The impact of the initial public health response to COVID-19 on swine health surveillance in Ontario

Tatiana Petukhova [a,*], David L. Pearl [a], Maria Spinato [b], Jim Fairles [b], Murray Hazlett [b], Zvonimir Poljak [a]

[a] Department of Population Medicine, University of Guelph, ON N1G 2W1, Canada
[b] Animal Health Laboratory, University of Guelph, ON N1G 2W1, Canada

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ABSTRACT

COVID-19 restrictions and the pandemic have affected animal health and food production through the disease's effects on human activities. COVID-19 impact on swine health surveillance can be assessed by investigating submissions and test positivity for pathogens before and after COVID-19 restrictions. PRRSV, Influenza A virus, *Mycoplasma hyopneumoniae* and PCV-2 are considered important and economically challenging respiratory diseases for the swine populations. By reviewing test results from swine samples submitted for diagnostic testing to a regional diagnostic laboratory, and by assessing total submissions, total positive tests, and the proportion of positive tests at weekly intervals with time series techniques and generalized linear regression models, we evaluated COVID-19's impact on the monitoring of these respiratory pathogens in Ontario, Canada. We classified weeks that fell from week 12 through week 24 in each year as pandemic equivalent weeks and the non-pandemic weeks included all other weeks. The pandemic period in 2020 resulted in a significantly higher number of submissions ($p < 0.05$) and PRRSV positive submission counts ($p < 0.05$) when compared to equivalent time periods in previous years; however, no changes could be detected in the odds of weekly PRRSV submission positivity. Weekly positive proportions of PCV-2 tests were higher during the pandemic period in 2020 compared with the pandemic equivalent period in 2018 and 2017. The counts of submissions that requested tests for PRRSV, Influenza A virus and *M. hyopneumonia* combined, as well as the number of submissions and the proportions of submissions that tested negative for these multiple respiratory pathogens were not significantly different between the pandemic period in 2020 and other periods examined. Our findings indicate that swine producers, in conjunction with various private and public veterinary support services, continued monitoring and performing diagnostic screening on farms for economically important animal diseases despite complications resulting from COVID-19 public health restrictions. PRRSV continues to have a serious impact on swine health. The absence of an increased proportion of negative tests for individual or groups of pathogens, or an accompanying increase in submissions during the 2020 pandemic period suggests that no new undetected pathogens with an impact on respiratory signs in swine were introduced during this time.

1. Introduction

Severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2), the causative agent of COVID-19, was initially detected in December 2019 and soon thereafter spread globally [1]. SARS-CoV-2 was first detected in Canada on January 25, 2020 [2,3]. In March 2020, different levels of government in Canada introduced social distancing measures. In Ontario, these measures included: social gathering restrictions in private residences, staffed businesses and facilities; closing high-contact locations; and physical distancing between non-family individuals, among others [4]. COVID-19 may also have had effects on the health and production of food animal populations through the disease's effects on human activities. In some jurisdictions, outbreaks of COVID-19 among workers in abattoirs resulted in the euthanasia of animals that could no longer be processed [5,6]. The impact of these supply chain issues may have also influenced the willingness and financial ability of producers to

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pay for diagnostic testing. Furthermore, social distancing measures and increased biosecurity concerns may have decreased indirect contacts between farms, leading to a decrease in transmission of pathogens. Studies have demonstrated that management practices that limit between farm contacts can reduce the prevalence of infections on swine farms [6]. Surveillance of infectious diseases in swine is a major issue for the pork industry due to high population turnover, and the frequent emergence of novel pathogens and variants of endemic pathogens [7,8]. Consequently, identifying if the COVID-19 pandemic is compromising infectious disease surveillance on swine farms is important for the
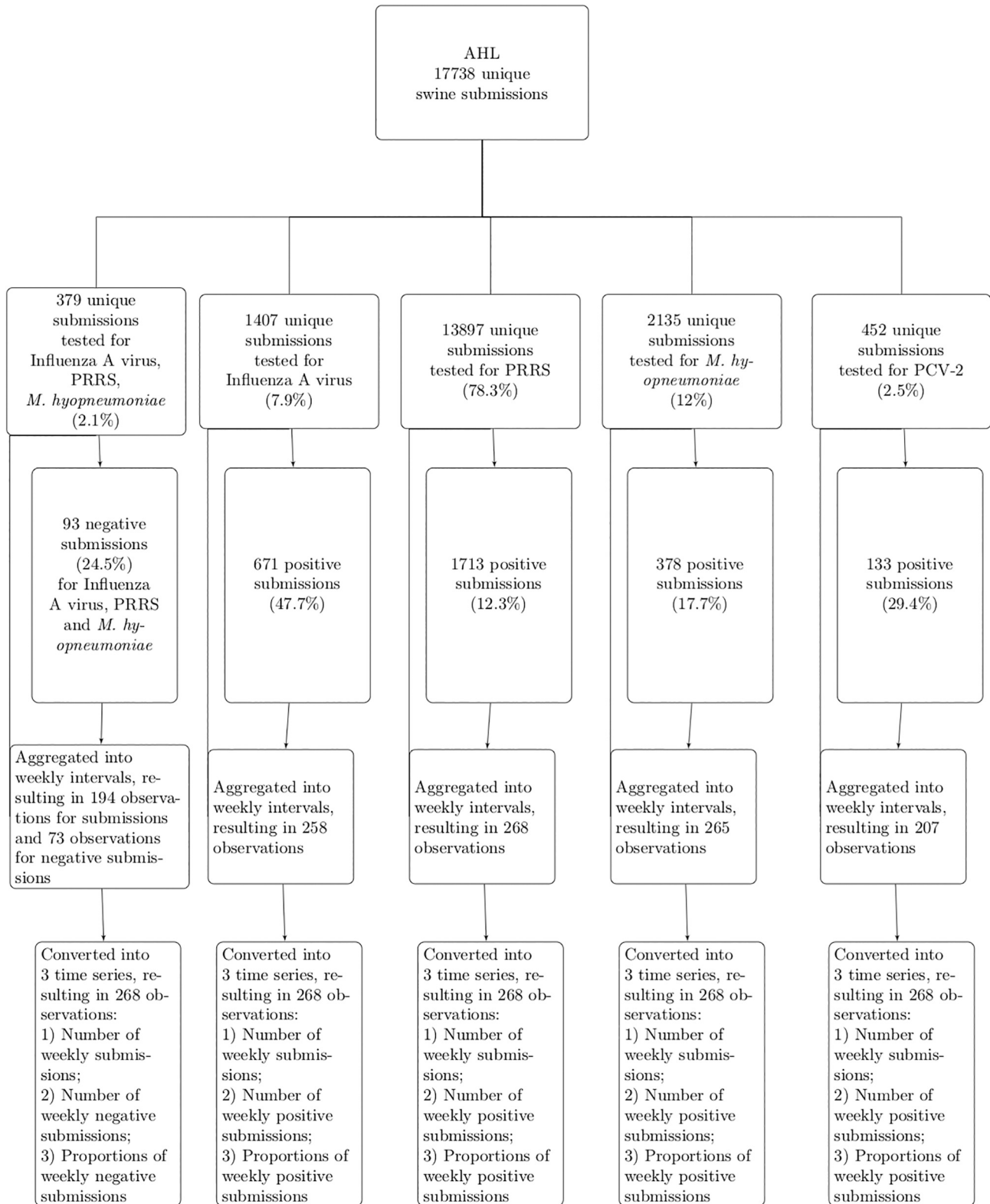

Fig. 1. Graphical illustration of extracted data based on unique submissions. Data were obtained from records of samples submitted from swine farms in Ontario, Canada, to the Animal Health Laboratory from May 1, 2015 through June 30, 2020.

industry. In addition, emergence of a new pathogen that consistently affects one body system (e.g., respiratory), could have caused an increase in the number of negative tests for other pathogens that cause similar clinical signs. The latter scenario has been previously reported by O'Sullivan et al. *who* observed an increase in the proportion of negative tests for porcine respiratory and reproductive syndrome virus during the emergence of porcine circovirus type 2 (PCV-2) [9,10] . Although SARS-CoV-2 does not affect swine [11], the increasing rate of discovery of emerging pathogens in swine has been documented [12], with the 2018 emergence of African swine fever in East Asia [13] being of notable concern throughout the global agricultural community. Thus, unexpected changes in the frequency of negative tests for common pathogens could be suggestive of the incursion of a new pathogen and useful for early detection. The objective of this study was to determine whether measures implemented during the early phase of the COVID-19 pandemic in Ontario (Canada) had an impact on testing for common swine respiratory pathogens.

2. Materials and methods

2.1. Data processing

Surveillance data were obtained from the Animal Health Laboratory (AHL, University of Guelph, ON, Canada). The original data consisted of univariably structured diagnostic assay results performed on 169,745 unique swine specimens submitted to the laboratory from May 1, 2015 to June 12, 2020 inclusive. Specimens were received daily from swine farms in Ontario and were supplied voluntarily. We processed the observations and extracted records relevant to Influenza A virus, PRRSV, *M. hyopneumoniae*, and PCV-2. As a result, we obtained records on 17,738 unique swine diagnostic submissions (Fig. 1). These records were results from tests applied to the same specimen or different specimens within a submission. That is, each diagnostic submission contained one or more samples from a swine facility on a specific date, and each sample was tested either for one pathogen or for several pathogens. The tests were from either traditional polymerase chain reaction (PCR) or real-time reverse transcription polymerase chain reaction (RT-PCR) procedures. Test results were reported categorically (positive/negative results). Any test that indicated a positive result for a pathogen was considered a positive individual test. A submission with at least one positive test for a specific pathogen was considered a positive submission for this pathogen.

Based on the laboratory records, the number of daily submissions and the number of daily positive submissions related to each disease were aggregated into weekly intervals with variables corresponding to the date of the beginning of the week, resulting in 15 individual datasets (Fig. 1). A week was considered to run from Monday to Sunday and each study year included 52 weeks. In those study years that included 53 weeks, the 53rd week was omitted to ensure the same number of weeks in each study year in order to convert outcome measures into comparable time series. Furthermore, the number of positive submissions for each pathogen counted by week was divided by the total count of submissions for the pathogen per week, resulting in the proportions of weekly positive submissions and the proportions of monthly positive submissions. As a result, we obtained the time series of the number of weekly submissions, the number of weekly positive submissions, and the proportions of weekly positive submissions for each disease. Each dataset and each time series were analyzed individually.

2.2. Statistical methods

We analyzed the total submission counts per week that were tested for Influenza A virus, PRRS virus, *M. hyopneumoniae* and PCV-2, the total submission counts per week that tested positive to these pathogens, and the proportions of these positive counts per week. That is, we converted these outcomes into 12 individual time series for time series analysis,

and we also used these outcomes as response variables for generalized linear regression models (GLMs). Furthermore, we examined the possibility of a new undetected respiratory pathogen by considering submissions that were tested for Influenza A virus, PRRS virus, and *M. hyopneumoniae* combined, and that resulted in negative tests. The total number of these submissions per week, the total number of negative submissions per week and the proportions of these negative counts were also analyzed using time series analysis and GLMs.

In total, 15 time series were decomposed to visualize trend, seasonal, and noise components using the "stl" function in the "stats" package in R. In addition, the 15 response variables were modeled with GLMs to examine the associations between years and pandemic vs. non-pandemic equivalent weeks. Years from 2015 to 2020 were fitted as a categorical variable. Weeks that fell from week 12 through week 24 were classified as pandemic equivalent weeks and the non-pandemic weeks included all other weeks. The dates for the pandemic equivalent weeks were defined based on the week when the Government of Ontario declared a state of emergency [2,4,14,15] until the end of the study period.

We modeled the count data with quasi-Poisson regression to account for overdispersion in the counts. The dispersion parameter was calculated by dividing the deviance χ^2 by its degrees of freedom, and the obtained value was assessed with the goodness-of-fit test. The proportions of weekly confirmed case counts were modeled using binomial/logistic regression. We assessed the overall significance of the interaction term between the variables year (modeled as a categorical variable) and pandemic$-$/non-pandemic-equivalent weeks using analysis of deviance. We then performed multiple pairwise comparisons to compare the pandemic period of 2020 with pandemic-equivalent periods of previous years in models with significant interaction terms. The multiple pairwise comparisons were adjusted with the Tukey correction using the "ghlt" function in the "multcomp" package. The focus of the latter comparison was to evaluate whether the pandemic period of 2020 was different from the pandemic-equivalent periods of previous years when this interaction effect was statistically significant. The scatter plots of residuals were visually assessed to identify outliers. GLMs were fitted using the "glm" function in the "stats" package with R statistical software version 4.0.0 [16] with a 5% significance level.

3. Results

3.1. Descriptive analysis

During the study period, the proportion of positive test results for swine submissions related to the respiratory pathogens being examined were the following: 47.7% for Influenza A virus; 12.3% for PRRSV; 17.7% for *M. hyopneumoniae*; 29.4% for PCV-2 (Fig. 1). Almost a quarter of submissions (24.5%) tested negative where they were tested for Influenza A, PRRSV, and *M. hyopneumoniae* combined (Fig. 1).

3.2. Time series analyses

Visual inspection of the time series decompositions revealed an increase in the long-term trend for the number of weekly swine submissions for Influenza A, PRRSV, and *M. hyopneumoniae* testing, while the trend for submissions for PCV-2 testing remained relatively stable (Fig. 2; Supplementary Figs. 1–13). Trends in weekly positive swine submissions and the proportions of weekly positive swine submissions varied over the study period with an increasing trend in the final year for most time series studied (Fig. 2). Trends in weekly counts of submissions that were tested for PRRSV, Influenza A virus and *M. hyopneumoniae* combined and weekly counts testing negative to these three pathogens seem to be relatively stable, while the trend in the proportions of triple-negative swine pathogen submissions appears to have an inconsistent behaviour.

Visual inspection of the count time series for Influenza A virus, PRRSV, and *M. hyopneumoniae* combined suggests that the majority of
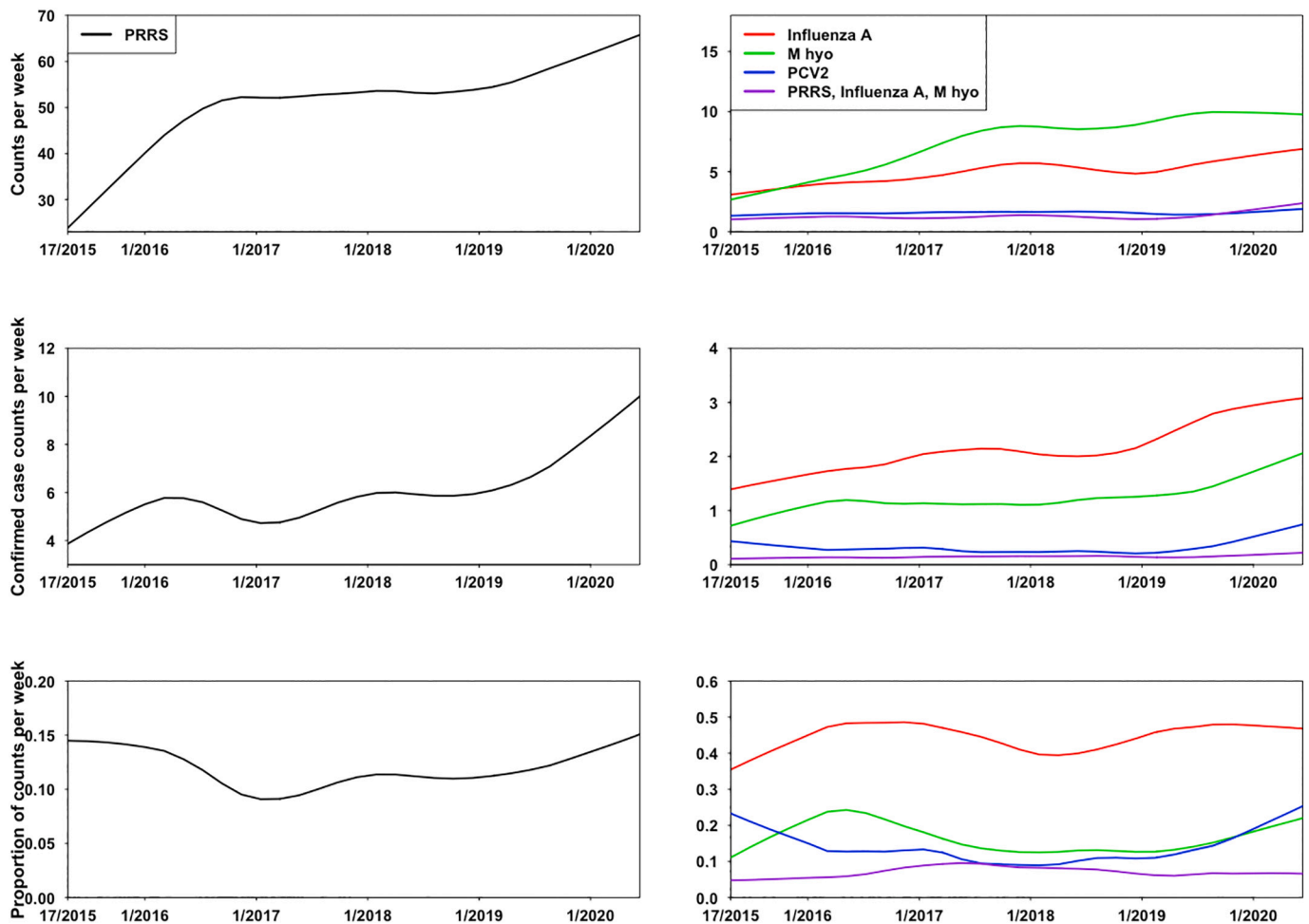
Fig. 2. Trends in four respiratory infectious diseases based on submissions to the Animal Health Laboratory from swine farms in Ontario. The trends for Porcine Reproductive and Respiratory Syndrome virus (PRRSV) are shown in black; Influenza A virus, shown in red; *Mycoplasma hyopneumoniae* bacteria (M. hyo), shown in green; Porcine circovirus type 2 (PCV-2), shown in blue. The trends for three respiratory pathogens combined were extracted after the decomposition of each time series, shown in purple.

submissions that were tested for all these respiratory pathogens were tested in fall 2015 (6%), from fall 2017 to spring 2018 (21%), and from fall 2019 to spring 2020 (21%) (Fig. 3A). About 27% of the submissions for the three respiratory pathogens tested negative from fall 2017 to fall 2018, and 18% of the submissions tested negative for the three pathogens from the end of the fall 2019 through winter 2020 (Fig. 3B).

The overall significance from global tests for an interaction between year and pandemic-/non-pandemic-equivalent weeks for four swine pathogens and for triple-negative swine pathogen submissions are summarized in Table 1. Based on these global tests, significant interactions were identified in models with the following outcomes: the number of weekly swine submissions, the number of weekly positive swine submissions, and the proportions of weekly positive swine submissions for PRRS virus (Table 1); and in the proportions of weekly positive swine submissions for PCV-2 (Table 1).

3.3. PRRSV

In the pandemic equivalent weeks, the number of submissions and number of positive submissions were significantly higher in 2020 compared to all previous years (Table 2). However, the odds of testing positive during the pandemic weeks of 2020 were not significantly different from the odds of testing positive in pandemic equivalent weeks of previous years (Table 2). In the non-pandemic weeks, the submission counts and positive submission counts were significantly higher in 2020

compared to 2017 and 2015 (Table 2), while the odds of testing positive were significantly higher in 2020 compared to only 2017 (Table 2). Full model results and contrasts comparing years for all pandemic-equivalent and non-pandemic-equivalent periods are presented in Tables S1 and S2, respectively.

3.4. PCV-2

The interactions between year and pandemic−/non-pandemic-equivalent weeks were not significantly associated with submission counts, positive submission counts, or the proportion of positive submissions when evaluated through a global test (Table 1) or contrasts after adjusting for multiple testing (Table 3), indicating no significant differences in the number of submissions, number of positive submissions, or the proportion of positive submissions for PCV-2 in the pandemic period of 2020 compared to equivalent periods in other years. The odds of testing positive were notably greater in 2020 compared to 2018 and 2017 (Table 3). Full model results and contrasts comparing years for all pandemic-equivalent and non-pandemic-equivalent periods are presented in Tables S3 and S4.

3.5. Influenza A virus

The global tests for interactions between year and pandemic−/non-pandemic equivalent weeks were not statistically significant for any of
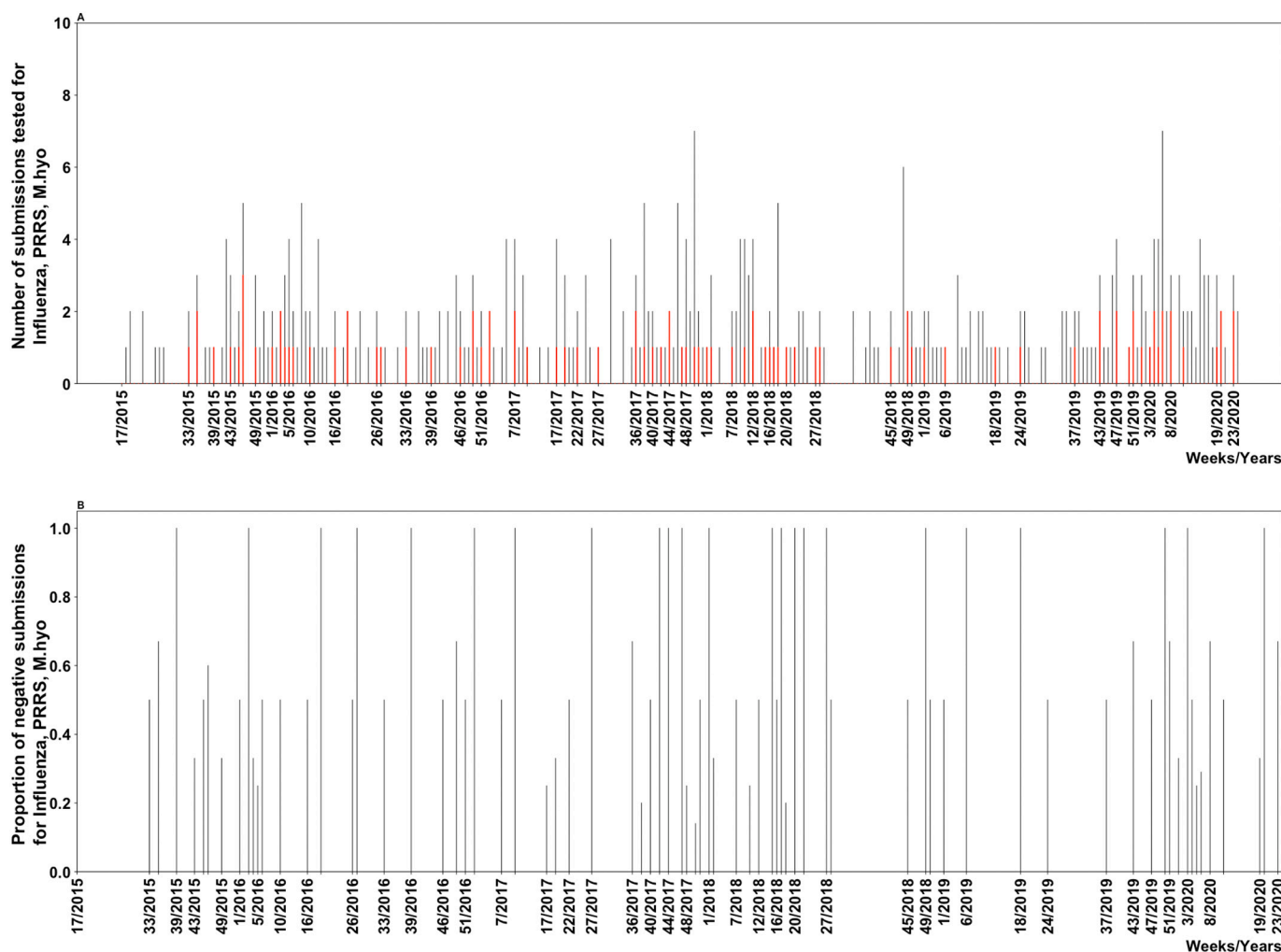
Fig. 3. Time series of the number of weekly unique swine submissions tested for the three respiratory infectious diseases combined. A) Number of weekly swine submissions tested for Influenza A virus, Porcine Reproductive and Respiratory Syndrome virus (PRRSV), and *M. hyopneumoniae* (M.hyo) are shown in black, and the number of weekly swine submissions negative to all three pathogens are shown in red. B) The proportions of weekly swine submissions negative for all three pathogens.

Table 1

Overall statistical significance from global tests for an interaction between year and pandemic-/non-pandemic-equivalent weeks for four swine pathogens and for triple-negative swine pathogen submissions in Ontario (2015–2020).

Pathogens	Submission rate[a]	Positive submission rate[a]	Proportion of positive submissions[b]
	P-values	P-values	P-values
PRRSV	0.001	0.004	0.04
Influenza A virus	0.61	0.62	0.24
Mycoplasma hyopneumoniae	0.98	0.53	0.29
PCV-2	0.41	0.38	0.01
Triple negative submissions	0.88	0.44	0.68

[a] Submission rate (counts/week); positive submission rate (positive counts per week); proportion of positive submissions (proportion of weekly submissions that tested positive).

[b] Except for triple negative submissions (negative for PRRSV, Influenza A virus, and *M. hyopneumoniae*).

the weekly parameters evaluated (Table 1). The results from regression analyses for Influenza A virus are summarized in Table S5. The number of weekly submissions and positive submissions were significantly higher in 2020 compared to 2015, but there were no significant

differences between the pandemic-equivalent and non-pandemic-equivalent weeks. In contrast, the odds of testing positive were significantly greater in the pandemic-equivalent weeks than in the non-pandemic-equivalent weeks, but no significant differences were identified between years.

3.6. M. hyopneumoniae

The global tests for interactions between year and pandemic−/non-pandemic-equivalent weeks were not statistically significant for any of the weekly parameters evaluated for *M. hyopneumoniae* (Table 1). The results from regression analyses for *M. hyopneumoniae* are presented in Tables S6. The number of weekly submissions and positive submissions were significantly higher in 2020 compared to 2015, but there was no significant difference between the pandemic-equivalent and non-pandemic-equivalent weeks.

3.7. Submissions for PRRSV, Influenza A virus and M. hyopneumoniae combined

The global tests for interactions between year and pandemic−/non-pandemic equivalent weeks were not statistically significant for any of the following weekly parameters evaluated: (i) the total number of submissions for the three major respiratory pathogens (i.e., PRRSV,

Table 2
Contrasts between 2020 and previous study years in pandemic-/non-pandemic-equivalent weeks for the generalized linear models fit on Porcine Reproductive and Respiratory Syndrome virus data. The weekly submission rates and positive submission rates were fitted with quasi-Poisson regression models. The proportions of weekly positive submissions were fitted with a binomial/logistic regression model.

Variables	Submission rate			Positive submission rate			Proportion of positive submissions		
	IR	95%CI	P	IR	95%CI	P	OR	95%CI	P
Pandemic: 2020–2019	1.1	(1.01,1.3)	0.04	1.4	(0.9, 2.2)	0.09	1.4	(0.9, 2.2)	0.46
Pandemic: 2020–2018	1.3	(1.1, 1.5)	0.01	1.6	(1.1, 2.4)	0.02	1.5	(1, 2.4)	0.66
Pandemic: 2020–2017	1.3	(1.1, 1.5)	0.01	1.7	(1.1, 2.6)	0.01	1.7	(1.1, 2.6)	0.07
Pandemic: 2020–2016	1.4	(1.1, 1.6)	0.01	1.7	(1.1, 2.7)	0.01	1.7	(1.1, 2.7)	0.40
Pandemic: 2020–2015	2.0	(1.6, 2.4)	0.01	2.1	(1.3, 3.3)	0.01	2.0	(1.3, 3.3)	1.00
Non-Pandemic: 2020–2019	1.1	(0.9, 1.4)	0.42	1.5	(0.9, 2.6)	0.18	1.5	(0.9, 2.6)	0.35
Non-Pandemic: 2020–2018	1.2	(0.9, 1.5)	0.08	1.6	(0.9, 2.7)	0.08	1.6	(0.9, 2.7)	0.32
Non-Pandemic: 2020–2017	1.2	(1.1, 1.5)	0.03	2.1	(1.1, 3.6)	0.01	2.0	(1.1, 3.6)	0.01
Non-Pandemic: 2020–2016	1.1	(0.8, 1.3)	0.98	1.0	(0.6, 1.6)	1.00	1.0	(0.6, 1.6)	1.00
Non-Pandemic: 2020–2015	2.3	(1.7, 3.1)	0.01	3.2	(1.4, 7.1)	0.01	2.0	(0.8, 4.8)	0.82

Submission rate (counts/week); positive submission rate (positive counts per week); proportion of positive submissions (proportion of weekly submissions that tested positive); P: p-value (significance level was 0.05); 95% CI: 95% confidence interval; IR: Incidence rate ratio; OR: Odds ratio.

Table 3
Contrasts between 2020 and previous study years in the pandemic-equivalent and non-pandemic-equivalent weeks of the proportions of weekly positive submissions of PCV-2 based on a model fitted with binomial/logistic regression using a generalized linear model.

Variables	OR	95%CI	P
Pandemic: 2020–2019	2.2	(0.4, 11.4)	0.87
Pandemic: 2020–2018	5.2	(1, 28.0)	0.05
Pandemic: 2020–2017	5.2	(0.9, 28.4)	0.06
Pandemic: 2020–2016	2.9	(0.5, 15.6)	0.55
Pandemic: 2020–2015	2.5	(0.4, 13.3)	0.75
Non-Pandemic: 2020–2019	4.2	(0.3, 58.4)	0.78
Non-Pandemic: 2020–2018	0.7	(0.1, 4.9)	1.00
Non-Pandemic: 2020–2017	2.1	(0.2, 17.8)	0.98
Non-Pandemic: 2020–2016	3.7	(04, 36.1)	0.73
Non-Pandemic: 2020–2015	0.4	(0.02, 5.7)	0.98

P: p-value (significance level was 0.05); 95% CI: 95% confidence interval; OR: Odds ratio.

Influenza A virus and *M. hyopneumoniae)*; (ii) the number of submissions for the three major respiratory pathogens that tested negative (Table 1); and (iii) the proportion of submissions that tested negative for the three major respiratory pathogens (Table 1). In addition, there were no statistically significant differences in these outcomes between years or the pandemic-equivalent and non-pandemic-equivalent weeks (Tables 1 & S7). All the results of these regression analyses involving the different outcomes related to the combined testing of the three major swine respiratory pathogens are presented in Table S7.

4. Discussion

The data used for this study were obtained from the Animal Health Laboratory (AHL, University of Guelph, Guelph, Canada) which is the largest provincial animal health laboratory in Canada. During the study period, the majority of swine operations in Ontario would regularly submit specimens for diagnostic and surveillance purposes to this laboratory. It should be noted that in 2015 matrices validated for RT-PCR analysis in the laboratory may have been different compared to recent years because new matrices, such as oral fluids, had just become available in that year. Thus, comparisons of time periods were probably most relevant between other years. To avoid any impact of seasonality, our data analysis strategy was focused on comparing equivalent time periods (i.e., pandemic vs. non-pandemic equivalent periods. Importantly, the period characterized by stringent application of public health measures in the early phase of the COVID-19 pandemic in Ontario [4] could not be linked with a decrease in the number of submissions for any swine respiratory pathogens examined or a decrease in the number of positive

submissions. The only pathogen for which important differences were observed was PRRSV; both the number of weekly submissions and the number of positive weekly submissions were higher during the pandemic period of 2020, when compared to pandemic-equivalent periods of previous years. Simultaneously, changes in the percent weekly positivity could not be detected for this pathogen over identical periods of 2020 and previous years. These results should be interpreted while taking into consideration underlying reasons for testing, common infection control practices on farms, some of which are informed through the results of regular diagnostic testing, and the overall high awareness of biosecurity among owners and operators of commercial swine herds.

In general, although the results of testing for a single pathogen were analyzed as a single time series in this and other studies [17,18], the underlying reasons for submissions to test for the same pathogen may be different. Many factors contribute to the submission of specimens for testing for pathogens causing production-limiting diseases and the subsequent reporting to provincial veterinary authorities in Ontario including a pathogen' clinical impact and its epidemiological features [19,20]. In a recent survey of North-American swine veterinarians, participants indicated that disease control and emerging diseases are the two most important reasons for seeking scientifically researched information [21]. Diagnostic testing and surveillance are fundamental for disease control of endemic and emerging diseases, and from this perspective, the findings of this study are not surprising. The emergence of African swine fever in East Asia in 2018 marked another pivotal event that had an impact on the emergency preparedness of North American jurisdictions, including Ontario; producer organizations and veterinary authorities became more vigilant and increased emergency preparedness activities. It is difficult to speculate whether this had an impact on the results of our study. From a regulatory perspective, any suspicion of a disease resembling African swine fever or another reportable disease would have to be reported to the federal and provincial veterinary authorities and would result in a different sampling and testing pathway in the laboratory compared to non-reportable diseases.

For the diagnostic laboratory that provided the study data, veterinary practitioners had the opportunity to indicate if the sample was submitted for diagnostic or for monitoring purposes. Although the distinction between these categories was left to the veterinary practitioners, specimens submitted for diagnostic purposes were likely to be submitted as a response to clinical presentation. In contrast, specimens submitted for monitoring were more likely to be submitted in order to detect the circulation of a pathogen, commonly in the absence of clinical signs and could serve the purpose of early detection or confirming / establishing freedom from infection in individual herds. For example, the confirmation of a PRRSV outbreak in swine herds could be done with a small number of specimens from animals with a typical clinical

presentation, whereas monitoring for PRRSV in herds that are under a disease control program usually requires a higher number of specimens and follows widely-accepted procedures [22,23] that are used in North American jurisdictions by a substantial number of commercial swine farms. Although similar principles could be applied to multiple pathogens, the distinction between diagnostic testing and monitoring is probably most pronounced for PRRSV, because it is currently the most important viral disease in swine populations [23,24] due to its prevalence and impact, and because the results of monitoring directly inform herd-level decisions about disease control in a prescribed manner. Low average percent positivity for PRRSV (12.3%) suggests that a substantial proportion of submissions were tested for monitoring purposes. Equally important, however, is that the odds of testing positive submission did not change for PRRSV during the pandemic period of 2020, suggesting that the nature of PRRSV testing did not substantially change despite an increase in the number of total weekly submissions for PRRSV and number of PRRSV-positive weekly submissions that occurred during the same period. The finding that the number of submissions did not drop for any of the tested pathogens during the pandemic period may also be attributed to wide acceptance of disease surveillance as a necessary component of good production practices.

In this study, we only investigated the early phase of the COVID-19 pandemic in Canada, and it remains speculative whether these findings could be extrapolated to the subsequent time periods. Early surveys that were investigating social contact patterns among people in response to COVID-19 public health measures in Canada indicated high average compliance with public health measures and high average reductions in human contacts in May 2020 in Ontario. In contrast, later surveys showed an increase in human contacts in September and December 2020 in part because some public health restrictions were lifted [25,26]. However, to what extent the results of these surveys could be directly extrapolated to the population stratum involved in swine production is unknown. The diagnostic laboratory that provided the study data was able to continue operating during the initial pandemic phase. Any testing on swine samples was not affected and did not slow down despite some challenges in sourcing supplies and in rearranging some staffing, such as splitting teams and arranging longer workdays, to comply with required personnel separations in the laboratory to meet turnaround times and client test needs. As far as we know, the AHL has never had a unit significantly reduced because of COVID-19 and has never stopped testing. Considering all the above, we conclude that animal disease surveillance programs and the diagnostic laboratory were able to handle the challenges imposed by the COVID-19.

This specific aspect of animal health is contrary to the findings in human populations, where the number of procedures and some diagnostic testing experienced delays as a consequence of COVID-19 restrictions [27]. Nonetheless, any comparison to other sectors should be made cautiously since the impact of the latter restrictions could be dependent on the specific health sector and multiple criteria influencing services in the sector. In addition, the finding that there was no decline in the odds of testing positive with either an increase in demand for testing, or with no change in number of weekly submissions among either individual pathogens or the three major respiratory pathogens combined also suggests that no another unknown emerging respiratory infectious agent was introduced during this period.

The number of positive submissions also did not change during the pandemic period of 2020 for Influenza A virus, *M. hyopneumoniae,* and PCV-2, unlike the increase observed with PRRSV. If measures implemented during the pandemic further reduced indirect contacts between farms, a reduction in cases would be expected. However, the absence of such a result is not completely surprising. The frequent emergence of novel pathogens [7,8], the incidence and prevalence of important endemic pathogens, and the economic impact of swine pathogens have contributed to the implementation of high biosecurity standards in many commercial swine farms [28,29].

The only pathogen where the odds of testing positive was notably higher during the pandemic period of 2020 compared to equivalent periods in any other years was PCV-2. Specifically, our findings suggest that the nature of surveillance was different in the pandemic period of 2020 compared to the pandemic-equivalent periods in 2018 and 2017. However, this finding is challenging to interpret because PCR tests could be used for monitoring of the porcine circovirus type 2 virus, but positive PCR test is rarely used alone in order to confirm a case of porcine circovirus-associated disease (PCVAD). This is one of the reasons why PCV-2 test results were not used in the time series of negative tests.

5. Study limitations

One of the limitations in this study was that we could not determine the underlying reason for submitting specimens to the AHL for a pathogen test. It was also not clear if the nature of surveillance for the pathogens of interest had changed during the last six years, which also might have contributed to the intensity of surveillance and number of submissions. For example, the massive increase in the use of oral fluids and various environmental samples for specific pathogen testing could have influenced the convenience of sampling, the number of specimens required, and ultimately the frequency of testing in individual herds or the entire population.

6. Concluding remarks

In conclusion, we found that swine producers together with those providing veterinary services continued to prioritize monitoring and diagnostic screening for disease detection and monitoring on farms despite the impact of COVID-19 on human activities. In addition, the nature of PRRSV testing did not substantially change during this period, and PRRSV continued to have a serious impact on swine health. The nature of surveillance for PCV-2 appeared to be different, with the odds of testing positive in pandemic period of 2020 being higher, in comparison to equivalent periods in some earlier years. Finally, our results offered additional evidence that no new novel pathogens with an impact on respiratory signs in swine were introduced during this period.

Ethics statement

The authors declared that this research did not deal with animals. The University of Guelph Research Ethics Board (REB) approval number is 20-06-032.

Consent for publication

All authors read and approved the final version for publication consideration.

Declaration of Competing Interest

The authors affirm that there are no interests to declare.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.onehlt.2021.100338.

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