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Review

Harmless or Just Neglected? Revisiting the Role of 'Minor' Pig Viral Infections in Italy

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Abstract

In 2023, the Italian National Livestock Registry estimated that the pig population in Italy exceeded 8.1 million animals, with approximately 26,000 pig farms nationwide. The pig farming sector is highly concentrated in the northern regions, which account for about 89% of the national swine stock (ISMEA, 2024). Pig farming worldwide can generally be divided into intensive, semi-intensive, and extensive systems, each characterized by different management practices and biosecurity levels (Racewicz et al., 2021). In Italy, intensive systems predominate in the north and parts of the centre, often with a high degree of specialization and integrated production chains. Conversely, in the remaining central and southern regions, pig farming tends to be less specialized, frequently family-run, and strongly influenced by local customs and traditions (Bellini et al., 2009). This coexistence of diverse farming systems results in significant differences in herd management, biosecurity standards, production inputs, and market demands, all of which can directly or indirectly influence the spread of infectious diseases. In recent years, several emerging and re-emerging viral pathogens have been identified in swine populations worldwide, some with considerable clinical and economic impact, while others remain largely understudied, with uncertain effects on pig health. Advances in diagnostic technologies, such as next-generation sequencing (NGS), have improved virus detection, revealing the presence of previously undetected agents. This review aims to provide an updated overview of emerging swine viruses reported in the Italian pig industry, with particular attention to those whose roles within current farming systems are still unclear.

Keywords

emerging viruses, pigs, Italy, swine diseases

Introduction

In 2023, the Italian National Livestock Registry estimated the pig population in Italy at over 8.1 million, with approximately 26,000 pig farms. From a geographical perspective, 89% of the pig population is concentrated in the northern regions. Lombardy is the leading region in pig farming, accounting for about half of the national stock. It is followed by Piemonte and Emilia-Romagna, which contribute approximately 16% and 12%, respectively. The central and southern regions account for just over 11% of the national supply, with Umbria and Sardinia being the main contributors in these areas (ISMEA 2024). Worldwide, pig farming is generally categorized into three main systems: intensive, semi-intensive, and extensive. Intensive systems typically involve housing large groups of pigs indoors under tightly controlled management practices and stringent biosecurity protocols. In contrast, semi-intensive and extensive systems generally allow pigs to be raised in outdoor or partially outdoor settings (Racewicz et al., 2021). Currently, two distinct livestock farming systems coexist in Italy. In the northern regions and parts of Central Italy, intensive pig farming predominates, and in some areas, a high level of specialization is achieved through integrated production chains. In contrast, in the remaining central regions and in the south, pig farming tends to be less specialized, often characterized by mixed production systems, frequently family-run, and strongly influenced by local customs and traditions (Bellini et al., 2009). The coexistence of different pig farming systems results in a variety of management approaches, leading to differences in production scale, health standards, biosecurity levels, production

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inputs, market demands, and production costs. All these factors, directly or indirectly, influence the potential risk of disease spread (Julio Pinto & Santiago Urcelay, 2003). In recent years, several viral agents have emerged or re-emerged in swine populations globally. While some are associated with significant clinical disease and economic losses, others appear to have minimal or still uncertain effects on pig health (Meng & Thiel, 2020). The aim of this review is to provide an updated overview of emerging viral pathogens reported in the Italian pig industry, with a particular focus on those whose role within current management systems remain unclear.

Criteria used to select the reviewed studies

To identify emerging and understudied viral pathogens relevant to the Italian pig industry, we adopted a two-step approach. First, we examined reviews and scientific reports presented at national veterinary congresses, which were used to compile a preliminary list of pathogens of interest. Subsequently, we conducted a systematic search of the scientific literature published between January 2000 and June 2025. The search was performed in PubMed, Scopus, and Web of Science databases using combinations of keywords related to emerging infectious diseases, pigs, and the pathogens under investigation.

Porcine Astrovirus (PAstV)

Porcine astrovirus (PAstV) is a non-enveloped, single-stranded RNA virus belonging to the *Astroviridae* family. Its genome is approximately 6.8 to 7.9 kilobases in length (Monroe et al., 1993). Based on complete ORF2 gene sequences, PAstV is classified into five distinct genotypes (PAstV1 to PAstV5) (Wu et al., 2020). The virus has a global distribution, with an estimated prevalence of 28.19%, underscoring its significant impact on the pig farming industry and its contribution to increased economic losses in pig production worldwide (Ge et al., 2025). PAstV is particularly associated with enteric disease in piglets, especially around the weaning period (Kour et al., 2021; Ren et al., 2022; Puente et al., 2023). It is frequently detected in co-infections with other enteric pathogens such as rotavirus and coronavirus, which can exacerbate clinical symptoms (Shi et al., 2021). The data available on PAstV in Italy are limited. One study on faecal samples collected between 2012 and 2014 from swine herds in the northern, central, and southern regions of the country reported a prevalence of 67.4% (Monini et al., 2015). In a separate metagenomic study conducted on pig samples collected in 2015 from Northeast Italy, PoAstV2 was also detected (Tassoni et al., 2019).

Porcine Torovirus (PToV)

Porcine torovirus (PToV) is an enveloped virus with a linear, non-segmented, positive-sense single-stranded RNA genome. The genus *Torovirus* (ToV) belongs to the family *Tobaniviridae*, although it was historically classified under the family *Coronaviridae* (Ujike & Taguchi, 2021). PToV was first detected and characterized in piglet feces in the Netherlands in 1998 (Kroneman et al., 1998), but it has not yet been propagated in cell culture. Although PToV is more frequently detected in piglets with diarrhea than in healthy ones, its clinical significance remains unclear. Coinfections with other pathogens may contribute to the severity of symptoms. PToV has been reported worldwide, often at high prevalence (Hu et al., 2019). However, although its presence has been reported in Italy, there are no consistent data on its prevalence in pig farms. The only available evidence comes from a 2009 study in which torovirus-like particles were identified by electron microscopy in fecal samples from piglets with diarrhea, collected in 2002 in the province of Brescia, Northern Italy. Genetic analysis confirmed their identity as porcine torovirus (PToV-BRES) (Pignatelli et al., 2009).

New Porcine Parvovirus (PPV2-8)

Parvoviruses are small, non-enveloped viruses, approximately 25 nm in diameter, with a linear single-stranded DNA (ssDNA) genome ranging from 4 to 6 kilobases in length. They are widespread pathogens capable of causing various diseases in both animals and humans. In swine, eight distinct porcine parvoviruses (PPV1 to PPV8) have been identified, each classified within different genera and subfamilies of the *Parvoviridae* family. Specifically, PPV1 and PPV8 are members of the genus *Protoparvovirus*, PPV2 and PPV3 belong to *Tetraparvovirus*, and PPV4 and PPV6 are assigned to *Copiparvovirus*. PPV5 remains unclassified, whereas PPV7 has been placed in the newly established subfamily *Hamaparvovirinae*, within the genus *Chaphamaparvovirus* (Lau et al., 2008; Xiao et al., 2013; Ni et al., 2014; Palinski et al., 2016; Guo et al., 2022; Vargas-Bermudez et al., 2023). PPV2 through PPV8 are collectively referred to as "novel" porcine parvoviruses. Among these, PPV2 was first described in 2001 and has been proposed as a potential etiological agent of the porcine respiratory disease complex (PRDC) (Novosel et al., 2018; Nelsen et al., 2021). In contrast, the pathogenic roles of PPV3 through PPV8 remain unclear, and their involvement in disease processes is still under investigation (Jager et al., 2021; Vargas-Bermudez et al., 2023). Epidemiological investigations conducted worldwide indicate that the prevalence of novel porcine parvoviruses (nPPVs) tends to be higher in fattening and finishing pigs, while it is comparatively lower in suckling and weaned piglets (Milek et al., 2019; Lagan et al., 2021). The presence of novel porcine parvoviruses (nPPVs) has also been reported in recent years in Italy. A retrospective study conducted in Northern Italy identified emerging PPVs both as single infections and in co-infection with other pathogens commonly associated with reproductive failure in pig farms (Faustini et al., 2024). In addition, PPV3 was detected in wild boar populations in Southern Italy (Amoroso et al., 2019). Between 2020 and 2022, PPV7 was identified in domestic pigs and, for the first time, in wild boar on the island of Sardinia, with a prevalence of 20.59% (Dei Giudici et al., 2024).

Porcine Bocavirus (PBoV)

Porcine bocavirus (PBoV) is a single-stranded DNA virus classified within the *Bocaparvovirus* genus of the *Parvoviridae* family. The genome is 4–6 kb and encodes three open reading frames (ORFs) (Prpić et al., 2024). Based on the complete VP1 gene, PBoV is divided into three groups, with Group 3 further subdivided into five subgroups (Zhou et al., 2018). It was first identified in 2009 in Sweden, alongside porcine circovirus 2 (PCV2) and torque tenovirus (TTV), in lymph nodes of pigs affected by postweaning multisystemic wasting syndrome (PMWS). Since its discovery, PBoV has been detected globally, primarily in weaned piglets sometimes at high prevalence, and is known for its wide tissue tropism. Nevertheless, significant variability has been reported depending on the study, country, animal category and diagnostic approach (Zhou et al., 2014). However, because it is frequently found in both healthy and symptomatic pigs, often in co-infection with other viruses, its role in causing disease remains uncertain (Aryal & Liu, 2021). In Italy, the presence of PBoV Group 1 was detected in an Italian Large White pig slaughtered in 2003 (Bovo et al., 2017). Later, in September 2011, a molecular study conducted in pig farms in Northern Italy showed that 16.4% of the samples and 22% of the farms tested positive, highlighting that weaning pigs are the most susceptible to infection (Canelli et al., 2012).

Torque teno sus virus (TTSuV)

Torque teno sus viruses (TTSuVs) are small, non-enveloped viruses characterized by a circular, single-stranded, negative-sense DNA genome of about 2.8 kilobases. They belong to the *Anelloviridae* family and contain a highly conserved untranslated region (UTR) along with several open reading frames (ORFs), including ORF1, ORF2, ORF3, and a gene encoding an NF-kB-like protein. Two major genera infect pigs and wild boars: *Iotatorquevirus*, which includes the species TTSuV1a, and *Kappatorquevirus*, encompassing TTSuVk2a and TTSuVk2b (Righi et al., 2022). These viruses are widespread globally, with prevalence rates in swine populations reported between 24% and 100% (Kekarainen & Segalés, 2012). Because of their common presence in both healthy and diseased animals, a direct causal role of TTSuVs in specific diseases has not been confirmed (Meng, 2012). However, co-infections involving TTSuVs and other significant swine pathogens, particularly PCVs, have been documented and may impact disease progression (Kekarainen et al., 2006; Ellis et al., 2008). The first investigation of TTSuV in Italy was carried out in 2006 and involved ten farms located in north-central regions of the country. The results indicated that TTSuV infection was widespread among intensively farmed swine, with an overall prevalence of 24%. Infection rates were notably higher in fattening farms (40%) compared to closed-cycle operations (11%), regardless of herd size (Martelli et al., 2006). A subsequent study conducted in Sardinia between 2012 and 2013 on clinically healthy pigs revealed a high overall infection rate of 83.2%. Among the detected species, TTSuV1 (20.4%) and TTSuVk2a (16%) were the most frequently identified. Additionally, co-infections involving multiple TTSuV species were common, affecting 45.4% of the animals examined (Blois et al., 2014). A study conducted on liver samples collected from 400 wild boars during the 2016-2020 hunting seasons in two provinces of Northern Italy (Sondrio and Parma) showed a prevalence of 4.5%. TTSuV1 and TTSuVk2a were detected in 2.7% and 2.5% of the positive liver samples, respectively. TTSuV1a and TTSuVk2a co-infection was observed (Righi et al., 2022).

Porcine kobuvirus (PKV)

Kobuvirus, a member of the *Picornaviridae* family, is a non-enveloped virus with a positive-sense single-stranded RNA genome. Porcine kobuvirus (PKV) was initially identified in 2007 in fecal samples from healthy neonatal piglets in a Hungarian herd (Reuter et al., 2008). Since that discovery, PKV has been reported globally in both symptomatic and asymptomatic pigs. However, its specific role in causing gastrointestinal disease remains uncertain. Current evidence suggests that PKV is unlikely to be a primary pathogen but may instead contribute as part of a complex of factors in the pathogenesis of multifactorial diseases (Eriksen, 2023). In Italy, molecular analyses confirmed PKV in fecal samples from 2000 and 2012, with detection rates of 57.5% and 49.7% in clinically healthy and diarrheic pigs, respectively (Di Bartolo et al., 2015). However, a survey conducted in Central Italy from November 2008 to December 2011 found a much lower PKV detection frequency, i.e. 3.85% of fecal samples from healthy pigs (Di Profio et al., 2013).

Porcine Calciviridae: Norovirus (NoV), Sapovirus (SaV) and Valovirus (ValV)

The family *Caliciviridae* currently includes 11 genera, with members of the genera *Norovirus* (NoV), *Sapovirus* (SaV), *Valovirus* (ValV), and *Vesivirus* (VESV) known to infect swine (Vinjé et al., 2019). Among these, NoVs, SaVs, and ValVs, collectively referred to as porcine enteric caliciviruses, are primarily transmitted through the fecal–oral route (Desselberger, 2019). These viruses are non-enveloped, single-stranded, positive-sense RNA viruses with genome lengths ranging from 7.3 to 8.5 kb (Green et al., 2000; Vinjé et al., 2019). Based on genome organization, members of the *Caliciviridae* family are divided into two groups. In NoVs, ORF1 is separated from ORFs 2 and 3 near the 3′ end, and an additional ORF4 (contained within ORF2) encodes a virulence factor (VF1). In contrast, SaVs and ValVs exhibit a large ORF1, a standard ORF2 (homologous to NoV ORF3), and a proposed ORF3 functionally analogous to NoV ORF4 (Goodfellow & Taube, 2016; Vinjé et al., 2019). Porcine caliciviruses are classified into genogroups and genotypes based on the sequence of the major capsid protein (VP1). NoVs are currently divided into 12 genogroups (GI–GX, GNA1, and GNA2), with porcine NoVs belonging to genogroup GII, specifically P-types GII.P11, GII.P18, and GII.P19 (van der Poel et al., 2000; Scheuer et al., 2013; Vinjé, 2015; Chhabra et al., 2020; Lucero et al., 2021; Cavicchio et al., 2022; Winder et al., 2022). SaVs exhibit substantial genetic diversity and are classified into 19 genogroups (Farkas et al., 2005; Scheuer et al., 2013; Oka et al., 2015; Yinda et al., 2017). Eight genogroups (GIII, GV, GVI, GVII, GVIII, GIX, GX, GXI) have been detected in pigs, while three (GIII, GV, GVI) have been found in wild boars (Reuter et al., 2010; Nagai et al., 2020; Davidson et al., 2022). Genogroup GIII is predominant in swine and includes several unassigned genotypes (>11), characterized by high intra- and inter-genotypic diversity (Nagai et al., 2020). To date, only a single genogroup (GI) and genotype (GI.1) of swine ValV has been described (Wang et al., 2011; Vinjé et al., 2019). NoVs infect various vertebrates, including humans and swine, and represent the leading cause of acute gastroenteritis outbreaks worldwide. In pigs, NoVs have been detected mainly in asymptomatic animals, with sporadic cases of detection in diarrheic swine. Detection spans all age groups, from suckling to finishing pigs, although prevalence remains generally low (<16.6%), with higher rates typically observed in older animals (>90 days) (Cunha et al., 2010; Cavicchio et al., 2020, 2022; Davidson et al., 2022). SaVs have been identified in numerous studies of pig herds worldwide, in both asymptomatic and diarrheic animals (Mauroy et al., 2008; Collins et al., 2009; Keum et al., 2009; Reuter et al., 2010; Stamelou et al., 2022). Experimental infections have confirmed the ability of SaVs to cause enteric disease in pigs (Guo et al., 2001). SaVs are found across all age groups but are most prevalent during the post-weaning period and can be involved in outbreaks (Cavicchio et al., 2022; Davidson et al., 2022). Reports of co-infection with other enteric caliciviruses or different SaV types in swine remain infrequent (Oka et al., 2015; Davidson et al., 2022). ValVs, originally described as St-Valérien-like caliciviruses, have been detected in Canada, the USA, Japan, and Italy, exclusively in fecal samples from older asymptomatic pigs (>4 months), with reported prevalence ranging from 2.6% to 23.8% (L'Homme et al., 2009; Di Martino et al., 2011; Wang et al., 2011; Sato et al., 2014). However, knowledge of their epidemiology, pathogenesis, and genetic diversity remains limited. In Italy, multiple studies have contributed to understanding the circulation of porcine caliciviruses. Between 2003 and 2006, fecal samples from diarrheic piglets in Northern and Central Italy were analyzed for porcine enteric caliciviruses. Calicivirus RNA was detected either alone or in co-infection with rotaviruses group A and C. No NoVs were found, whereas the majority of SaVs belonged to genogroup GIII (Martella et al., 2008a; Martella et al., 2008b). A retrospective molecular analysis of fecal samples collected from asymptomatic pigs in Emilia-Romagna (2006–2007) and diarrheic pigs sampled in 2012 revealed one NoV-positive case and 14 SaV-positive samples out of 201 (6.9%) in the first group. In the second group, no NoVs were detected, whereas 18 out of 89 samples (20%) were SaV-positive (Reuter et al., 2010; Di Bartolo et al., 2015). In 2007, two distinct NoV strains (GII.P11) were detected in swine farms in Northeastern Italy (Laconi et al., 2020). A follow-up investigation conducted in the same region between 2018 and 2019 revealed a prevalence of 11.4% and demonstrated the co-circulation of NoVs belonging to two different P-types, GII.P11 and, for the first time in Italy, GII.P18 (Cavicchio et al., 2020). Meanwhile, a study conducted between 2012 and 2014 on fecal samples collected from pigs at different production stages on swine farms located in Northern, Central, and Southern Italy showed no presence of NoV (Monini et al., 2015). ValV was first reported in Central Italy between 2008 and 2009 in five healthy pigs aged 24–36 weeks (Di Martino et al., 2011). Evidence of its widespread presence in Italian pig herds was further supported by a serological survey reporting a seroprevalence of 10.3% (Di

Martino et al., 2012).

Conclusion

In recent years, the incidence of emerging and re-emerging swine diseases has risen considerably. This trend is partly due to the introduction of advanced diagnostic technologies, such as next-generation sequencing (NGS), which target nucleotide sequences in complex diagnostic cases and enable the identification of previously undetected viruses. While emerging viruses that cause significant clinical disease in pigs or have zoonotic potential such as PRRSV, PCVs, and hepatitis E virus, have rightly attracted substantial attention, there remains limited knowledge about other emerging or re-emerging swine viruses whose impact on pig health is still uncertain. Many of these viruses are widespread in swine populations around the world but remain largely understudied. As a result, their biology, epidemiology, and pathogenic potential are not well understood (Meng, 2012; Perfumo et al., 2020). Moreover, the consequences of co-infections involving multiple swine pathogens on animal health warrant further investigation. This review highlights emerging swine viruses detected in Italy that have limited or unclear clinical relevance and emphasizes the need for comprehensive studies using conventional approaches, including in vivo and in vitro models. Considering globalization, which has facilitated the movement of animals and animal products, together with climate change, which has drastically modified the pig industry and influenced the spread of several vectors, there is a pressing need to establish national surveillance networks. These networks should be able to provide accurate data on the distribution of newly emerging swine diseases, while the routine implementation of next-generation sequencing (NGS) is essential to promptly identify novel pathogens and, in particular, monitor their evolution while circulating in pigs. The limited knowledge regarding newly emerging swine viruses, often detected as co-infecting pathogens, does not accurately depict the real risks they may pose for outbreaks and for pig production. Productive losses in subclinically infected animals are difficult to identify and are often overlooked by farmers and veterinarians, yet they can be highly detrimental to overall farm profitability. Only through longitudinal studies, systematic correlation of viral detection with clinical and productive data, and carefully designed *in vivo* trials involving individual emerging viruses will it be possible to generate reliable knowledge about the actual risks and impact these pathogens represent for the swine industry at the national level.

Ethical approval

Ethical approval was not required for these studies because no biological samples were used.

Conflict of interest

The authors declare that they have no conflict of interest.

Author Contributions

Conceptualization: UM, GF; Writing original draft preparation: UM, GF; Writing, review and editing: UM, GF.

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