

## First molecular characterization of a Marek's disease virus strain detected from tumour-bearing turkeys

### Introduction

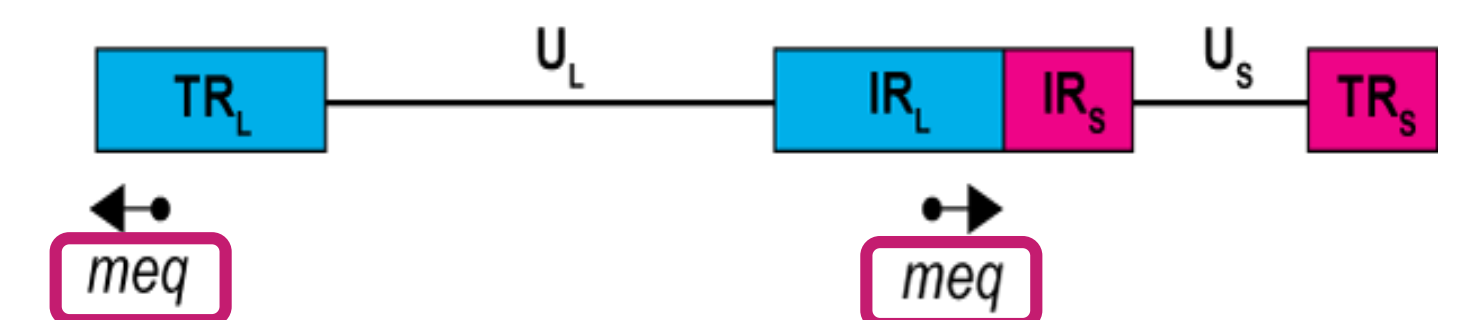
Marek's disease (MD) is a lymphoproliferative disease caused by *Gallid alphaherpesvirus 2* (GaHV-2), which affects primarily the chicken. The virus is able to induce tumours also in turkeys, even if this finding is unusual when compared to the frequency of occurrence in chickens. GaHV-2 embraces four pathotypes: mild, virulent, very virulent and very virulent plus. In the present study is reported the first description of GaHV-2-caused visceral tumours in Italian commercial turkeys, along with the molecular characterization of the GaHV-2 strain through *meq* gene sequence analysis and phylogeny.



### Commercial turkeys

During the year 2016, 3-4 months old white meat turkeys, reared on a commercial free-range farm located in the Lazio region of Italy, experienced mortality, associated, at post-mortem exam, to enlarged livers showing whitish lesions of lymphoproliferative nature. The flock was reared indoor since 50 days of age, then in outdoor pens adjacent to free-range broiler chickens' pens.

### PCR targeting the *meq* gene



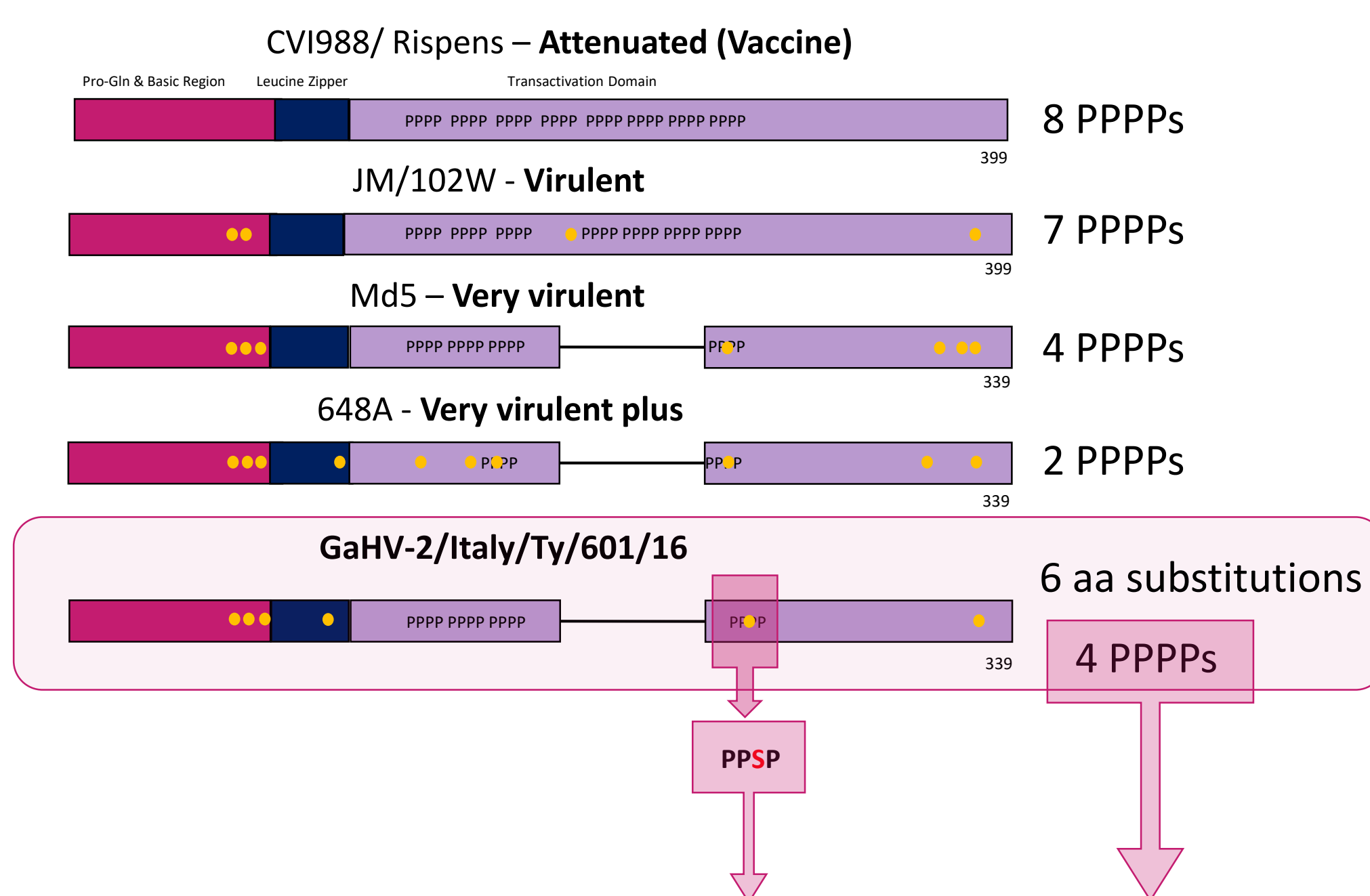
Tumour-bearing livers served for the genomic DNA extraction. The virus was detected with a specific PCR protocol targeting the full-length *meq* gene (Mescolini et al., 2019), the principal GaHV-2 oncogene. The *meq* gene carries virulence specific markers such as the number of four proline stretches (PPPP) within the transactivation domain: strains with a lower number of PPPPs and disrupted PPPP motifs, due to amino acid (aa) substitutions, showed higher virulence (Shamblin et al., 2004; Renz et al., 2012).

### Sequence and phylogenetic analysis

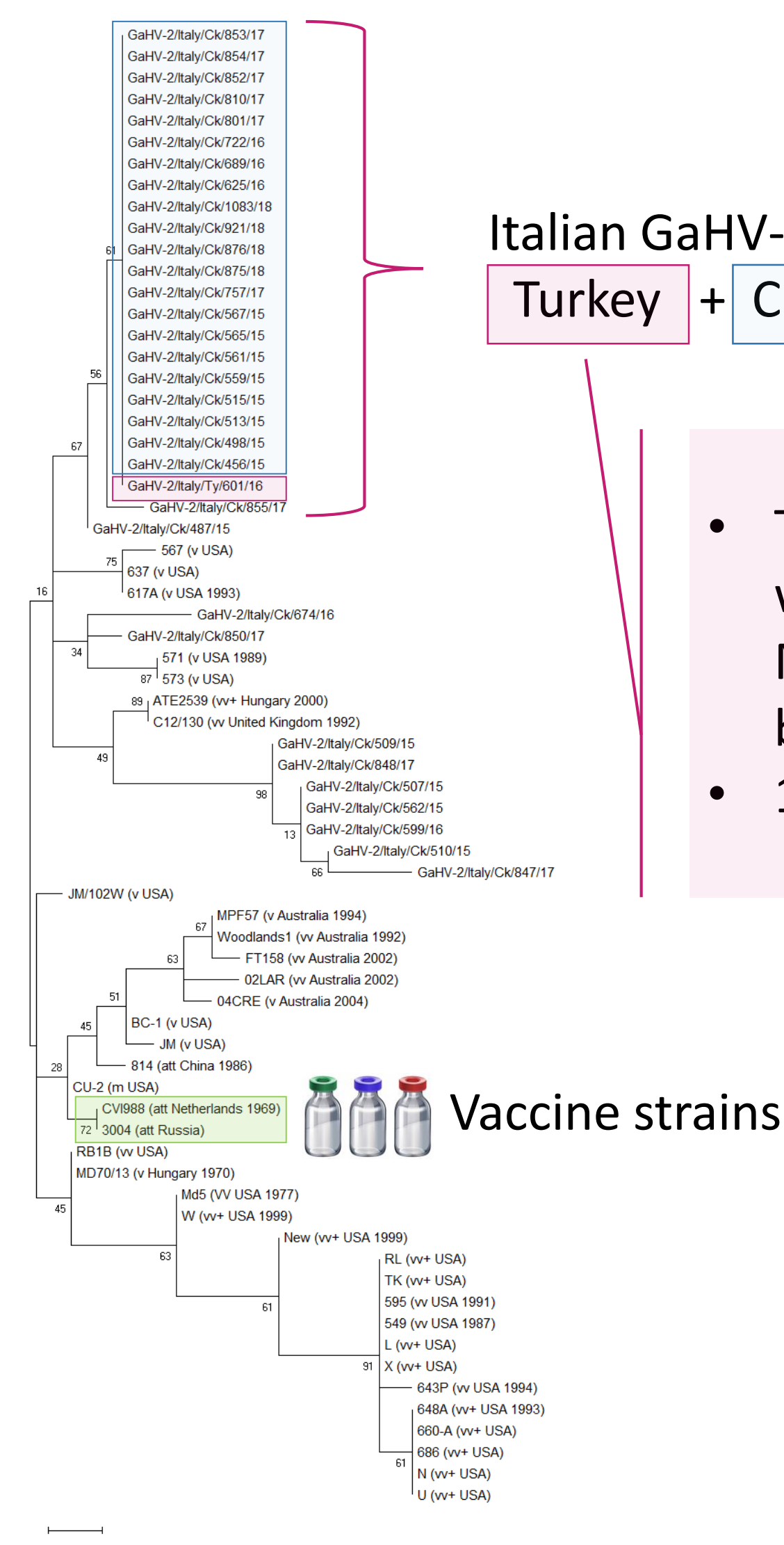
The amplicon was sequenced and the *meq* gene aa sequence was analyzed, using BioEdit software, and compared to prototype strains of known pathotype.

Phylogenetic analysis, was performed with the Maximum Likelihood method under the Jones–Taylor–Thornton model in MEGAX, using selected *meq* gene sequences retrieved from *GenBank*.

### Results

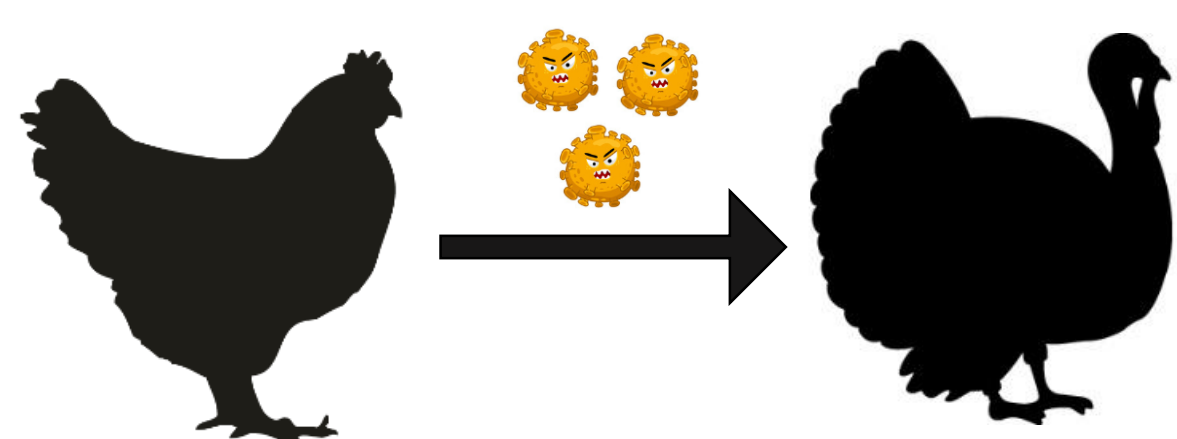


The Turkey strain encodes for a Meq protein with molecular characteristics of high virulence.



- The turkey strain clustered together with Italian strains detected during MD outbreaks in commercial and backyard chickens;
- 100% nucleotide sequence identity.

### Conclusions



- The turkey GaHV-2 showed molecular features of **high virulence** and was **closely related to chicken GaHV-2 strains** detected during MD outbreaks in commercial and backyard chicken flocks in Italy;
- GaHV-2 is ubiquitous among chickens, despite the vaccination, and **chicken-to-turkey transmission** was hypothesized due to the presence of broilers in neighboring pens.

### References

- Mescolini, G., Lupini, C., Felice, V., Guerrini, A., Silveira, F., Cecchinato, M., & Catelli, E. (2019). Molecular characterization of the *meq* gene of Marek's disease viruses detected in unvaccinated backyard chickens reveals the circulation of low- and high-virulence strains. *Poultry Science*, pii: pez095. doi: 10.3382/ps/pez095. [Epub ahead of print]
- Renz, K. G., Cooke, J., Clarke, N., Cheetham, B. F., Hussain, Z., Fakhru'l Islam, A. F. M., Tannock, G.A., & Walkden-Brown, S. W. (2012). Pathotyping of Australian isolates of Marek's disease virus and association of pathogenicity with *meq* gene polymorphism. *Avian Pathology*, 41(2), 161–176.
- Shamblin, C. E., Greene, N., Arumugaswami, V., Dienglewicz, R. L., & Parcells, M. S. (2004). Comparative analysis of Marek's disease virus (MDV) glycoprotein-, lytic antigen pp38- and transformation antigen Meq-encoding genes: Association of *meq* mutations with MDVs of high virulence. *Veterinary Microbiology*, 102(3–4), 147–167.