions within the framework of working groups “Molecular Virology” and “Epidemiology” on AvCoV nomenclature.

Avian Coronaviruses (AvCoV) include Infectious Bronchitis Virus (IBV), Turkey Coronavirus (TCoV), Pheasant Coronavirus (PhCoV), Duck Coronavirus (DuCoV), Goose Coronavirus (GoCoV), Pigeon Coronavirus (PiCoV), and Guinea fowl Coronavirus (GfCoV) group within Gamma-coronaviruses (gammaCoV) in the *Coronaviridae* family. AvCoV are highly infectious. Distributed worldwide, they cause severe diseases in layer-type and meat-type galliform birds. In turkeys and guinea fowls the virus affects the enteric system, whereas in chickens, the respiratory tract, gut, kidney, and reproductive system are main target organs. Decreases in performance, higher mortality, and poor meat and egg quality induce vast economic losses for European poultry producers. Another very important aspect is the increased prevalence of secondary bacterial infections in AvCoV affected flocks and the subsequently increased use of antibiotics. The risk of antibiotic resistance is thereby enhanced.

AvCoV show rapid mutation and high recombination rates, resulting in many different antigenic forms, serotypes, or variant strains worldwide. New serotypes arise by recombination or spontaneous mutations. They can emerge as a result of only a few

changes (2–3%) within the amino acid sequence of the S1 subunit of the viral spike protein. This S1 subunit is the major inducer of protective immunity and induces virus neutralizing antibodies. Although changes in the S1 subunit of the spike protein may occur, the majority of the virus genome remains largely unchanged. This may be the reason why a few serotypes provide protection against virus strains belonging to different serotype(s), which have therefore become known as protectotypes.

Most of the time mutations do not lead to the emergence of new variant strains/serotypes that pose a problem for poultry producers. Nevertheless, sometimes an economically important new pathogenic variant strain may arise. However, birds infected with different serotypes are quite differently affected, even though the sequence differences in part of the S1 subunit are sometimes insignificant; hence in regard of disease control it may be more relevant to think in terms of protectotypes rather than only genotype and/or serotype.

The more frequent use of molecular techniques to detect and classify AvCoV directly from clinical samples increased the reported data over the world. However it reduced the routine virus isolation and it is often unclear whether authors report data on clinical specimen or isolated virus.

The result of the high genetic and antigenic variability of AvCoV is an inconsistent nomenclature and classification of virus strains, leading to confusion and loss of valuable information. Furthermore there are currently no standard detection and classification methods defined. Fruitful discussions within the framework of the working groups “Molecular virology” and “Epidemiology” of the European Union COST Action FA1207 “Towards control of avian coronaviruses: strategies for diagnosis, surveillance and vaccination” led to the agreement that the following pieces of information are minimal to refer to AvCoV strains:

- Coronavirus Genus: gammaCoV for the large majority of domestic poultry AvCoV strains, deltaCoV in rare cases AvCoV, the official nomenclature for avian coronaviruses including infectious bronchitis virus, turkey coronavirus and their counterparts
- Host of origin

- Geographic site of detection (country or area depending on the part of the world and the surface of the country)
- Specimen identification (unique code given by the laboratory that should start with either an “S” for sample or an “I” for isolate depending on whether the original specimen was isolated or not)
- Year of specimen collection (4 digit)

We therefore recommend the following nomenclature for AvCoV specimens and isolates: CoV Genus/AvCov/host/country*/specimen id**/year [*country or area (depending on the part of the world and the surface of the country), ** S for sample and I for isolate + specimen unique identifier].

This standardized nomenclature should enable a better understanding between researchers worldwide on circulating AvCoVs and will allow larger scale epidemiology studies where the quality of the initial dataset information is a crucial prerequisite.

While we aimed at keeping the standardized nomenclature as simple and as short as possible to promote its use in practice, we still

recommend that researchers add more data on their virus strains when available both in genetic databases such as GenBank or EMBL and in research articles. We recommend that “old” names (given before this recommendation) stay as initially stated to avoid any confusion, unless researchers want to update their own records on public databases.

Sincerely,

The European Union COST Action FA1207

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