Swine Health Information Center

Swine Disease Reporting System (SDRS) report

February 28, 2018

What is the SDRS?

SHIC-funded, VDLs collaborative project, with **goal to** aggregate swine diagnostic data from participating reporting VDLs, and report in an intuitive format (web dashboards), describing dynamics of disease detection by pathogen or disease syndrome over time, specimen, age group, and geographical space.

Collaborators:

Iowa State University: Giovani Trevisan*, Leticia Linhares, Bret Crim; Poonam Dubey, Kent Schwartz, Rodger Main, Daniel Linhares**.

University of Minnesota: Mary Thurn, Kimberly VanderWaal, Andres Perez, Jerry Torrison.

Advisory Council:

The advisory group reviews the data to discuss it and provide their comments to try to give the data some context and thoughts about its interpretation: Clayton Johnson, Douglas Marthaler, Emily Byers, Hans Rotto, Jane C. Hennings, Jeremy Pittman, Mark Schwartz, Paul Sundberg, Paul Yeske, Pete Thomas, Rebecca Robbins, Tara Donovan

* Giovani Trevisan: Project coordinator. E-mail: trevisan@iastate.edu.
** Daniel Linhares: principal investigator. E-mail: linhares@iastate.edu.

How was the data aggregated?

SAS scripts were used to import raw data from LIMS, delete identifiers for clinic, producer, veterinarian, and addresses, preserving only information of diagnostic results, farm type, age group, specimen, date, and state of sample origin. The data was consolidated at a *case level* (accession ID).

For each pathogen, a cases was considered ‘positive’ when at least one sample tested positive by PCR.

The data was then exported from SAS to Microsoft Power BI, which is a business intelligence web-platform to visualize the data on a user-friendly manner (i.e. disease-specific dashboards).

Results

For this first report, all data was from the Iowa State University Veterinary Diagnostic Laboratory (ISU-VDL). The dashboards include data from molecular tests (PCR-based assays, and virus genotyping)

We are working with the University of Minnesota VDL (UMN-VDL) to incorporate their data, which should be available in the next report.

There was an effort to exclude research-related cases, preserving 'field' data. Thus, the following filters were applied:

- non porcine ➔ 248 cases 0.09 %;
- research-related cases ➔ 1,437 cases 0.52 %;
- exhibition and export lab results ➔ 222 cases 0.08 %;
- vaccine test ➔ 129 cases 0.04 %;
- vehicles, lagoon, manure tests ➔ 4,589 cases 1.68%;
- serology department tests ➔ 29,675 cases 10.84%;
- virology department tests ➔ 5,038 cases 1.84%;

In total, there were 234,408 PRRS cases, from January 2007 to February 2018; and

92,693 Porcine Enteric Coronaviruses (PED + PDCoV + TGE) cases from January 2007 to February 2018.

Increased proportion of PRRS submission in 2010, followed by relative decrease in 2013:

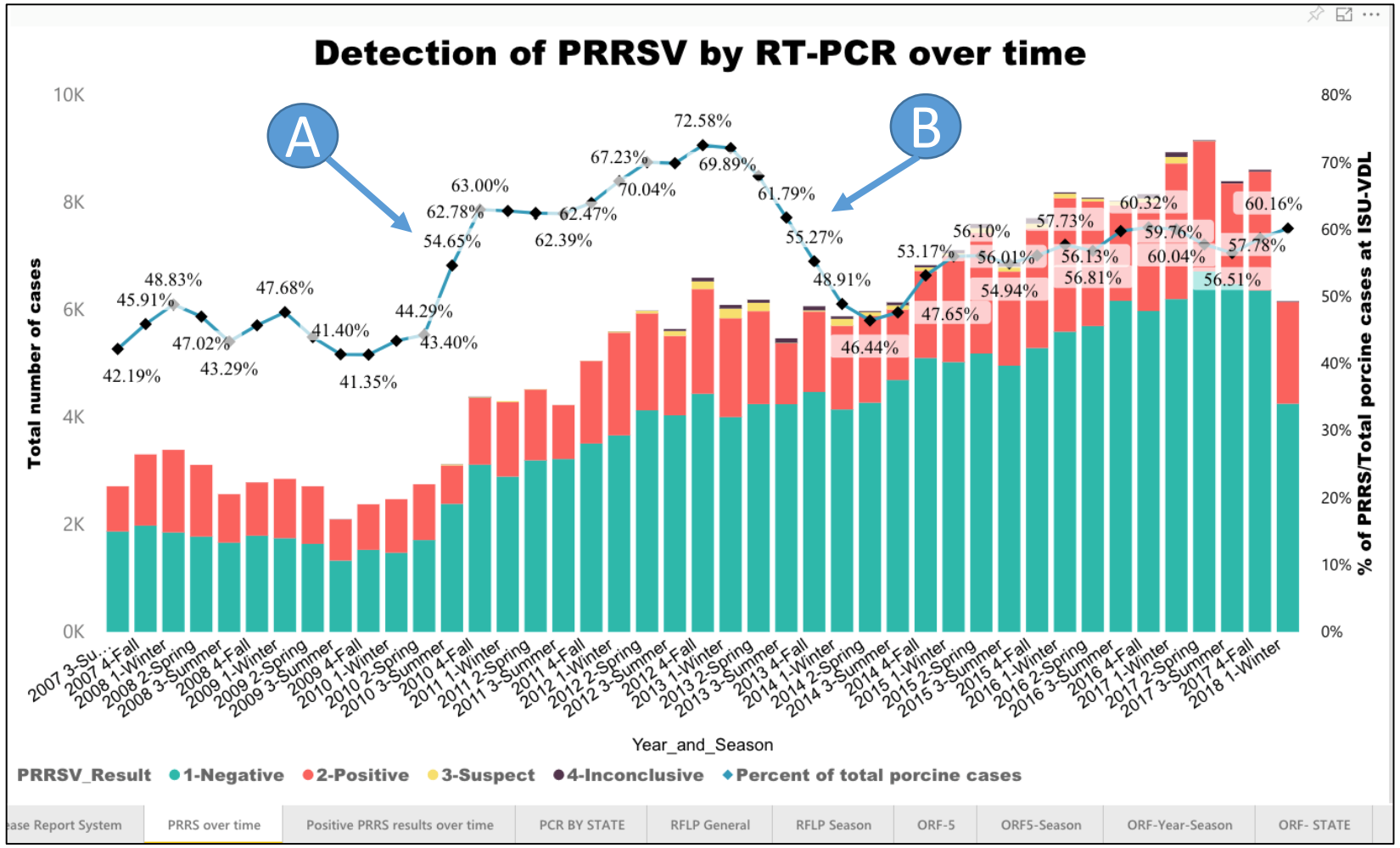


Figure 1 PRRSV RNA detection over time by rRT-PCR. Each bar indicates a season (Winter, Spring, Summer, Fall). Blue indicate cases that tested negative. Red represents cases with at least 1 positive sample. The line (secondary Y axis) represent percentage of cases tested for PRRS PCR relative to all other porcine submissions for molecular testing.

SDRC Advisory Council highlights:

A: Relative increase on % cases tested for PRRSv by rRT-PCR compared to all other porcine submissions at ISU-VDL in 2010, likely due to:

a) increase in OF-based monitoring;
b) publication of AASV guidelines for PRRSv terminology, stimulating people to monitor sow farms to define status;
c) increased use of MLV vaccination in sow farms, requiring people to monitor closely farms to differentiate wild type vs MLV-like virus.
d) The great majority of the increased testing was from cases with 'no tissue', suggesting that testing was for additional surveillance.

B: Relative decrease on % cases tested for PRRSv by rRT-PCR compared to all other porcine submissions at ISU-VDL in 2013, likely due to:

a) Increase of molecular testing for enteric coronaviruses (TGE and PED). With that, the total number of cases tested increased (larger denominator), decreasing the % cases tested for PRRS.

Increased proportion of PRRS submission in 2010, followed by relative decrease in 2013:

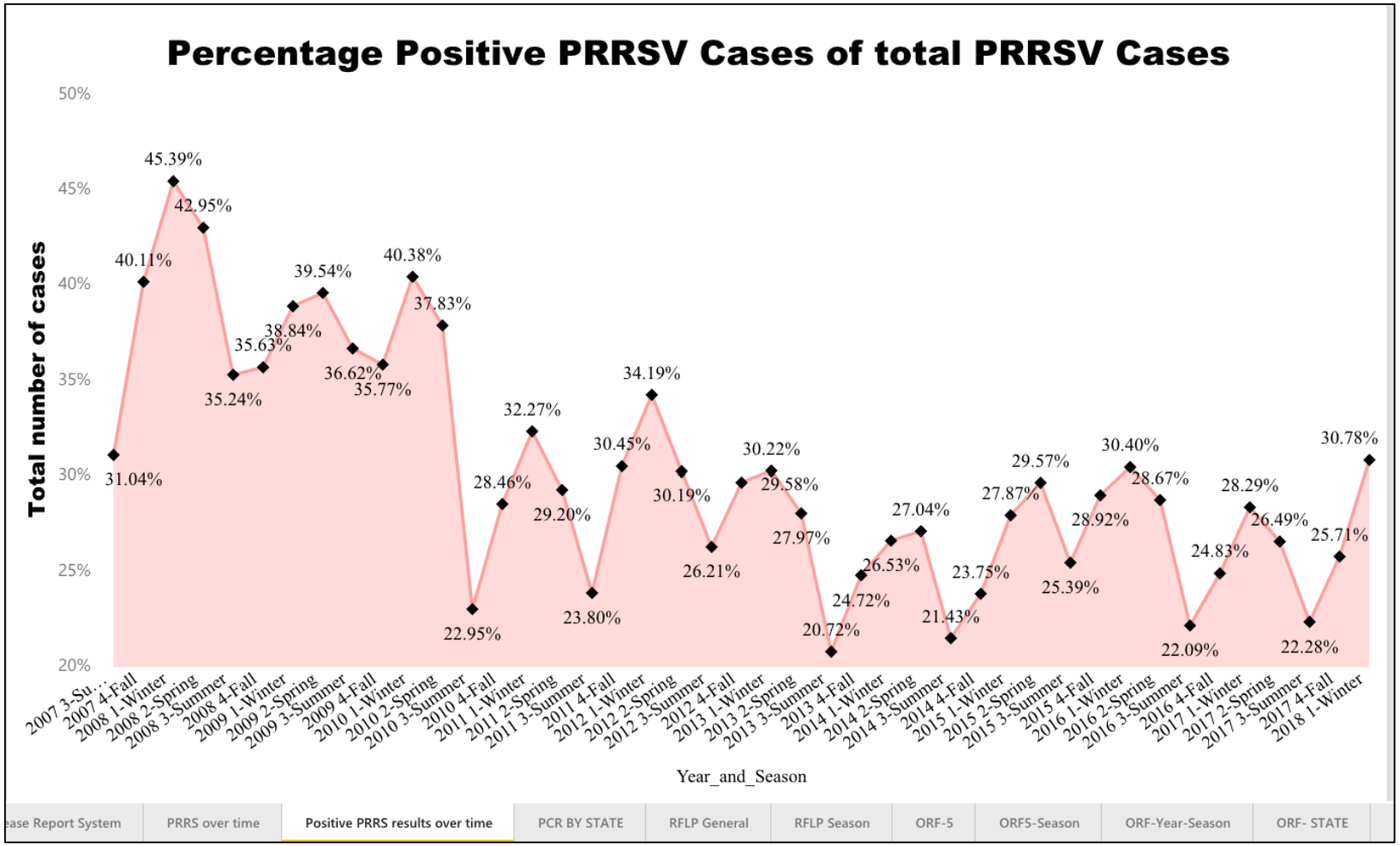


Figure 2 Percentage of cases tested positive for PRRSV RNA by rRT-PCR, over time.

SDRC Advisory Council highlights:

a) Clear seasonal (cyclic) pattern of increased percentage of PRRS-positive cases during Winter months (December, January, February).

b) The relative reduction of percentage positive cases after 2011 may also reflect increased monitoring for PRRSv due to same reasons indicated in the figure 1: incrased use of MLV vaccination, availability of the AASV guidelines for classifiying herds according to PRRS status, and increased use of oral fluids-based monitoring.

History of PRRSv detection by rRT-PCR, and Predicted Percentage of Positive Cases in 2018: not suggestive of significant deviation.

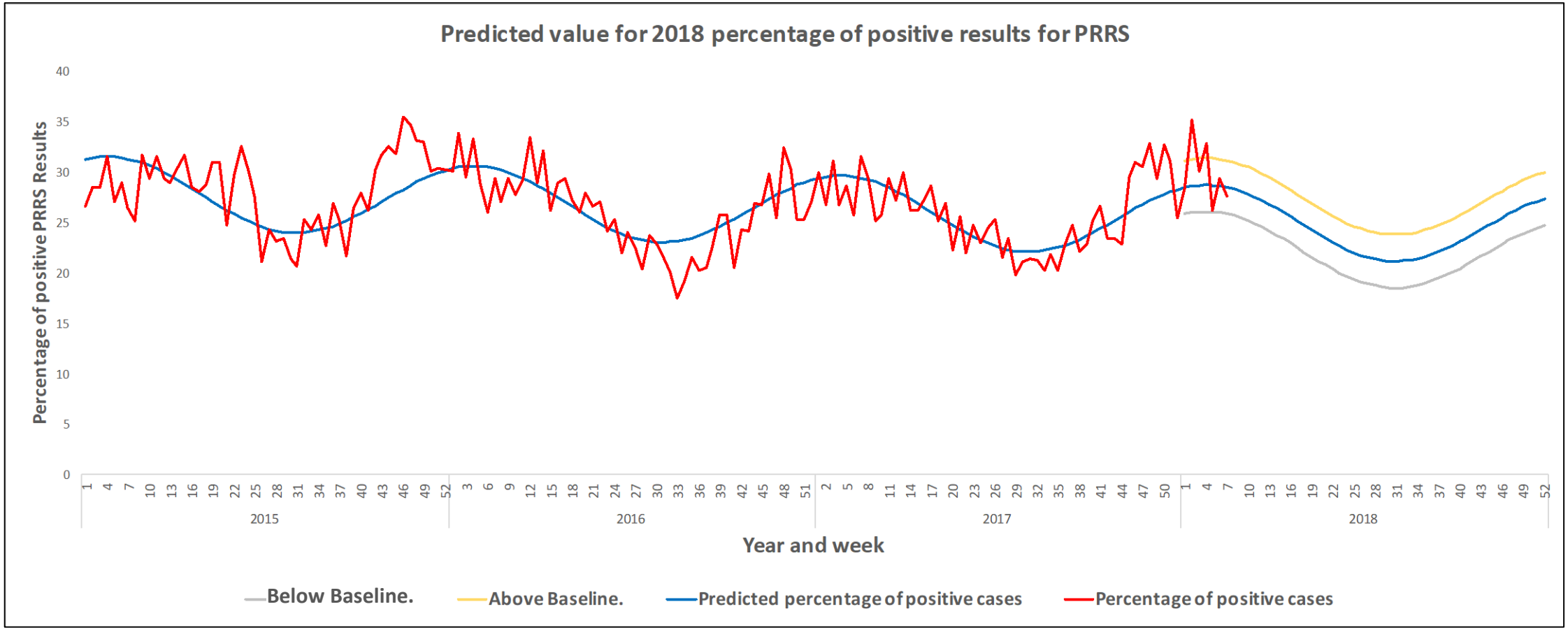


Figure 3 Cyclic pattern of PRRSv RNA detection by RT-PCR between 2015-2018. The red line represents the observed (real) values for percentage cases tested positive for PRRSV by RT-PCR. The blue line represents the expected moving average of percentage cases tested positive over time. The yellow and gray lines represent the upper and lower thresholds, respectively, based on 1 standard deviation of the blue (expected) line.
In other words, the number of expected positive cases in 2018 were built based on historic cyclic pattern observed between 2015-2017. The graph shows that the percentage of PRRSv-positive cases were within the expected based on historical data. This method was developed by Dr. Trevisan, in partnership with Dr. David J. Muscatello.

PRRS RFLP patterns over time:

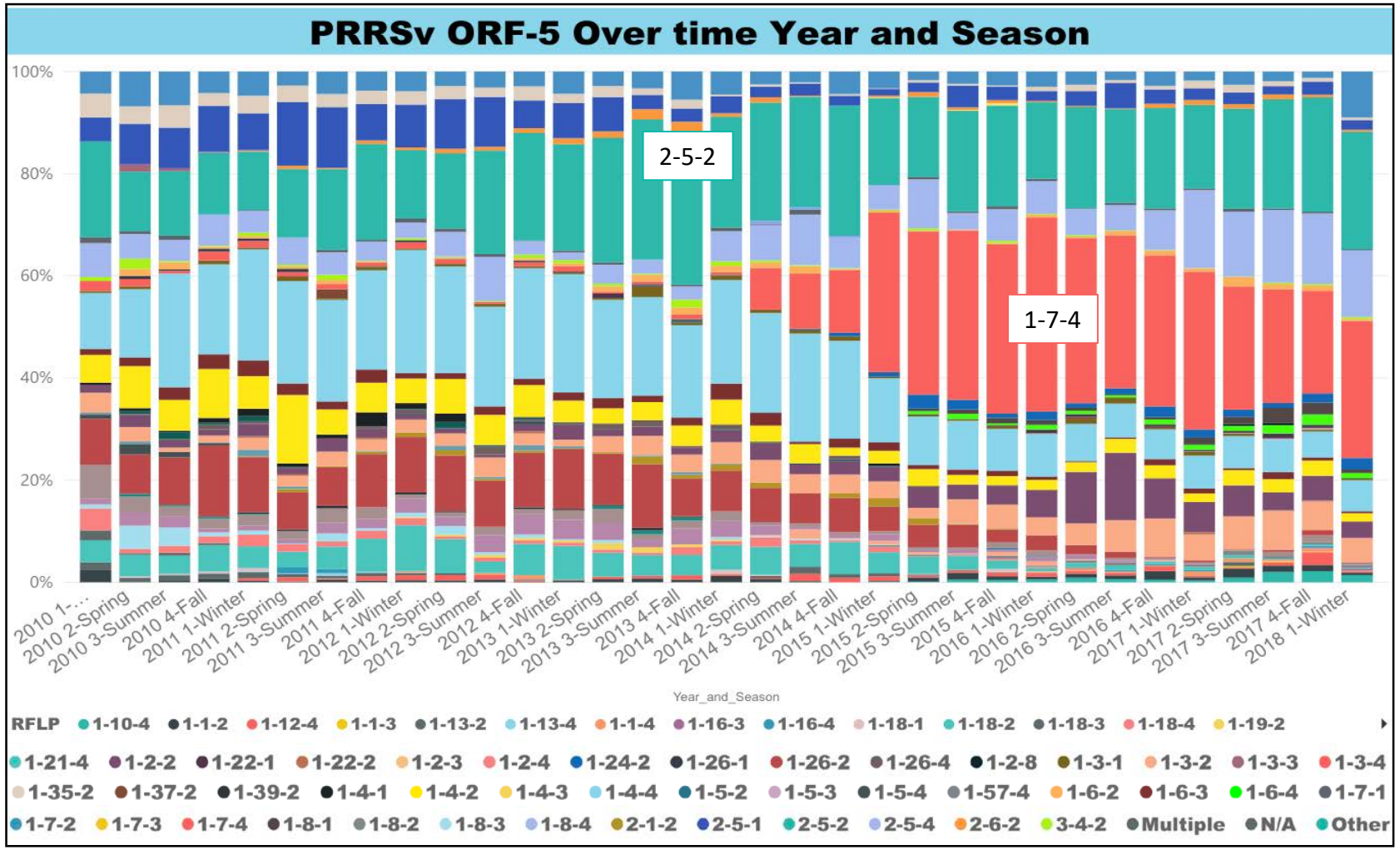


Figure 4 Porcine reproductive and respiratory syndrome virus (PRRSv) restriction fragment length polymorphism (RFLP) over time.

SDRC Advisory Council highlights:

a) Relative increase of 2-5-2 after 2011 (to about 20%, compared to about 13% before 2011), coinciding with the MSHMP report demonstrating increase use of modified-live virus (MLV) vaccine in breeding herds.

b) Increase of the 1-7-4 family on Spring of 2014.

Relative higher percentage of European PRRSV in NC, compared to other states

SDRC Advisory Council highlights:

a) The detection rate of European PRRSV is higher NC, compared to other states, in part due to endemic EU-PRRS circulation in some NC's flows/systems
b) Virulence of EU-PRRS is low compared to NA-PRRS
c) Veterinarians overseeing Midwest finisher flows that are importing NC pigs are aware of the EU-PRRS, and may not monitor finishing pigs, not detecting the virus in the Midwest in the same frequency that it is detected in NC sow farms.

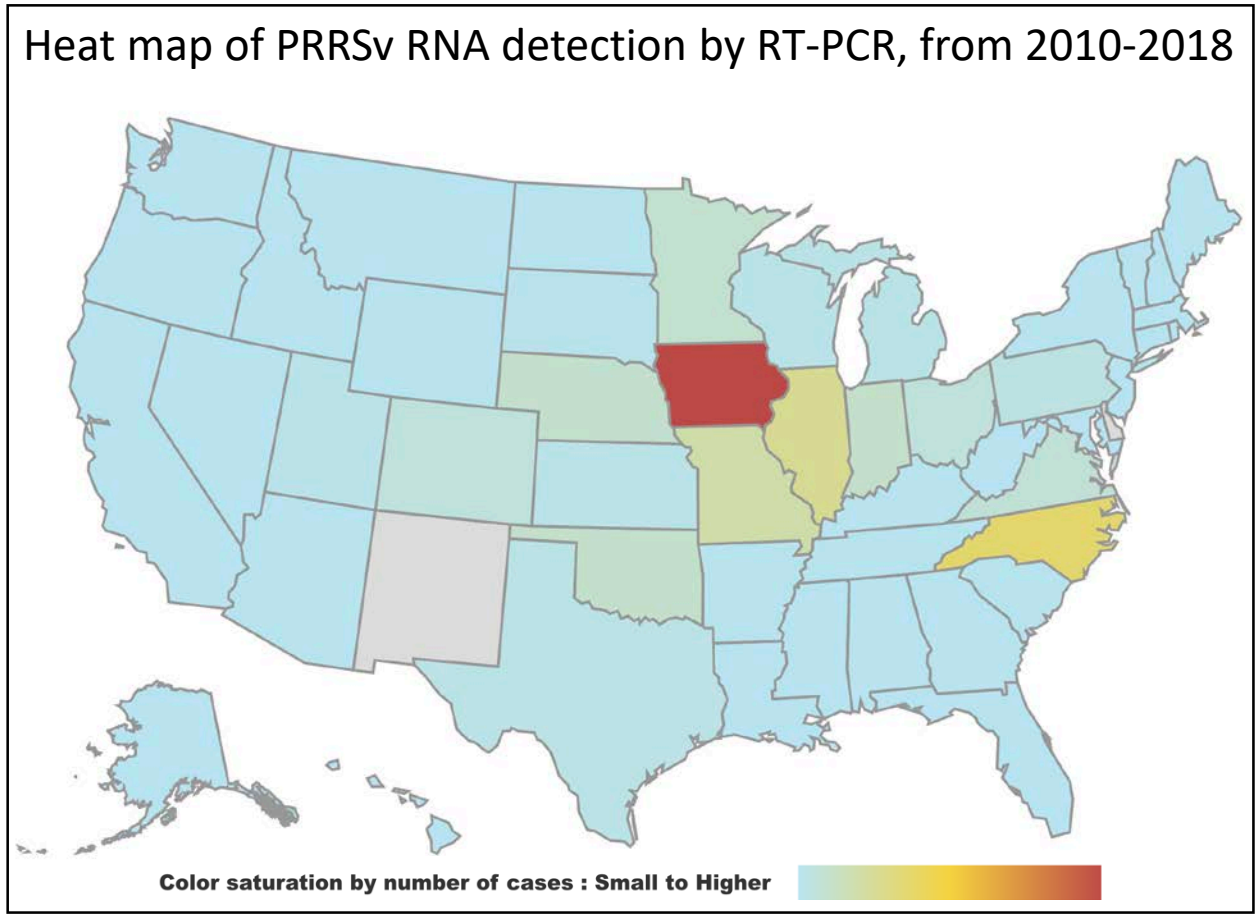


Figure 5a Number of positive cases for PRRSv, by State (**no filters**).

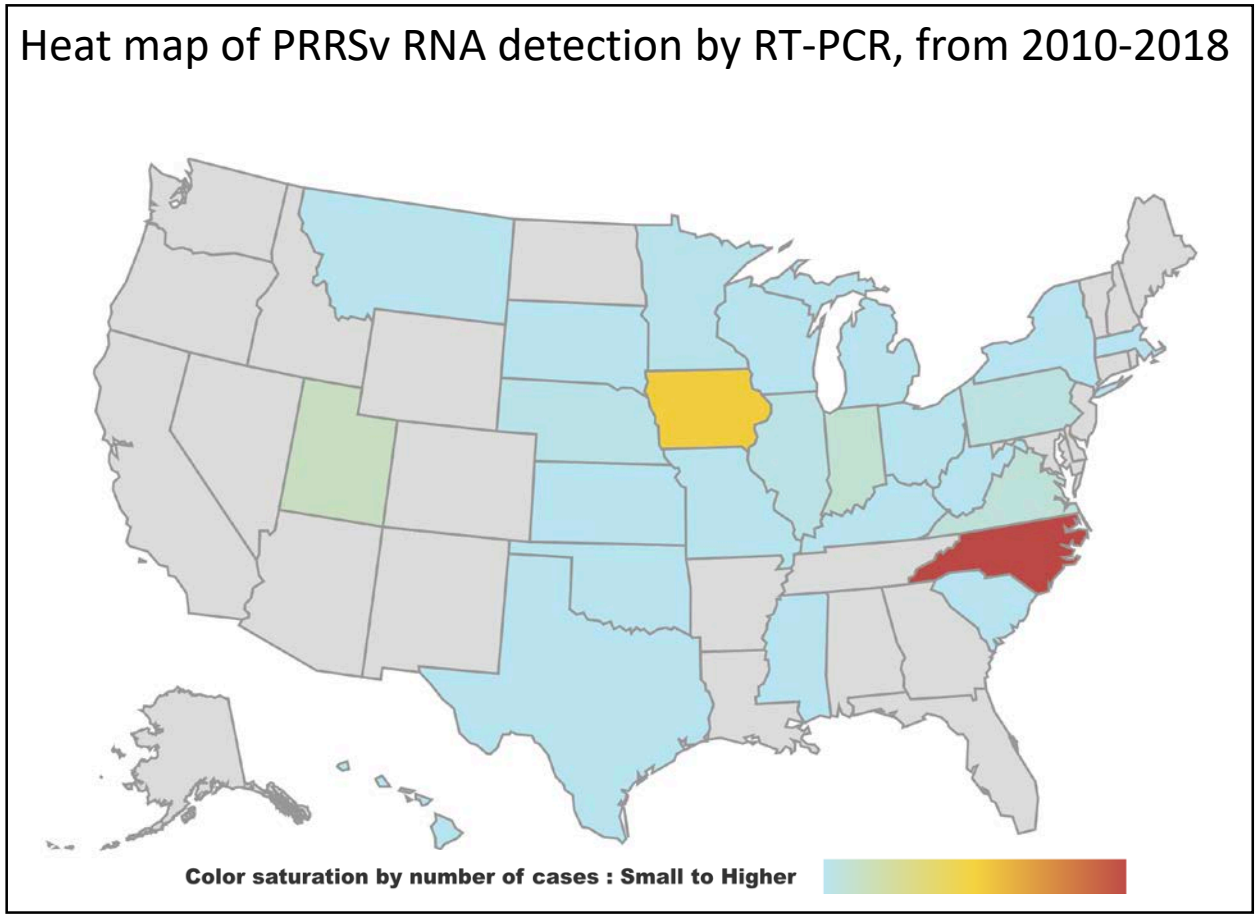
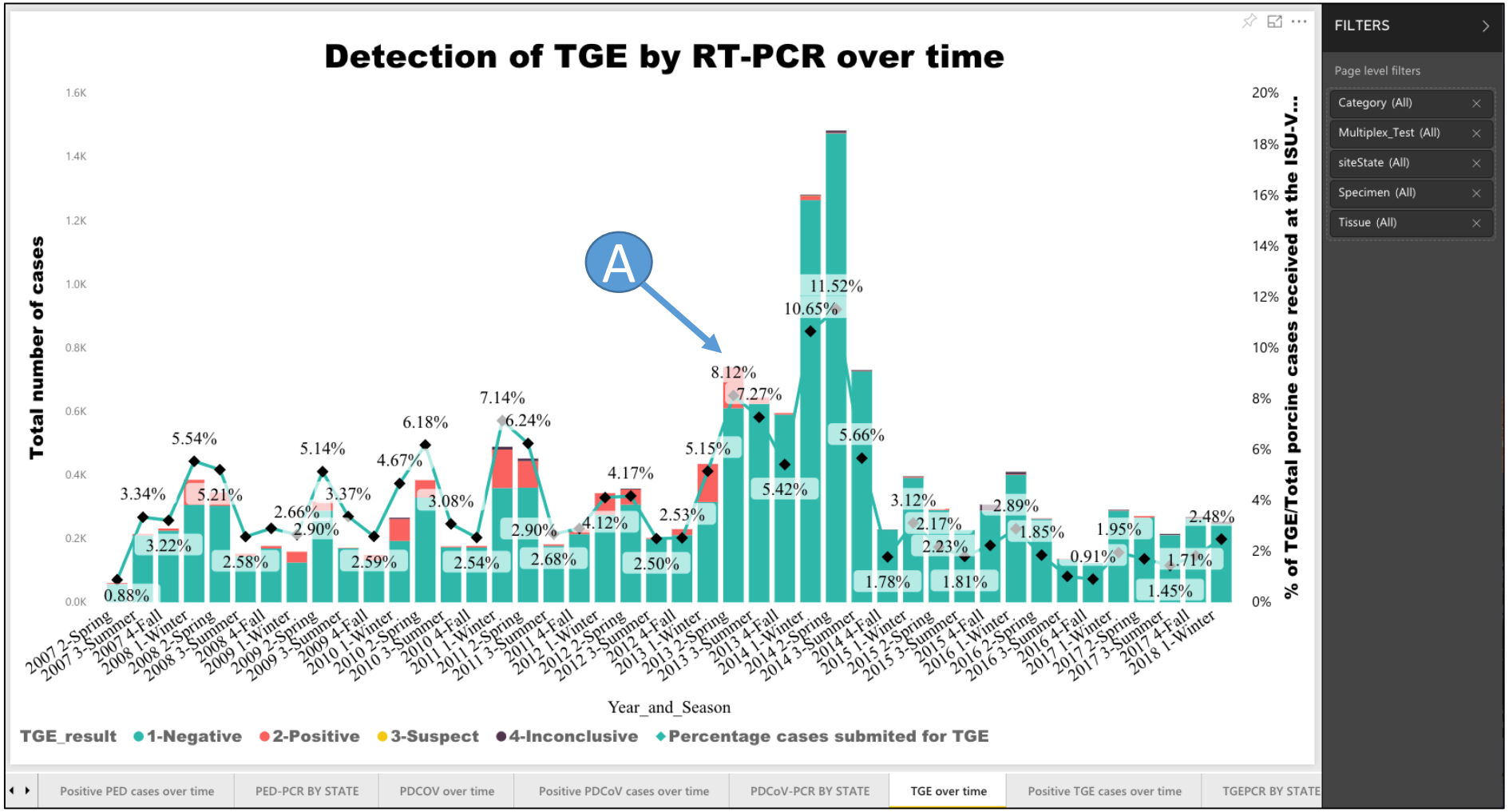


Figure 5b Number of positive cases for PRRSv, by State (**filtered EU-PRRS only**).

Significant increase of TGE testing by RT-PCR early 2013



SDRC Advisory Council highlights:

A: Relative increase of TGE testing by PCR in 2013:

a) The great majority of the increased testing was from cases of 'Grow-Finishing` category, suggesting increased monitoring;

b) In 2013 there was a concern with TGE infection in late finishing pigs around slaughter time;

c) Concomitantly with PED introduction in USA, more tests for TGE were performed in a effort to detect the TGE virus.

Figure 6a TGE RNA detection over time by rRT-PCR. Each bar indicates a season (Winter, Spring, Summer, Fall). Blue indicate cases that tested negative. Red represents cases with at least 1 positive sample. The line (secondary Y axis) represent percentage of cases tested for TGE PCR relative to all other porcine submissions for molecular testing.

Starting 2013, the detection rate of TGEV by RT-PCR decreased significantly

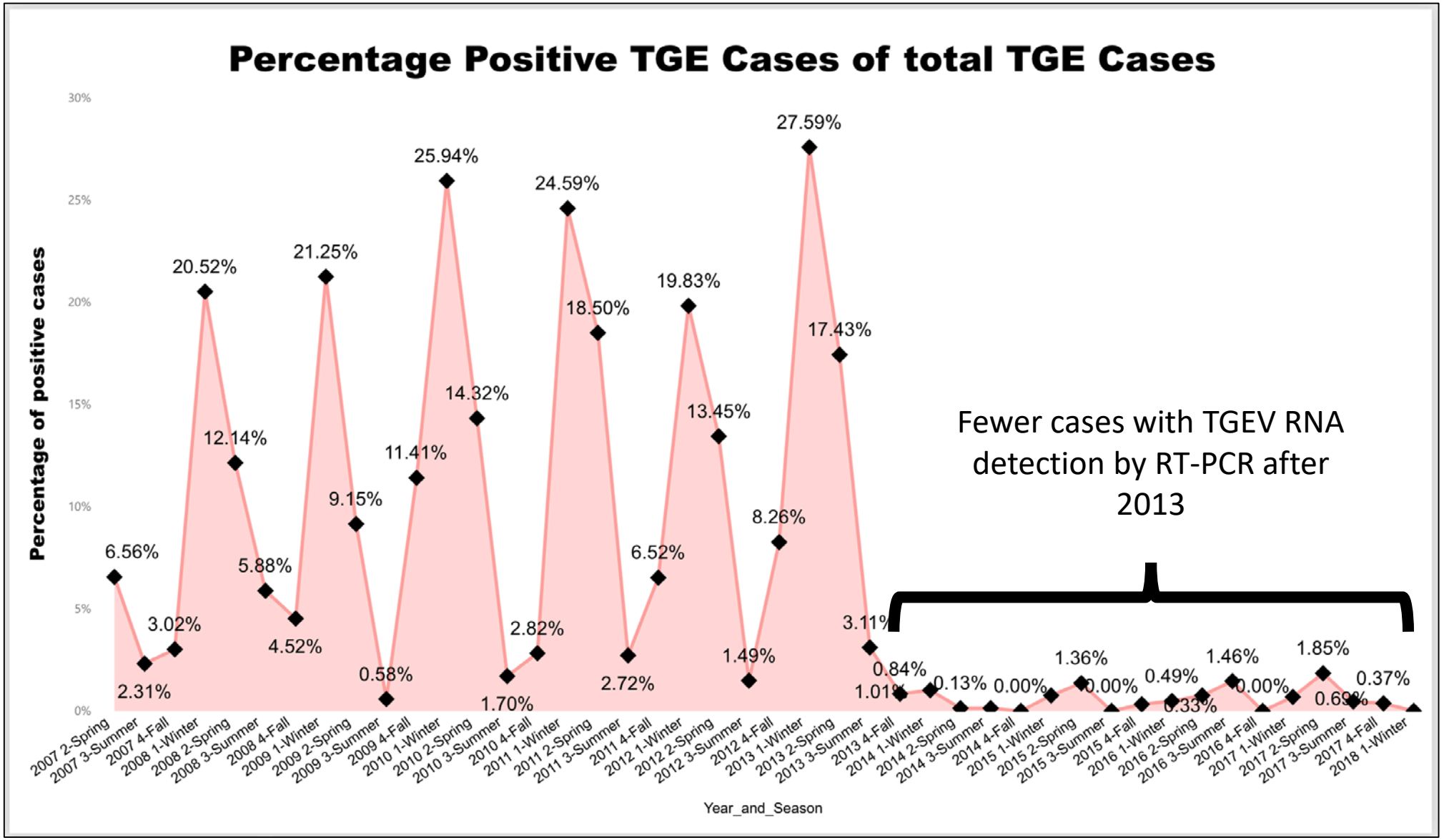


Figure 6b Percentage of cases tested positive for TGEV RNA by RT-PCR, over time.

Cyclic pattern of PEDv detection by RT-PCR over time

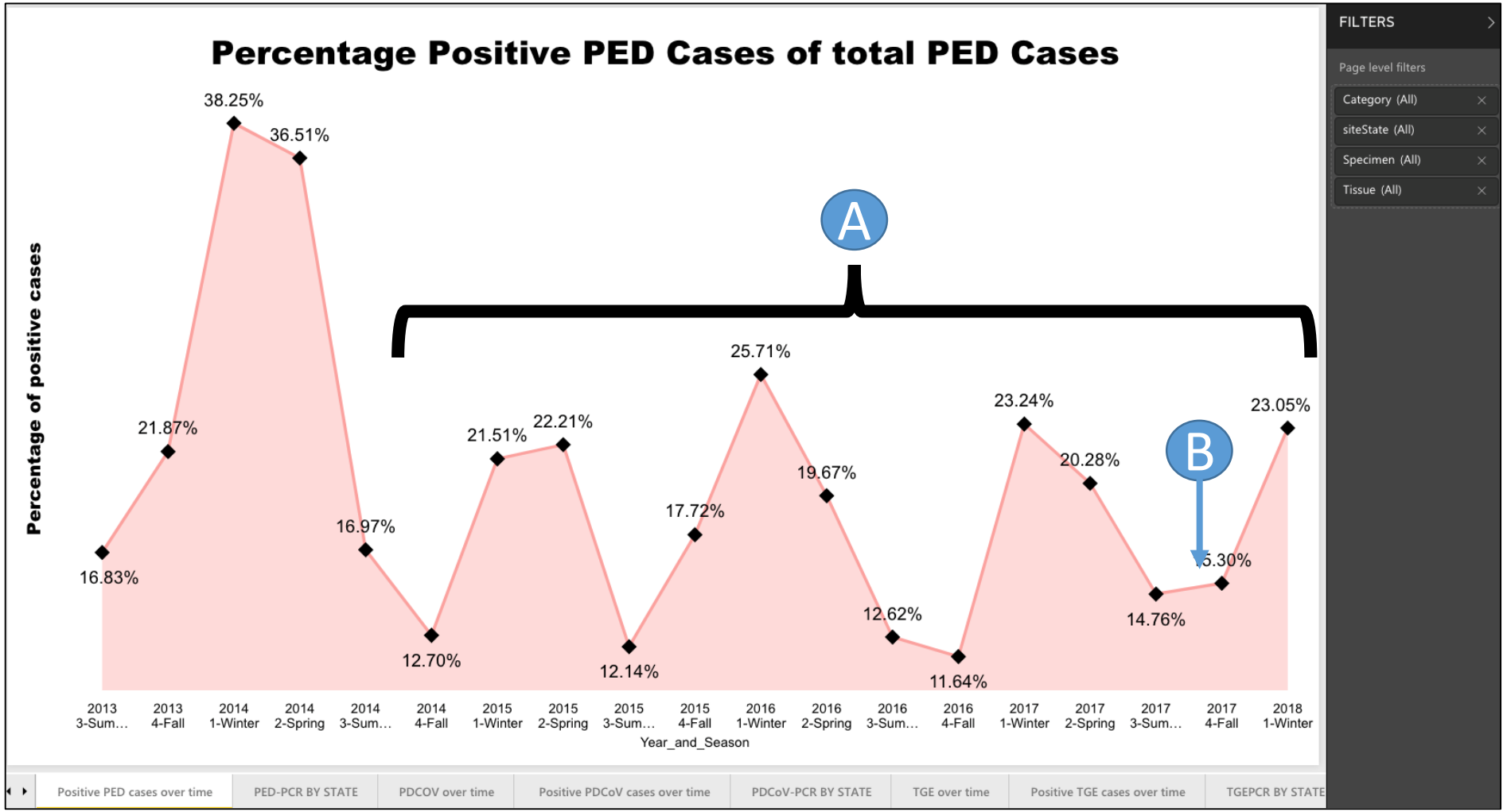


Figure 7 Percentage of cases tested positive for PED virus RNA by rRT-PCR, over time.

SDRC Advisory Council highlights:

A: Relative lower detection in 2014-2018 compared to 2013, likely in response of the implementation of management and biosecurity measures.

B: Relative increase in percentage of PED detection in the Summer and Fall of 2017:

a) Possible introduction of naïve pigs for replacements in 2016 and 2017 at sow farms;

b) Low immunity of the offspring's for PED potentially leading to increased detection;

c) Potentially reflecting increased monitoring of (exposed) gilts, not necessarily reflecting PED—associated disease in suckling pigs or growing pigs.

History of PEDV detection by rRT-PCR, and Predicted Percentage of Positive Cases in 2018: not suggestive of significant deviation.

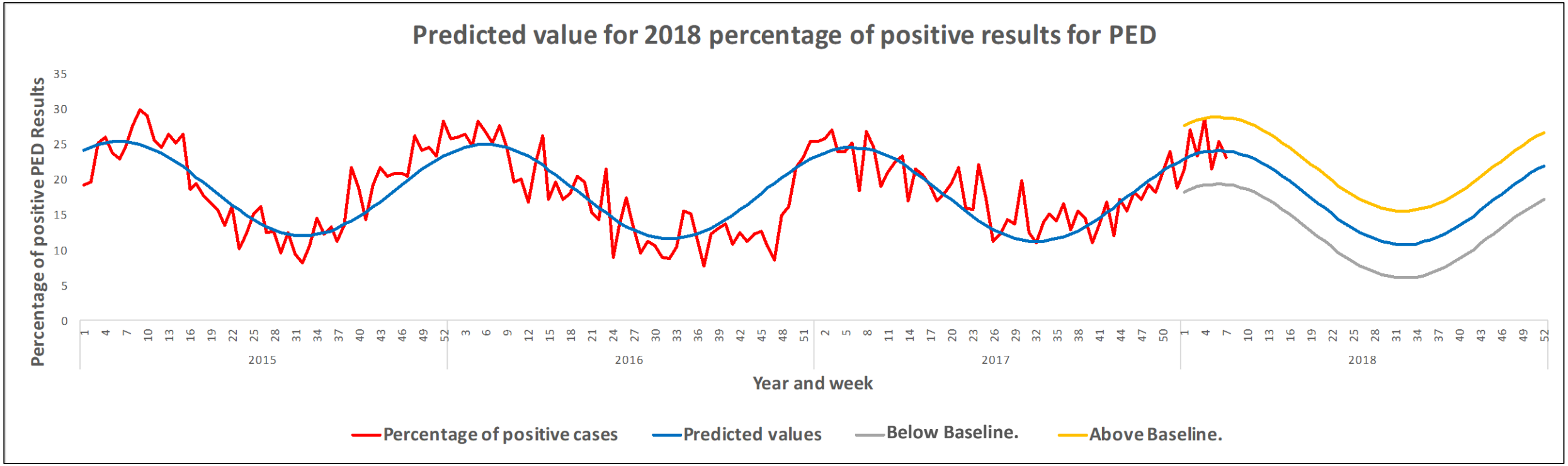
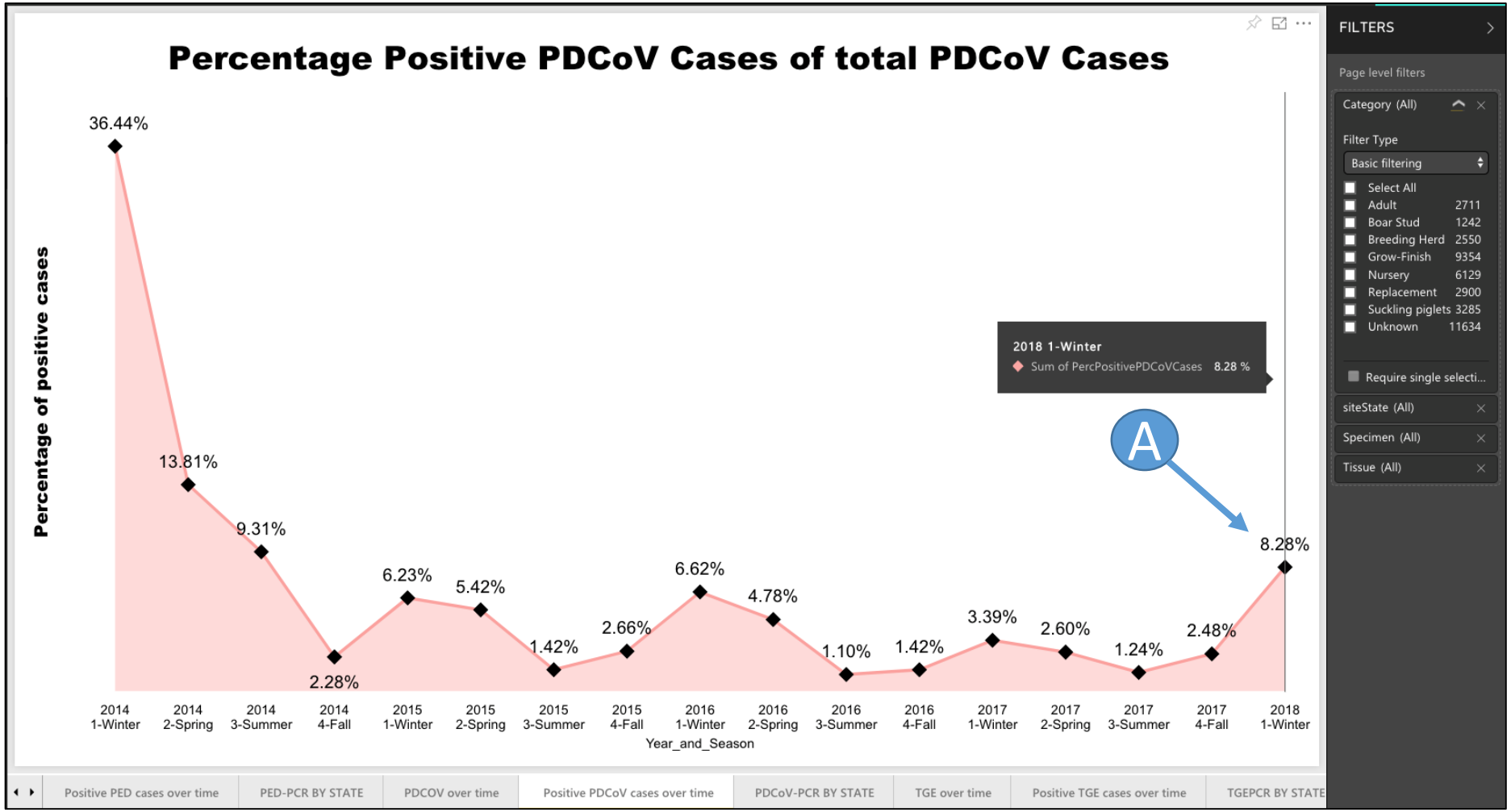


Figure 8 Cyclic pattern of PEDv RNA detection by RT-PCR between 2015-2018. The red line represents the observed (real) values for percentage cases tested positive for PEDv by RT-PCR. The blue line represents the expected moving average of percentage cases tested positive over time. The yellow and gray lines represent the upper and lower thresholds, respectively, based on 1 standard deviation of the blue (expected) line.
In other words, the number of expected positive cases in 2018 were built based on historic cyclic pattern observed between 2015-2017. The graph shows that the percentage of PEDV-positive cases were within the expected based on historical data. This method was developed by Dr. Trevisan, in partnership with Dr. David J. Muscatello.

PDCoV (Deltacoronavirus): cyclic pattern, and recent outbreak (winter 2018)



SDRC Advisory Council highlights:

A: Relative increase in % of detection of PDCoV at 2018 winter:

a) In most part linked to `Adult`; `Breeding Herd`; `Suckling piglets`; and `Grow-Finish` age categories;

b) Currently there is a field concern with higher detection of PDCoV in finishing animals;

c) Recent increase in PDCoV may also be related to change in immune status of pig populations (i.e.: increase in naïve status, leading to more breaks).

Figure 9 Percentage of cases tested positive for Porcine Deltacoronavirus RNA by rRT-PCR, over time (no filters applied).

History of PDCoV detection by RT-PCR, and Predicted Percentage of Positive Cases in 2018: strong evidence of significant increase in % cases tested positive.

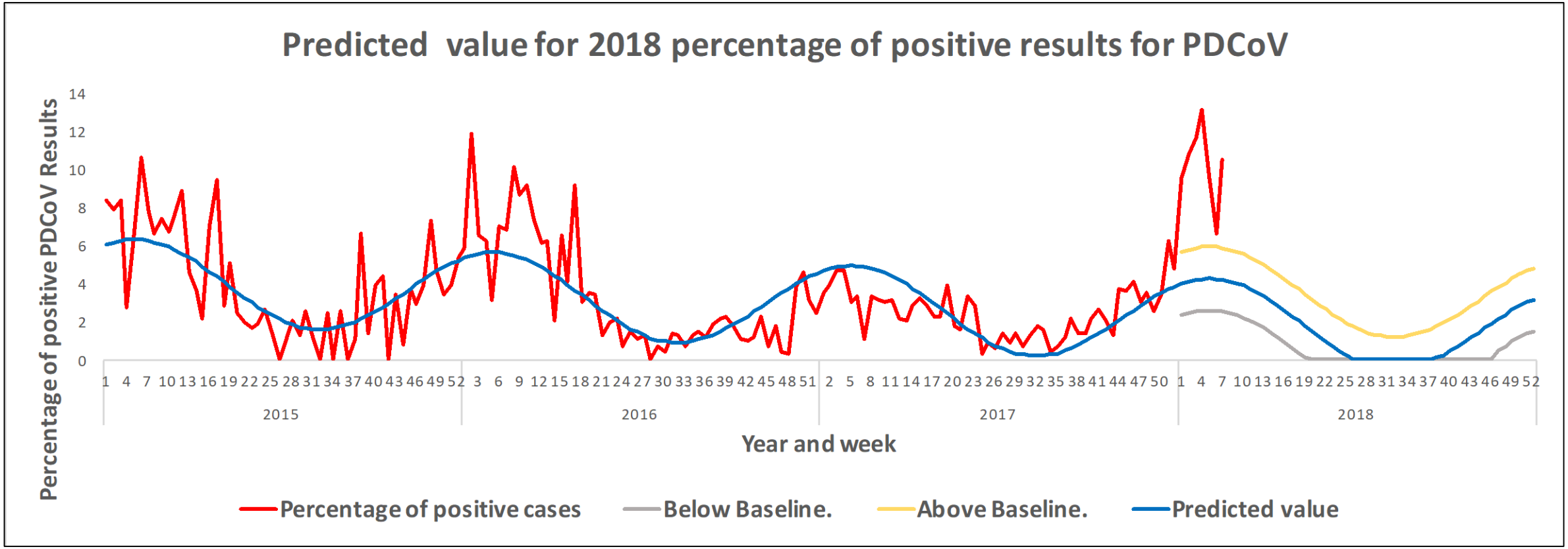


Figure 10 Cyclic pattern of PDCoV RNA detection by RT-PCR between 2015-2018. The red line represents the observed (real) values for percentage cases tested positive for PDCoV by RT-PCR. The blue line represents the expected moving average of percentage cases tested positive over time. The yellow and gray lines represent the upper and lower thresholds, respectively, based on 1 standard deviation of the blue (expected) line.
In other words, the number of expected positive cases in 2018 were built based on historic cyclic pattern observed between 2015-2017. The graph shows that the percentage of PDCoV-positive cases were significantly above the expected based on historical data. This method was developed by Dr. Trevisan, in partnership with Dr. David J. Muscatello.

Next steps

This was the first publication of this information, and thus the graphs included a long history of data (2007-2018), which required *Power point* style to better describe the data.

Going forward, for next reports we will focus on more recent data, which will allow using a more user-friendly reporting format.

Next report will will include additional data analysis on VDL data, and will include results from central nervous system diseases.

To access the full data, use steps as outlined below:

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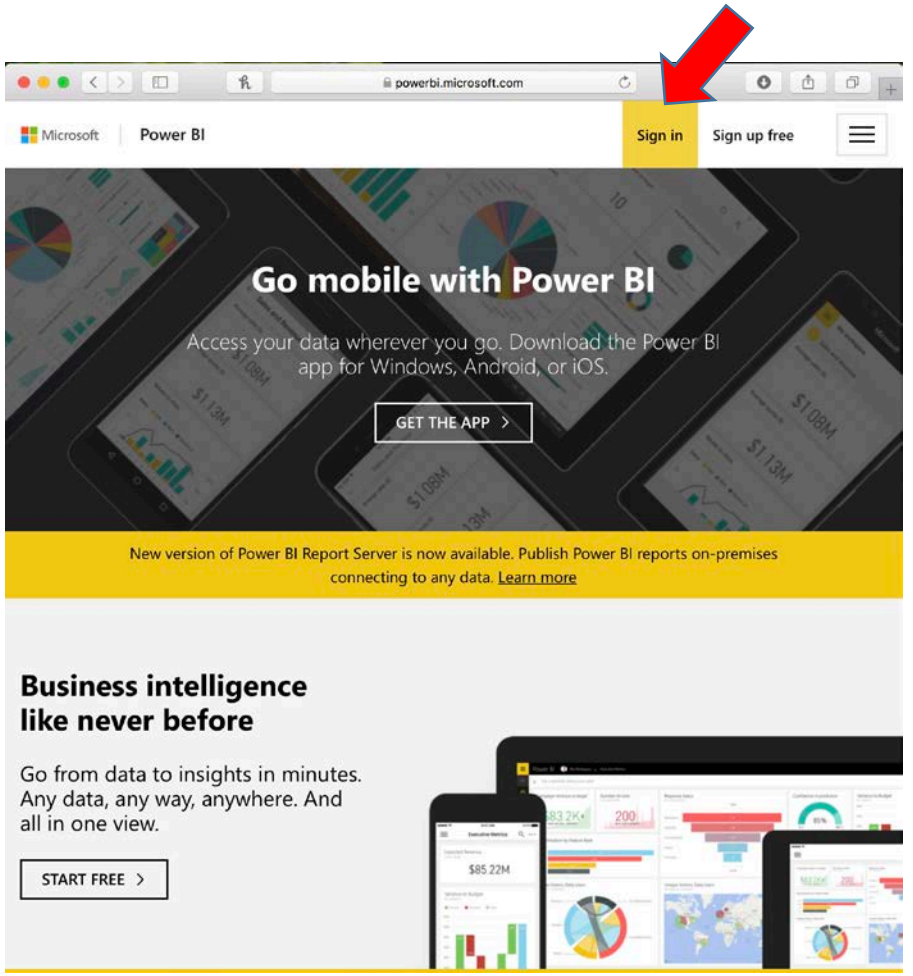
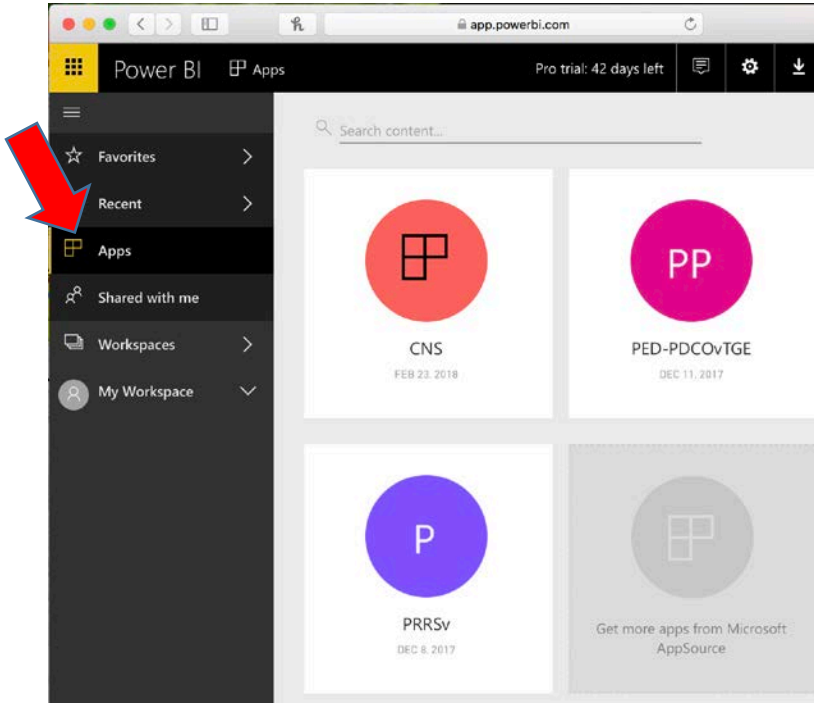
Steps to access the data:

1) Scan the code below, or go to: www.powerbi.com.

Power BI

2) Login: sdrs@iastate.edu
3) Password: Bacon 100
4) Click on ‘Apps’: left bar
5) Select your dashboard of interest (e.g. PRRv)





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Any questions? Contact us:

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