



ORAL COMMUNICATION(S)

MOLECULAR DETECTION AND CHARACTERIZATION OF SELECTED VIRUSES IN CAPTIVE PET BIRDS IN SICILY

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Birds are popular household pets and are frequently hosted at bird shows and zoological gardens. Their susceptibility to different viral infections poses a threat to animal health, with possible consequences for the economy and biodiversity. Psittacine beak and feather disease virus (PBFDV) from the Circoviridae family, and Gammapolyomavirus avis (APyV) from the Polyomaviridae family are two highly contagious viruses which can be associated with lethal outcome in young birds or chronic disease characterized by immunosuppression, feather loss, and concurrent infections in older/adult individuals [1]. Adenoviruses (AdV) are other common viruses in birds (as well as in psittacines) [2]. This viral group includes well-recognized pathogens together with a number of species with unclear clinical significance in birds. Despite the relevance of the topic, information on the spread and prevalence of these diseases across Italy remains very limited. Aiming, to partially fill this gap of information, this study investigated the molecular prevalence of PBFDV, APyV, and AdV in Sicily, analyzing individual risk factors associated with higher prevalence and sequencing some of the detected isolates to identify the most common strain or variant. A total of 166 oral-cloacal swabs were collected in captive pet birds from four Sicilian provinces (Messina, Catania, Palermo, Trapani) and belonging to various orders (Psittaciformes, Galliformes, Passeriformes and Musophagiformes). Both clinically healthy animals and those with symptoms were sampled. Symptomatic animals (45%) showed a wide range of clinical manifestations, including infectious-related, aspecific, or secondary signs such as lethargy, anorexia, diarrhea, respiratory and neurological distress, plumage disorders, feather damaging behavior, and alterations in hemato-biochemical profiles and complete blood

counts. After DNA extraction, each sample was assessed for the presence of specific nucleic acids using different PCR protocols described in the literature. The most prevalent pathogen was AdV (8.7%), followed by PBFDV (6%), which was identified as well in a Japanese quail for the first time, while APyV showed the lowest prevalence (0.6%). Fisher's exact test revealed a correlation between PBFDV positivity and age (young animals showed higher prevalence) and clinical signs. No risk factors were found to be associated with higher AdV prevalence. The sequencing results revealed a high nucleotide identity between PBFDV, APyV and PsAdV isolates and those described in other countries. The PBFDV and APyV (the first ever described in Italy), revealed a high similarity with genogroup I-c and I, respectively. The PsAdV sequence belonged to PsAdV-12 (the first documented sequences in Europe) from *Agapornis roseicollis* and PsAdV-2 from several parrot species. This study documented the spread of three different viruses in the bird population from Sicily, revealing risk factors that support virus dissemination and contributing to a better definition of the current epidemiological picture and the genetic features of the circulating strains.

[1] Kraberger et al. Incidence and diversity of circoviruses, polyomaviruses, and adenoviruses in exotic free-roaming rosy-faced lovebirds from Phoenix, Arizona, USA. *Virology*. 2025 Oct;611:110640.

[2] Molini et al. Investigation and sequence analysis of psittacine beak and feather disease virus and avian polyomavirus from companion birds in Windhoek, Namibia. *Acta Trop*. 2023 Feb;238:106739.