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SDEC Partners Research Update

Project Update: Detection of large genetic diversity of porcine group B rotavirus strains in the United States, resulting in a modified classification proposal for G genotypes

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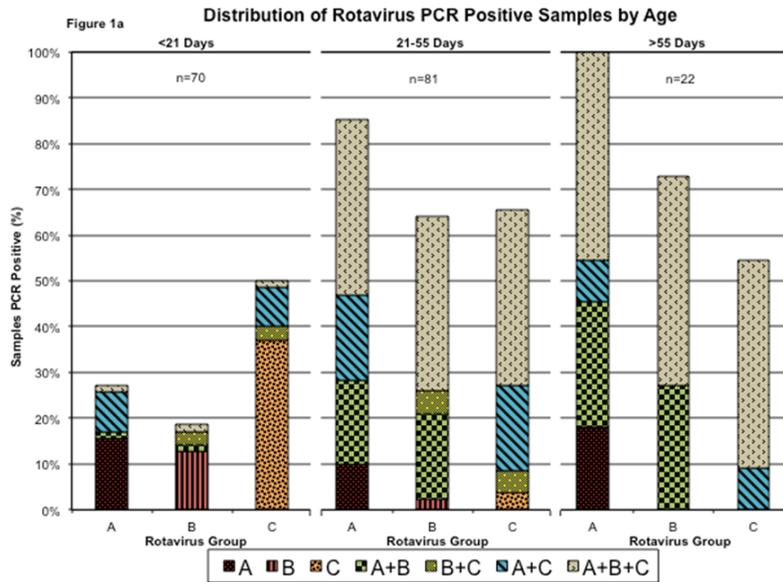
Background

- Rotaviruses (RVs) are a major etiological agent of acute viral gastroenteritis in young animals and children worldwide and possess a genome composed of 11 segments double-stranded RNA (dsRNA) and are currently classified into eight groups (A-H) based on antigenic properties and sequence based classification of the inner viral capsid protein 6.
- RVA is considered the most important rotavirus group because of their high prevalence and pathogenicity in both humans and a variety of domestic and wild animals. While porcine RVB were first identified in 1980's four other rotavirus groups, RVA, RVC, RVE, and RVH have also been described in pigs.
- Serological and molecular characterization of RVB strains is limited due to the difficulty of adapting RVB strains to cell culture. Kuga and colleagues (2009) sequenced the VP7 of 38 porcine RVB strains and constructed phylogenetic trees and pairwise identity frequency graphs for G genotype classification, resulting in proposed 5 clades which were further divided into 12 clusters, using 67% and 76% nucleotide cut-off values, respectively.

Objective

In order to better understand the ecology of rotavirus in porcine diarrhea cases, diagnostic samples from pigs of different ages were tested for RVA, RVB, and RVC as well as common pathogens associated with porcine diarrhea. Samples were collected from pig tissues submitted to the University of Minnesota, Veterinary Diagnostic Laboratory, United States. The VP7 open reading frame (ORF) for 68 swine RVB samples in the United States was determined, revealing a large genetic diversity of porcine RVB strains.

Results



Distribution of Samples by Group and Age

Category	<21 Days (n=70)		21-55 Days (n=81)		>55 Days (n=22)		Total (n=173)	
Total Positive	56	80.0%	78	96.3%	22	100.0%	156	90.2%
Negative	14	20.0%	3	3.7%	0	0.0%	17	9.8%
Total RVA positives	19	27.1%	69	85.2%	22	100.0%	110	63.6%
Total RVB positives	13	18.6%	52	64.2%	16	72.7%	81	46.8%
Total RVC positives	35	50.0%	53	65.4%	12	54.5%	100	57.8%
RVA only	11	15.7%	2	2.5%	4	18.2%	17	9.8%
RVB only	9	12.9%	2	2.5%	0	0.0%	11	6.4%
RVC only	26	37.1%	3	3.7%	0	0.0%	29	16.8%
RVA and RVB	1	1.4%	15	18.5%	6	27.3%	22	12.7%
RVB and RVC	2	2.9%	4	4.9%	0	0.0%	6	3.5%
RVA and RVC	6	8.6%	15	18.5%	2	9.1%	23	13.3%
RVA, RVB, and RVC	1	1.4%	31	38.3%	10	45.5%	42	24.3%

Conclusions

- The genetic diversity observed in VP7 sequences of porcine RVB strains suggests that RVB strains have been probably circulating in the porcine population for decades and may be more prevalent than originally thought.
- Failure to detect the true prevalence of RVB strains in the swine population may have been overshadowed by the high prevalence, pathogenicity, and zoonotic properties of RVA. Most likely, the lack of proper diagnostic assays has concealed the prevalence of RVB in the swine population.
- The newly developed RT-PCR can be used to further increase our diagnostic capabilities and help in genetic diversity studies of RVB strains in the future.
- The increased number of VP7 sequences of RVB strains has permitted its classification into 20 G genotypes based on an 80% nucleotide cut-off value by using the approach and guidelines used by the RCWG to classify RVA strains.

Implications

- Porcine RVB strains found in 46.8% of samples tested in the United States in 2009.
- Majority of RVB-positive samples (86.4%) contained mixed RV infections.
- Unexpected higher prevalence of RVC (50.0%) than RVA (27.1%) in <21 day age group.
- High detection rate (24.3%) of RVA/RVB/RVC co-infections.
- Updated RVB VP7 classification, using 80% nucleotide cutoff, yields 20 G genotypes.
- Proper identification of rotavirus B as a causative agent of pig diarrhea may lead to more appropriate control and lessen inappropriate antibiotic usage.