

# **Study of enteric virus infection and parenteral vaccines in the gnotobiotic pig model**

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# **Study of enteric virus infection and parenteral vaccines in the gnotobiotic pig model**

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## **Academic Abstract**

Human rotavirus (HRV) and human norovirus (HuNoV) are the most common causative agents of acute gastroenteritis- (AGE) related morbidity and mortality around the world. Gnotobiotic (Gn) pigs are the ideal large-animal model that allows for accurate, and precise, preclinical evaluation of vaccine efficacy. Similarities in gastrointestinal anatomy, physiology, and immune system allows for direct translation of results from Gn pigs to humans. Commercially available HRV vaccines perform significantly poorer in low- and middle- income countries as compared with developed countries. Non-replicating rotavirus vaccines (NRRVs) have been proposed as a viable solution to the problems facing currently available live-, attenuated oral vaccines and evaluation of a NRRV was the first research project in this dissertation. Three doses of a novel parenterally administered nanoparticle-based RV vaccine, P24-VP8\*, adjuvanted with Al(OH)<sub>3</sub> adjuvant, was able to prime VP8\*-specific mucosal and systemic T cell responses (IFN- $\gamma$  producing CD4+ and CD8+ T cells), and to induce strong systemic B cell responses (IgA, IgG and serum neutralizing antibodies). A significant reduction in the mean diarrhea duration, fecal virus shedding titers, and significantly lower fecal cumulative consistency scores was observed among vaccinated pigs demonstrating the efficacy of the vaccine against RV infection and diarrhea.

Next, we determined the median infectious dose ( $ID_{50}$ ) and median diarrhea dose ( $DD_{50}$ ) of the GII.4/2003 Cin-1 variant of HuNoV in Gn pigs to better standardize the pig model for HuNoV vaccine evaluation. Gn pigs were inoculated with 7 different doses of Cin-1 at 33-34 days of age. Pigs were monitored daily from post-inoculation day (PID) 1 to 7, for fecal virus shedding and fecal consistency to evaluate the virus infectiousness and associated diarrhea. The  $\text{Log}_{10} ID_{50}$  and  $DD_{50}$  were determined based on various mathematical models to be between 3.11 to 3.76, and 3.37 to 4.87 RNA copies, respectively. The Beta-Poisson was identified to be the best-fitting statistical model for estimating both the  $ID_{50}$  and  $DD_{50}$  of Cin-1. Determining the  $ID_{50}$  of the challenge virus strain is crucial for identifying the true infectiousness of HuNoVs and for accurate evaluation of protective efficacies in pre-clinical studies of therapeutics, vaccines and other prophylactics using this reliable animal model.

The lack of an easily reproducible cell culture model for HuNoV has significantly delayed the development of effective vaccines. There is still no HuNoV vaccine available. Currently, the vaccine development efforts are mostly based on genetically engineered virus-like particles (VLPs) comprised of the major HuNoV capsid protein VP1. We tested the immunogenicity of a novel tetravalent VLP vaccine containing 4 major HuNoV genotypes (GI.1, GII.3, GII.4 and GII.17) using Gn pigs and evaluated its protective efficacy when challenged with GII.4 Cin-1 HuNoV. Three doses of the VLP vaccine with  $Al(OH)_3$  adjuvant administered to Gn pigs intramuscularly (IM), induced high levels of VLP-specific serum IgA and IgG antibody and hemagglutination inhibition antibody responses in the vaccinated pigs. VLP-specific  $IFN-\gamma$  producing  $CD4+$  and  $CD8+$  T cells were also elevated among vaccinated pigs at post-challenge day (PCD) 7 in the spleen and blood, but not in the ileum. However, the vaccinated pigs were not protected from infection and diarrhea when challenged with any one of the three different doses

( $2 \times 10^5$ ,  $8 \times 10^4$ , and  $2 \times 10^4$  genome RNA copies) of Cin-1 HuNoV. These results indicated that the IM tetravalent VLP vaccine was highly immunogenic, but the presence of high levels of immune effectors induced by the vaccine were not sufficient for protecting the Gn pigs from Cin-1 challenge. Amino acid (aa) sequence analysis showed that the GII.4 Sydney 2012 strain which was included in the VLP vaccine, had 23 aa substitutions in the major receptor binding domain (P2) compared to the Cin-1, a GII.4 Farmington Hills 2002 strain. Our findings, for the first time, provided *in vivo* experimental evidence for the total lack of cross-genogroup, cross-genotype and cross-variant protection among HuNoV. This finding has importance implications for HuNoV vaccine development. HuNoV vaccines have to include multiple variants and have to be routinely updated in order to ensure sustained protection among the population.

Together these three studies in this dissertation demonstrate the versatility of Gn pigs as a reliable large animal model for studying the pathogenesis and immunity of enteric viruses and the evaluation of immunogenicity and protective efficacy of novel enteric viral vaccines.

# **Study of enteric virus infection and parenteral vaccines in the gnotobiotic pig model**

Ashwin Kumar Ramesh

## **General Audience Abstract**

People of all age groups are susceptible to acute gastroenteritis (AGE), a condition characterized by sudden onset of diarrhea, nausea and abdominal cramps. The two most important viral pathogens responsible for causing AGE are rotavirus (RV) and norovirus (NoV). Gnotobiotic (Gn) pigs have been valuable in helping us understand the mechanism of infection, pathogenesis, immunity and have played a key role in the expediting development of novel vaccines and therapeutics against both of these viruses. Live oral RV vaccines are available but they are not very effective in low income countries where the vaccines are needed the most. Next generation parenteral vaccines are proposed to improve the RV vaccine efficacy. Our first study showed that a nanoparticle-based intramuscular (IM) RV vaccine effectively reduced the duration and severity of human RV infection and diarrhea in Gn pigs. Secondly, we examined in detail the infectivity of HuNoV and identified accurately using different mathematical models on how much virus would be required to infect and cause diarrhea in naïve Gn pigs. This knowledge would greatly help in the accurate assessment of the efficacy of NoV vaccines. Third, we evaluated the immunogenicity and protective efficacy of a tetravalent IM NoV vaccine in Gn pigs. Although the vaccine was highly immunogenic, it did not confer any protection against infection and diarrhea upon challenge with the NoV at different doses. NoVs are so diverse that one year we might be infected with one strain and a few years later, we might be infected again with another strain, even though they

belong to the same genotype, and experience the same symptoms. This is because, changes brought about due to mutation in the virus capsid protein allow the viruses to hide from neutralizing antibodies induced by previous infection or vaccination as we have revealed in this study. NoV diversity and lack of cross protection need to be taken into consideration during vaccine development. This thesis shows how Gn pigs can be used to study these components in order to further maximize our ability to understand and combat enteric viral diseases.

*Dedicated to my parents*

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## List of Abbreviations

<b>Abbreviations</b>	<b>Definitions</b>
3PLL	three-parameter log logistic
AGE	Acute gastroenteritis
AIC	Akiake Inference Criterion
Al(OH) <sub>3</sub>	Aluminum hydroxide
ANOVA	analysis of variance
ASC	antibody secreting cells
AttHRV	attenuated HRV
AUC	area under curve
CCIF	cell culture immunofluorescence
Cin-1	HuNoV GII.4/2003 Cin-1 virus
DAPI	4,6-diamidino-2-phenylindole
DB	Dragstedt-Behrens
DD50	median diarrhea dose
dsRNA	double-stranded RNA
ELISA	enzyme-linked immunosorbent assay
EM	electron microscopy
FFU	fluorescent focus-forming unit
GE	Gastroenteritis
GLM	general linear model
Gn	gnotobiotic
HAI	Hemagglutination inhibition
HBGA	histo-blood group antigen
HIE	human intestinal enteroid
HuNoV	human rotavirus
IACUC	Institutional Animal Care and Use Committee
ID50	median infectious dose
IFN- $\gamma$	Interferon gamma
Ig	immunoglobulin
IM	intramuscular
LIC	large intestinal contents
LIPS	Luciferase Immunoprecipitation Systems
LMIC	low- and middle-income countries
MEM	minimum essential media
MNCs	mononuclear cells

MNV	murine norovirus
MPL	monophosphoryl lipoprotein
mRNA	messenger RNA
NoV	norovirus
NRRV	nonreplicating rotavirus vaccine
NSP	non-structural protein
ORF	open reading frame
PCD	post-challenge day
PCV	Porcine circovirus
PD	proportionate distance
PID	post-inoculation day
PPD	post-partum day
PTA	phosphotungstate
RdRp	RNA dependent RNA polymerase
RM	Reed-Muench
RT-qPCR	Quantitative reverse transcription PCR
RV	rotavirus
SCID	severe combined immunodeficiency
sf-EMEM	serum free EMEM
SIC	small intestinal contents
SK	Spearman-Karber
VirHRV	virulent HRV
VLP	virus like particles
VN	virus-neutralizing
VP	viral protein

# **Chapter 1**

## **Literature Review**

### **Current state of vaccine development for rotavirus and norovirus infection and disease**

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- i.** Chapter 11. Rotavirus. In *Handbook of Foodborne Diseases*, Food Microbiology Series, Edited by Donyou Liu. CRC Press/Taylor & Francis Group. p121-136. (2018).
- ii.** Chapter 22. Molecular Mechanisms of Host Immune Responses to Rotavirus. In *Molecular Food Microbiology*, Edited by Donyou Liu. CRC Press/Taylor & Francis Group (in press).

## 1. Acute Gastroenteritis

Acute gastroenteritis (AGE) is a condition that is often characterized by a sudden onset of diarrhea, nausea and abdominal cramps, that affects people of all age groups. Diarrhea is the second leading cause of death among children under 5 years of age, with an estimated annual global mortality rate of 526,000 in 2015 (Keusch, Walker *et al.* 2016). Limited access to safe and clean drinking water, basic sanitation, poor hygiene practices, and lack of medical care are the main contributing factors to AGE in low-income countries (GBD 2016). The most common etiological agents responsible for AGE-related morbidity and mortality around the world are norovirus (NoV), rotavirus (RV) and enteropathogenic *Escherichia coli* (Lanata, Fischer-Walker *et al.* 2013). Diarrheal disease caused by rotavirus primarily affects children <5 years old, but NoV AGE affects people of all ages (Monroe 2011). Together both these viruses demand a unified interest among researchers in the field to understand the pathogenesis and to develop effective prophylactic and therapeutic approaches against these preventable diseases. This review will focus on the key aspects of RV and NoV infection in humans, briefly outline current research efforts focused on understanding the pathogenesis and immunity, and the efforts in vaccine development to reduce the disease burdens in the world. This work also introduces the gnotobiotic (Gn) pig model system and highlights their value to enteric viral research.

## 2. Rotavirus

Rotaviruses belong to the genus *Rotavirus* within the family *Reoviridae*, which are characterized by a segmented, double-stranded RNA (dsRNA) genome encapsulated within a non-enveloped, triple-layered icosahedral capsid. RV is the leading cause of severe, dehydrating diarrhea among children under 5 years of age globally (Tate, Burton *et al.* 2016). The RV genome consists of 11 segments that encode for six viral structural proteins (VP1 to VP4, VP6 and VP7) and six nonstructural proteins (NSP1 to NSP6). Each genome segment encodes a single protein (monocistronic), except for segment 11 which encodes two proteins (NSP5 and NSP6) (Mattion, Mitchell *et al.* 1991).

## 2.1 Virus Structure

Three concentric layers of protein, an inner core layer, a middle layer, and an outer layer form the icosahedral capsid of the viral particle (McClain, Settembre *et al.* 2010, Green 2013). The core of the virion is made up of 120 molecules of VP2 arranged as 60 dimers that enclose the dsRNA genome together with the viral RNA dependent RNA polymerase (RdRp) (VP1) (Valenzuela, Pizarro *et al.* 1991, Zeng, Wentz *et al.* 1996) and the mRNA capping enzyme (VP3) (Chen, Luongo *et al.* 1999). The middle layer is formed by 260 trimers of VP6 protein. The inner core and the middle layer form double-layered particles (DLP). The outer surface of the RV virion is composed of 260 trimers of VP7 glycoprotein and 60 VP4 spike proteins also presented as trimers. The spike proteins are divided into four regions (head, body, stalk and foot) which are formed by two VP4 trypsin cleavage fragments VP5\* and VP8\*.

## 2.2 RV-host cell binding and entry

The main capsid proteins of rotavirus are VP4 and VP7, with VP7 comprising the outer shell of the capsid and VP4 forming the spike protein (Greenberg and Estes 2009). As such, VP4 is primarily responsible for rotavirus attaching to enterocytes. It is enzymatically cleaved by trypsin, found in the host gastrointestinal tract, into VP5\* and VP8\*, with VP5\* forming the main stem and VP8\* forming the head of the spike that directly encounters receptors on small intestinal cells (Liu, Huang *et al.* 2012, Desselberger 2014).

Initially, sialic acid moieties were thought to be involved in rotavirus binding (Ciarlet, Ludert *et al.* 2002). Recent multidisciplinary studies involving structural biology and glycobiology, have revealed that rotavirus utilizes histo-blood group antigens (HBGAs) as cellular receptors (Hu, Crawford *et al.* 2012, Huang, Xia *et al.* 2012, Liu, Huang *et al.* 2012, Böhm, Fleming *et al.* 2015, Ma, Li *et al.* 2015, Ramani, Hu *et al.* 2016). These glycan ligands have previously been determined to be responsible for the cellular binding of another enteric virus, norovirus (Marionneau, Ruvoën *et al.* 2002, Huang, Farkas *et al.* 2003). HBGAs are carbohydrates found on RBCs and epithelial surfaces throughout the body. In certain individuals, known as secretors, they are also found in biologic fluids including blood, milk, saliva and intestinal contents

(Huang, Xia *et al.* 2012, Ma, Li *et al.* 2015). *In vitro* assays using human saliva, milk and synthetic oligosaccharides have thus demonstrated that VP8\* binds to HBGAs (Huang, Xia *et al.* 2012). Several HBGA phenotypes exist based on varied expression of ABO, Lewis and secretor genes; current knowledge indicates rotavirus strain-specific binding to A, H type 1 and/or Lewis<sup>b</sup> antigens (Hu, Crawford *et al.* 2012, Huang, Xia *et al.* 2012). Most studies have also determined increased susceptibility to symptomatic infection in secretor-positive individuals (Imbert-Marcille, Barbé *et al.* 2014, Nordgren, Sharma *et al.* 2014, Van Trang, Vu *et al.* 2014, Zhang, Long *et al.* 2016), though conflicting evidence of infection in non-secretors does exist (Ayouni, Sdiri-Loulizi *et al.* 2015). Since the expression of HBGA is determined genetically and regulated developmentally, variations in glycan binding between different RV strains have significant impacts on multiple aspects of RV pathogenesis, including interspecies transmission, host range restriction, and tissue tropism, as well as on the susceptibility of the host to different RV strains and vaccine viruses (Ramani, Hu *et al.* 2016).

HBGAs are not the only glycans that have been demonstrated to interact with rotavirus. VP8\* also interacts with gangliosides in a strain-dependent manner (Coulson 2015). As stated previously, some animal strains do bind sialic acid as confirmed by their sensitivity to sialidases. These strains are able to bind the sialic acid found as a terminal moiety on the ganglioside GM3 (Haselhorst, Fiebig *et al.* 2011, Yu, Coulson *et al.* 2011) and as terminal and internal moieties on ganglioside GD1a (Haselhorst, Fleming *et al.* 2009). In contrast, sialidase-insensitive rotaviruses, which include most human strains, appear to interact with the ganglioside GM1a that lacks a terminal sialic acid (Haselhorst, Fleming *et al.* 2009). Of note, GM1a contains an internal sialic acid moiety that can interact with VP8\* and it is not affected by sialidases.

In addition to VP8\*, VP5\* and VP7 have also been implicated for their role in cellular binding. VP5\* has been demonstrated to bind integrins  $\alpha 2\beta 1$ ,  $\alpha 4\beta 1$  and  $\alpha 4\beta 7$  (Coulson, Londrigan *et al.* 1997, Graham, Halasz *et al.* 2003, Graham, Fleming *et al.* 2005), while VP7 binds integrins  $\alpha x\beta 2$ ,  $\alpha v\beta 3$  and  $\alpha 4\beta 1$  found on surface of epithelial cells (Coulson, Londrigan *et al.* 1997, Graham, Fleming *et al.* 2005). Heat shock

cognate protein hsc70 (Guerrero, Bouyssounade *et al.* 2002) and tight junction protein JAM-A (Torres-Flores, Silva-Ayala *et al.* 2015) are also involved in RV-host cell interaction.

Once bound, rotavirus has been shown to enter enterocytes via endocytosis, though the exact mechanism appears to be strain dependent (Gutiérrez, Isa *et al.* 2010, Díaz-Salinas, Romero *et al.* 2013, Arias, Silva-Ayala *et al.* 2015). Several RV strains have been known to spread to other sites extraintestinally, in humans as well as animal models, suggesting a wider receptor as well as host tissue range than previously hypothesized (Kraft 1958, Uhnoo, Riepenhoff-Talty *et al.* 1990, Mossel and Ramig 2003, Azevedo, Yuan *et al.* 2005, Jaimes, Feng *et al.* 2005, Zhao, Xia *et al.* 2005, Blutt, Fenaux *et al.* 2006, Crawford, Patel *et al.* 2006, Fenaux, Cuadras *et al.* 2006, Blutt, Matson *et al.* 2007, Graham, O'Donnell *et al.* 2007, Minami, Tamura *et al.* 2007, Green 2013).

### **2.3 RV Classification**

The *Rotavirus* genus currently is comprised of ten different species (groups) designated from A to J (Matthijnssens, Otto *et al.* 2012, Mihalov-Kovacs, Gellert *et al.* 2015, Banyai, Kemenesi *et al.* 2017, Crawford, Ramani *et al.* 2017). Strains belonging to RVA, RVB and RVC groups are known to infect both humans and animals, whereas strains within RVD-RVJ groups have only been known to infect animals. Within groups, RV are further classified into different serotypes or genotypes. Serotypes are defined by reactivity of virus in plaque reduction (or fluorescent foci reduction) neutralization assays using polyclonal or monoclonal antibodies (Estes and Cohen 1989). Genotypes are defined by comparative sequence analysis (and/or nucleic acid hybridization in the old days). The two outer capsid proteins VP7 and VP4 carry the serotype neutralizing epitopes that are encoded by genomic segment 7 (VP7 glycoprotein and thus G serotype) and segment 4 (VP4 protease sensitive protein and thus P serotype). Since these two proteins are encoded by separate gene segments, RVs within the same genogroup can generate new G-P serotype antigen combinations through reassortment after dual infections of single cells (Gentsch, Laird *et al.* 2005).

The RVA group contains at least 36 G genotypes, and 51 P genotypes (RCWG 2019), with increasing

numbers of variants discovered each year. A standardized nucleotide (nt) sequence-based characterization scheme for RVA genotypes has been developed by the Rotavirus Classification Working Group (RCWG) to maintain, evaluate and develop the RV genotype classification system, in particular to aid in the designation of new genotypes (RCWG 2015). The genotypes based on complete genome sequence of VP7–VP4–VP6–VP1–VP2–VP3–NSP1–NSP2–NSP3–NSP4–NSP5/6 of circulating RV strains are being continuously identified and differentiated according to particular cut-off points of nt sequence identities, allowing for accurate identification (Matthijnssens, Ciarlet *et al.* 2008, Matthijnssens, Ciarlet *et al.* 2008, Matthijnssens, Ciarlet *et al.* 2011).

## **2.4 Pathogenesis of RV infection**

A low dose of 100-1000 infectious particles is sufficient to cause the clinical manifestation of disease presented as AGE (Ward, Bernstein *et al.* 1986). RV utilizes integrins, sialic acids, and HBGAs to trigger cellular entry of the viral particle (Lopez and Arias 2006, Coulson 2015). The virus invades the mature enterocytes lining the middle and apical portions of the villi, by direct membrane penetration or through endocytosis. RV NSP4s are able to increase intracellular  $Ca^{2+}$  levels, which degrades tight junctions allowing paracellular water transportation. This can trigger the enteric nervous system's release of additional  $Ca^{2+}$  as well as  $Cl^-$ , contributing to the RV secretory diarrhea mechanism (Ball, Tian *et al.* 1996, Greenberg and Estes 2009). The classic histopathological markers of RV infections include villus blunting, crypt hyperplasia, and increased numbers of intraepithelial lymphocytes, but no significant inflammation (Ramig 2004). Infectious virions are released from non-polarized cells (e.g. MA104) by lysis (McNulty, Curran *et al.* 1976), but from epithelial cells (e.g. Caco-2) by a budding process that does not immediately kill the cell (Gardet, Breton *et al.* 2006). During RV-associated diarrhea, stools of infected individuals are known to contain large amounts of infectious virus particles (Crawford, Ramani *et al.* 2017).

## 2.5 Epidemiology of RV infection

RV is the most common cause of severe, dehydrating diarrhea among children under 5 years of age globally. Annual mortality rates due to RV infections have declined from 528,000 (range, 465,000–591,000) in 2000 to 215,000 (range, 197,000–233,000) in 2013 (Tate, Burton *et al.* 2016) owing to the implementation of RV vaccines in the national immunization program in many countries. RV is highly contagious and transmitted through a fecal-oral route. It is commonly spread by contaminated food, water, hands, and fomites. A respiratory mode of transmission has also been proposed (Prince, Astry *et al.* 1986). It has been found to cause disease in the young of many different animal species including, but not limited to: humans, cats, dog, cattle, pigs, horses, rats, birds, and various exotic animal species such as giant pandas, raccoon dogs, emus, sugar gliders, salmon and sea lions to name a few (Ghosh and Kobayashi 2014). In humans, the median age when the first RV episode may occur ranges from 6 to 9 months old with 80% of infections occurring among infants less than 1-year-old, whereas the median age in high income countries is 2-5 years (WHO 2013). Mortality rates due to RV infections in high income countries are rare due to the availability of prompt rehydration measures. RV disease typically manifests with nausea, malaise, headache, abdominal cramping, diarrhea and fever (Anderson and Weber 2004). In conditions where access to healthcare is limited, excessive diarrhea due to RV-infections cause an electrolyte imbalance that ultimately leads to death (Desselberger 2014).

RV infection accounts for 38.2% of all the diarrhea cases that require hospitalization each year worldwide (Lamberti, Ashraf *et al.* 2016). Prior to the implementation of RV vaccination, RV disease in the United State accounted for 3 million episodes per year, requiring 500,000 outpatient visits, and 60,000 hospitalizations, leading to 20-40 deaths (Fischer, Viboud *et al.* 2007, Esposito, Holman *et al.* 2011). Similar numbers were reported in European studies apart from a higher mortality rate of 200 deaths per year (Soriano-Gabarro, Mrukowicz *et al.* 2006, Van Damme, Giaquinto *et al.* 2007). RV disease in sub-Saharan African and some south Asian countries has been associated with significantly high disease episodes usually accompanied with death at high numbers (Parashar, Burton *et al.* 2009, Tate, Burton *et al.*

2012). Patterns of year-round disease were more evident in low- and low-middle income countries compared with upper-middle and high-income countries where disease was more likely to be seasonal (Patel, Pitzer *et al.* 2013). High mortality rates in developing countries in sub-Saharan Africa and Asia are predominantly due to lack of access to adequate health care and oral or intravenous rehydration therapies (Tate, Burton *et al.* 2012).

Multiple occurrences of RVs happen throughout an individual's lifetime, leading to the development of life-long immunity over time (severe disease does not occur in individuals who have had more than 2 RV infections), hence lowering the risk of serious outbreaks among the healthy (Burke, Tate *et al.* 2018). After the initial sets of RV infection and once sufficient memory immunity has been generated, RV-memory is lifelong (Velazquez, Matson *et al.* 1996).

## **2.6 Vaccines against RV: Rotarix and RotaTeq**

RotaTeq<sup>®</sup> (Merck), a pentavalent human-bovine reassortant oral vaccine, and Rotarix<sup>®</sup> (GlaxoSmithKline), a monovalent attenuated human RV (HRV) oral vaccine, are two currently licensed, commercially available, RV vaccines worldwide. In 2009, the World Health Organization (WHO) recommended that all countries, in particular those with high prevalence of diarrhea associated deaths in children, introduce RV vaccines into their national immunization programs (WHO 2009). RV vaccination programs have now been implemented in over 100 countries (WHO 2018). Both these vaccines are highly efficacious (80-90%) in high income countries against severe RV AGE, but display only a moderate degree of protection (40-60%) in low income countries (Ruiz-Palacios, Perez-Schael *et al.* 2006, Vesikari, Matson *et al.* 2006, Armah, Sow *et al.* 2010, Zaman, Dang *et al.* 2010, Vesikari 2012, De Oliveira, Giglio *et al.* 2013, Pendleton, Galic *et al.* 2013, Glass, Parashar *et al.* 2014, Gilmartin and Petri 2015, Lamberti, Ashraf *et al.* 2016). Multiple factors have been associated with this discrepancy between vaccine efficacies in the two-income resource settings (Clarke and Desselberger 2015). The composition and diversity of intestinal microbiota, especially bacteria, have recently been shown to play a role on the immunogenicity of the oral RV and other vaccines. Particularly, members of gut bacteria belonging to *Actinobacteria* such as *Bifidobacterium longum*

subspecies *infantis*, were present in higher abundance and positively correlated with T cell responses to oral polio (OP), Bacillus Calmette-Guérin (BCG) and tetanus toxoid (TT) vaccines. On the other hand, the presence of *Clostridiales*, *Enterobacteriaceae*, and *Pseudomonadales*, were associated with poor vaccine responses (Huda, Lewis *et al.* 2014).

The majority of countries currently implementing RV vaccines as part of their national immunization programs are countries with low RV-related mortality, so the real impact of the vaccines on global estimates of RV mortality has been limited (Tate, Burton *et al.* 2016). HRV disease is most prevalent among the African, southern- and southeastern- Asian countries. A case study in 2013 analyzed the etiological causes of moderate to severe diarrhea in seven developing countries in sub-Saharan Africa and Southern Asia, and found that the vast majority of the diarrhea cases within the first two years of life were caused by HRV (Kotloff, Nataro *et al.* 2013). While WHO advises that all countries should implement RV vaccines and over 100 countries have licensed RotaTeq and/or Rotarix (WHO 2018), the countries with the highest rates of diarrheal deaths have seen the lowest rate of RV vaccine seroconversions, averaging 43% (Patel, Glass *et al.* 2013, WHO 2013, Kompithra, Paul *et al.* 2014). The reasons for lower vaccine efficacy in low income settings are not fully determined. A combination of factors has been proposed to be responsible for the differences in vaccine efficacy in high vs low income countries (Zaman, Dang *et al.* 2010, Valdez, Brown *et al.* 2014, Valdez, Brown *et al.* 2014, Becker-Dreps, Vilchez *et al.* 2015, Gilmartin and Petri 2015, Twitchell, Tin *et al.* 2016).

## **2.7 Risks associated with live RV vaccines: intussusception linked to RV vaccines and virus contaminations**

Intussusception is a condition where the intestine telescopes within itself leading to intestinal obstruction. If left untreated, it could lead to internal hernias and even sepsis and can be fatal (Jain and Haydel 2019). There are no definitive underlying causes of intussusception although an increase in gut motility during viral infections have been positively associated (Koch, Harder *et al.* 2017).

The very first vaccine that was manufactured and licensed in the United States, RotaShield® (Wyeth), only circulated in the market between September 1998 – July 1999 before its withdrawal due to its association with intussusception (CDC 1999). Due to this potential adverse effect, both RotaTeq and Rotarix underwent rigorous prelicensure clinical trials involving larger cohorts of 60,000-70,000 infants each, designed specifically to evaluate the safety of these vaccines. There was no difference in the risk of intussusception between vaccine, and placebo, recipients subsequently allowing for the vaccines to be licensed.

Post-licensure surveillance studies have revealed that children vaccinated with RotaTeq and Rotarix are prone to an increased risk of intussusception, potentially due to the high titers of replicating attenuated RV in the intestines (Parashar, Cortese *et al.* 2015). Rotarix vaccine stocks were identified to be contaminated with low levels of live porcine circovirus type 1 (PCV) viral particles, as well as viral DNA causing a safety concern in some countries (Victoria, Wang *et al.* 2010). This led to the temporarily withdrawal of Rotarix from circulation until it was confirmed that there was no immunological or clinical evidence of PCV1 infection among vaccine recipients pre- and post-licensure (Dubin, Toussaint *et al.* 2013). Benefit-risk studies have been carried out throughout the world in order to assess vaccine safety and efficacy (Clark, Jit *et al.* 2014, Ledent, Lieftucht *et al.* 2016, Lamrani, Tubert-Bitter *et al.* 2017, Ledent, Arlegui *et al.* 2018). These studies have shown that the benefits of currently licensed RV vaccines far outweigh the risks associated with their use.

## **2.8 Other live, attenuated oral RV vaccines**

With varying degrees of vaccine efficacies among different populations worldwide, local organizations funded by their governments have developed vaccines targeting rotavirus strains endemic among their populations.

Recently, two more live oral vaccines Rotasiil® (pentavalent bovine-human reassortant) and Rotavac® (monovalent G9P[11]), have been added to the WHO pre-qualification list for distribution (Pecenka, Debellut *et al.* 2018). Clinical trials carried out in India on Rotavac demonstrated an efficacy of 56% against

severe RV gastroenteritis (GE) requiring hospitalization in the first year of life and 49% in the second year of life (Bhandari, Rongsen-Chandola *et al.* 2014) while the efficacy of Rotasiil was observed to be 33% during the first year of life in India (Kulkarni, Desai *et al.* 2017) and 67% in Niger (Coldiron, Guindo *et al.* 2018). The complete post-market safety and reactogenicity of the recently introduced Rotasiil and Rotavac are still under evaluation, with current understanding is that there is no difference in rates of intussusception between infants receiving the vaccines and placebo (Burke, Tate *et al.* 2019).

Rotavin-M1 vaccine (Polyvac), is a live, attenuated oral vaccine, based on G1P[8] strain isolated from a child hospitalized for diarrhea in Nha Trang, Vietnam. This vaccine showed 73% seroconversion in an efficacy trial carried out using 160 infants. Based on these studies, Rotavin-M1 has been licensed in Vietnam and is available in the private market. Phase III immunogenicity trials are currently underway to further evaluate the liquid formulation of the vaccine.

Another live, attenuated oral vaccine, Lanzhou lamb rotavirus vaccine (Lanzhou Institute of Biological Products), has been licensed and available exclusively in China since 2000. One post-marketing study found that a single dose of the LLR vaccine confers ~50% protection rate when given to children between 9 and 35 months old (Fu, He *et al.* 2012).

RV3-BB (PT BioFarma, Bandung, Indonesia) is a naturally attenuated oral vaccine developed by the Murdoch Children's Research Institute based on G3P[6] RV strain which was isolated from the stool of asymptomatic infants. The RV3 strain is naturally adapted to the newborn gut allowing its replication despite the presence of maternal antibodies from breastfeeding. A study conducted in Indonesia administered 3 doses of this vaccine in two ways: (i) neonatal schedule when the vaccine was administered at 0-5 days, 8 and 14 weeks; or (ii) infant schedule when the vaccine was administered on 8, 14 and 18 weeks. Among the cohort that received the first dose of the vaccine immediately after birth (neonatal schedule), 75% of the infants were protected from severe RV infection while 51% the infants that were administered the vaccine based on the infant schedule were protected from severe RVGE. The vaccine was well tolerated among both vaccine groups and showed similar incidence of adverse events to the placebo

recipients (Bines, At Thobari *et al.* 2018). Further studies evaluating the safety and immunogenicity of this vaccine are being carried out in African neonates and infants (Burke, Tate *et al.* 2019).

## **2.9 Nonreplicating rotavirus vaccines**

Underperformance of oral RV vaccines in low income countries has been hypothesized to be caused by multiple factors, mostly centered around the inability of vaccine strains to reach their target cells in the intestine. Passively transferred anti-RV antibodies, in particular, IgA via breast milk, and transplacentally acquired IgG, have been associated with negative impacts on the immunogenicity of oral RV vaccines (Velasquez, Parashar *et al.* 2018). Co-administration of polio vaccine together with oral RV vaccine have shown to decrease RV-specific IgA seroconversion rates (Emperador, Velasquez *et al.* 2016, Ramani, Mamani *et al.* 2016). High stomach acidity has also been linked with virus degradation prior to accessing the intestines leading to a decreased immunogenicity of vaccines (Patel, Shane *et al.* 2009, Glass, Jiang *et al.* 2018). Nonreplicating rotavirus vaccines (NRRV) have been considered as suitable alternatives to mucosal-administered RV vaccines. In addition to being unaffected by a lower vaccine immunogenicity due to reasons hypothesized, NRRVs also completely eliminate the risk of intussusception making them safer than the currently available vaccines. Several new NRRV candidates are currently under various stages of development (Glass, Jiang *et al.* 2018).

## **2.10 Development of a VP8\*-based vaccine**

The binding of RV VP8\* proteins to host cell surface glycans initiates the process of virus entry into host cell leading to a successful infection. VP8\* proteins have been identified as important target epitopes for virus neutralization. Recombinant VP8\* proteins, produced using an *E. coli* expression system, were initially reported to elicit the production of high levels of VP8\*-specific IgG and/or neutralizing antibodies in intramuscularly vaccinated guinea pigs (Wen, Cao *et al.* 2012). The inclusion of a tetanus toxoid T cell epitope P2 sequence, and administering it together with an alum-based adjuvant further boosted the vaccine potency and enhanced the immunogenicity of VP8\* proteins originated from P[8] and P[6] strains, when

evaluated using guinea pig and Gn pig models (Wen, Wen *et al.* 2014). With ongoing Phase III human clinical trials, the P2-VP8\* vaccine has showed significant promise and is furthest along towards licensure. Phase I and Phase II clinical trials carried out to evaluate the effects of P2-VP8\* vaccine demonstrated that participants who received the full course (three doses) of vaccination, shed fewer attenuated rotavirus in feces as compared to trial participants who received either the placebo or two doses of P2-VP8\* after Rotarix oral inoculation (Fix, Harro *et al.* 2015, Groome, Koen *et al.* 2017).

## **2.11 Correlates of protection against RV**

The mechanisms responsible for generating protective immunity to rotavirus infections and illness following vaccination or natural infection are not completely understood, especially in humans where detailed examination of the acquired cellular immune response (B cells, T cells) in young children has been limited because of the difficulty in obtaining timely and sufficient specimens. RV infections elicit both nonspecific (innate) (Gonzalez, Azevedo *et al.* 2010, Holloway and Coulson 2013) and acquired virus-specific humoral and cellular immune responses (Angel, Franco *et al.* 2012). However, there has been no established correlate of vaccine-induced protection. The presence of certain levels (>20U/ml or 3-fold increase) of humoral RV-specific antibodies such as the presence of IgA in fecal contents, as well as the serum IgA and IgG have been accepted as correlates of protection (Angel, Franco *et al.* 2012, Patel, Glass *et al.* 2013). This general consensus is due to RV-specific serum IgA antibody levels generally following the same trend as, other, less-easily measured immune effector functions such as mucosal antibody titers or levels of virus-specific memory B cells in the gut associated lymphoid tissues. Fecal IgA titers of >1:80, serum IgA titers of >1:200, and serum IgG titers of >1:800 are correlated with protection in high income countries (Desselberger 2014). Interestingly, it has been demonstrated that high serum IgA titers do not confer the same degree of protection in low income countries as compared to initial studies carried out in high income countries (Lee, Carmolli *et al.* 2018).

## 2.12 Gn pig models and their utility in RV research

Animal models are very useful for the preclinical evaluations of vaccine candidates. The neonatal Gn pig is a valuable model for its contribution to the understanding of the underlying mechanisms of RV infection (Azevedo, Yuan *et al.* 2005), pathogenesis (Ward, Rosen *et al.* 1996, Azevedo, Yuan *et al.* 2006), and defining the correlates of protection (Saif, Ward *et al.* 1996, Yuan, Ward *et al.* 1996) against RV disease. Gn pigs have also been used for evaluating the protective efficacy of novel vaccines against RV infection (Yuan, Wen *et al.* 2008, Wen, Wen *et al.* 2014). RV infections in pigs manifest within 12-18 hours after infection with virus shedding lasting up to 4-7 days.

Signs of infection and intestinal pathology in Gn pigs due to RV infections are very similar to that in humans, making them a suitable model to study the course of RV disease (Ward, Rosen *et al.* 1996). Gn pigs that were fully protected from RV disease when challenged with virulent HRV had significantly different RV-specific intestinal IgA ASC numbers and intestinal IFN- $\gamma$  frequencies during the time of challenge as compared to unprotected pigs. Using Gn pig models, RV-specific intestinal IgA antibody secreting cells (ASC) and IFN- $\gamma$  producing T cells have been identified as important determinants of protective immunity (Yuan, Ward *et al.* 1996, Yuan, Wen *et al.* 2008). High frequencies of regulatory T-cells (CD4+CD25- Treg cells in particular) have been correlated with poor protective immunity against RV infections in Gn pig models (Wen, Li *et al.* 2012). On the other hand, frequencies of intestinal IFN- $\gamma$  producing CD4+ and CD8+ T cells induced by HRV infection or live attenuated HRV vaccination were significantly correlated with a significant protection rate against HRV diarrhea (Yuan *et al.*, 2008). Gn pigs have been instrumental for the validation of RV vaccines prior to their clinical trials.

Gnotobiotic (Gn) piglet models transplanted with unhealthy human gut microbiome to study rotavirus vaccine efficacy have demonstrated low effector T cell response (interferon  $\gamma$  producing T cells) to the oral RV vaccine (Twitchell, Tin *et al.* 2016). Conversely, Gn pigs colonized with healthy gut microbiome obtained from children with low gut enteropathy scores had a robust immune response to RV vaccine. Recently, humanized pig models have been developed to study the impacts of nutrition status (nutrition /

malnutrition) on the severity of RV infection (Kumar, Vlasova *et al.* 2018). The benefit of having a large animal model that closely mimics the infection and disease observed in humans provides the ability to modulate different aspects of the model, allowing for a better understanding of the disease in a way that cannot be carried out in humans. Continued research using this animal model will help with the understanding of many unanswered questions.

### **3. Norovirus**

With more RV vaccines being implemented as part of national immunization programs around the world, human noroviruses (HuNoV) are now the leading causative agents of AGE among all age groups (Hall, Glass *et al.* 2016, Mattison, Cardemil *et al.* 2018). HuNoV causes over 20% of all AGE cases annually (Ahmed, Hall *et al.* 2014). Among susceptible individuals, very low inoculum doses are sufficient to generate a full course of infection with high titers of virus shed in feces (Teunis, Moe *et al.* 2008, Atmar, Opekun *et al.* 2014, Messner, Berger *et al.* 2014, Schmidt 2015). HuNoVs are transmitted through a fecal-oral route and epidemics primarily occur most in healthcare facilities, restaurants, and schools among other settings. HuNoV outbreaks primarily occur due to individuals coming in contact with contaminated food and water (CDC 2011, Brennan, Cavallo *et al.* 2018, Free, Buss *et al.* 2019).

#### **3.1 Classification of NoV**

NoVs are single-stranded positive sense RNA viruses that belong to the genus *Norovirus* within the family *Caliciviridae*. NoV genome is composed of 3 open reading frames (ORFs). NoV classification is based on the genetic sequence of the entire virus genome or, the sequence of an individual virus gene (Kroneman, Vega *et al.* 2013). Each genogroup is further sub-classified into genotypes based on phylogenetic analysis of the capsid (VP1) and the RNA dependent RNA polymerase (RdRp) protein sequences (De Graaf *et al.*, 2016). NoV is currently categorized into 10 genogroups (G1-GX) which are further classified into 49 genotypes based on VP1 gene (Chhabra, de Graaf *et al.* 2019). There are 29 different virus strains spread

over 3 different genogroups (genogroup I, II, and IV), that are responsible for AGE in humans (Kroneman, Vega *et al.* 2013, Vinje 2015, Cortes-Penfield, Ramani *et al.* 2017).

### **3.2 Structure of NoV**

The NoV capsid is made up of two structural proteins, VP1 (major) and VP2 (minor), coded by ORF 2 and 3 respectively. VP1 is divided into a shell (S) domain and the protruding (P) domain that provide form and stability to the virus (Tan and Jiang 2005). The VP1 has been extensively studied for its antigenic properties and ability to be easily produced using different *in vitro* expression systems. The VP1 has been observed to self-assemble leading to the formation of virus-like particles (VLPs) that have been the basis of NoV vaccines (Tan and Jiang 2019). Recently, using a feline calicivirus model, the VP2 has been discovered to function as trans-capsid channel that is responsible for the delivery of viral genome upon host cell binding (Conley, McElwee *et al.* 2019).

### **3.3 Pathogenesis of NoV**

Over 80% of all HuNoV-associated GE around the world is caused by GII.4 NoVs (Riddle and Walker 2016). The absence of a cell culture system has delayed the progress made on the understanding of NoV pathogenesis and immunity and the development of effective vaccines or therapeutics against NoV disease in humans (Duizer, Schwab *et al.* 2004). The site of replication for NoVs has not been well established, but it is assumed that they replicate in the upper intestinal tract. Biopsies collected from the jejunum of volunteers who develop gastrointestinal illness following an oral administration of the Norwalk (GI.1) or Hawaii virus (GII.1) have exhibited histopathologic lesions (Karandikar, Crawford *et al.* 2016). Interestingly, broadening and blunting of the villi of the proximal small intestine has been observed, although the mucosa itself remains histologically intact (Glass, Parashar *et al.* 2009).

Jones *et al.*, reported that a human derived continuous B-cell line, BJAB, is capable of supporting HuNoV replication (Jones, Watanabe *et al.* 2014). Infectivity of a GII.4 HuNoV in the cell culture system was stimulated by the presence of enteric bacteria or HBGAs, which were proposed to facilitate attachment to

the B cells. The same group also showed that murine norovirus (MNV) were capable of replicating in continuous B-cell lines (M12 and WEHI-231). The poor repeatability and low viral titers yielded from using the BJAB cell line gave rise to new challenges that need to be overcome in order to establish a successful cell culture model. This theory of B-cells being permissive for HuNoV infections was tested in human patients with severe combined immunodeficiency (SCID). Two groups, those with intact (but sometimes dysfunctional) B cells (n = 10) and those without (n = 8), and all were tested for the presence of NoV RNA in stool. The viral RNA titers were similar between the two groups, leading to the conclusion that NoV infections do occur in the absence of B-cells (Brown, Gilmour *et al.* 2016). In a study involving severe combined immunodeficiency (SCID) Gn pigs that were deficient in B cells (and in T cells and NK cells by *RAG2/IL2RG* gene knockout), after an oral inoculation with HuNoV, fecal virus shedding was observed for a longer duration and the virus-tissue distribution was wider compared to the wildtype Gn pigs (Lei, *et al.* 2016). This could either mean that B-cells are not the primary targets of HuNoV infection or that HuNoVs are capable of infecting a broader range of cell-types similar to the findings in RVs. The results of this study were further supported by data recently published by another group that showed no difference between rates and severity of NoV infection among SCID and non-SCID Gn pigs indicating that the innate immune mechanism might be crucial for NoV clearance (Annamalai, Lu *et al.* 2019).

Successful NoV cell-culture has been achieved using a stem-cell derived human enteroid system. Bile acid and the presence of HBGA receptors on the cell surfaces were identified to be key determinants of virus entry and propagation (Ettayebi, Crawford *et al.* 2016). Enteroids derived from all three segments of the small intestine (duodenum, jejunum, and ileum) were permissive for NoV replication up to 96 hours post inoculation. Immunocytochemistry analysis on intestinal biopsies collected from a transplant patient who was suffering from severe GII.4 GE revealed that epithelial cells are the primary site of replication for NoV (Green, Kaufman *et al.* 2019). In another study, duodenal biopsies taken from an individual suffering from common variable immune deficiency who was chronically infected with HuNoV also showed viral antigens (capsid proteins and RdRp) within enterocytes (Estes, Ettayebi *et al.* 2019). The conclusion that epithelial

cells is the predominate target cell type for HuNoV in these studies of humans is consistent with the observation in Gn pigs infected with HuNoV (Bui, Kocher *et al.* 2013, Lei, Ramesh *et al.* 2016, Lei, Samuel *et al.* 2016).

### **3.4 Correlates of protection against NoV infections**

Current knowledge on immune responses to HuNoV comes predominantly from experimental human infection models and clinical studies with VLP vaccines. Similar to some RV species as mentioned earlier, HBGAs are host susceptibility determinants for NoV infections. HBGA found on the surface of intestinal epithelial cells of humans with the secretor phenotype (Marionneau, Ruvoen *et al.* 2002) have been determined as key regulators of susceptibility to HuNoV binding and entry in humans (Lindesmith, Moe *et al.* 2003, Hutson, Airaud *et al.* 2005). Furthermore, the ABO blood group antigens have also been linked to susceptibility to Norwalk (HuNoV GI.1 prototype) infection, with AB, and B blood group antigen individuals showing a lower incidence of infection and illness with HuNoV (Lindesmith, Moe *et al.* 2003). Understanding the binding capacity of HuNoV VLPs to blood group antigens allowed for the development of Hemagglutination Inhibition Assay (Czakó, Atmar *et al.* 2012). Hemagglutination inhibition (HAI) titers have since been used as a correlate of protection by determining the antibody titers that can effectively block the binding of blood group antigens with HuNoV (Ramani, Estes *et al.* 2016).

Antibodies found in serum that block NoV-HBGA binding (HBGA blocking antibodies) have been suggested as a direct correlate of protection from clinical illness (vomiting and diarrhea) following GII.4 HuNoV vaccination or challenge. In a HuNoV human volunteer challenge study, pre-challenge serum titer levels (>1:500) of functional antibodies that block binding of HuNoV VLPs to HBGAs correlated with lower risk of illness (Reeck, Kavanagh *et al.* 2010). High serum IgA but not serum IgG titers have also been linked with protection from HuNoV-associated illness (Atmar, Bernstein *et al.* 2015).

NoV-specific salivary IgA and NoV-specific memory IgG cells have also been identified as additional correlates of protection against NoV GE (Ramani, Neill *et al.* 2015). Pre-challenge, NoV-specific salivary

IgA levels correlated with reduced severity of GE. Rapid salivary IgA response following NoV challenge was previously demonstrated to be protective against infection. Pre-challenge, NoV-specific fecal IgA levels are associated with a lower peak viral load, while levels on day seven post-infection correlate with a shorter duration of virus shedding (Ramani, Neill *et al.* 2015).

A Luciferase Immunoprecipitation Systems (LIPS) assay, recently developed by Tin *et al.*, has made it possible to screen NoV genotype-specific IgG antibodies in the serum against the VP1 capsid protein (Tin, Yuan *et al.* 2017). The benefit of having an assay that is capable of identifying genotype specific serum or fecal antibody response would enhance the accuracy in determining the immunogenicity of vaccine candidates.

Interferon- $\gamma$  (IFN- $\gamma$ ) secreted by CD4<sup>+</sup> and CD8<sup>+</sup> T cells in response to NoV infections have been correlated with protection in humans (Lindesmith, Moe *et al.* 2005), mice (Zhu, Regev *et al.* 2013, Rodriguez, Monte *et al.* 2014), and Gn pig models (Kocher, Bui *et al.* 2014, Lei, Ramesh *et al.* 2016).

The host factors associated with HuNoV infection are poorly understood due to their host-specificity and the limited access to laboratory models to study its pathogenesis. Incremental advancements have been made by studying different aspects of NoV infection using different animal models and collating the results together to form a better understanding of the NoV infection. The importance of non-human models for the study of NoV pathogenesis has been reviewed in detail elsewhere (Wobus, Cunha *et al.* 2016). Cell-culture research using MNV, a surrogate virus model, has been ongoing and key highlights include the discovery of the MNV that grows in dendritic cells and murine macrophage-like cell lines (Wobus, Karst *et al.* 2004); the demonstration that transfection of a full-length cDNA clone of the NV genome (under control of the T7 promoter) into modified vaccinia Ankara (MVA)-T7 infected cells allowing the expression of viral proteins and subsequent NV RNA replication (Asanaka, Atmar *et al.* 2005); the expression of self-replicating NoV RNAs following the transfection of NoV RNA in a hepatoma cell line (Chang, Sosnovtsev *et al.* 2006); and most recently, cells expressing CD300lf, namely tuft cells, in the presence of secondary bile acids, have been identified as the target cells capable of facilitating MNV infection and replication (Wilén, Lee *et al.*

2018). A more recent study concluded that CD300lf is the primary physiologic receptor for MNV, but not for HuNoV (Graziano, Walker *et al.* 2019).

### **3.5 Animal models for NoV research**

Currently, there is no animal model that can directly recapitulate the full range of NoV disease symptoms that are observed in humans, but animals in which evidence for infection has been reported following challenge with HuNoV include Gn piglets and calves (Cheetham, Souza *et al.* 2006, Souza, Azevedo *et al.* 2008, Jung, Wang *et al.* 2012, Bui, Kocher *et al.* 2013, Lei, Samuel *et al.* 2016), monkeys and chimpanzees (Bok, Parra *et al.* 2011), and immunodeficient mice (Taube, Kolawole *et al.* 2013). MNV has been used as a surrogate to study the pathogenesis, immunology, and replication of HuNoV infections, and a large amount of data has been generated (Wobus, Karst *et al.* 2004). However, the limitations of this model are obvious due to the difference between the two viruses in clinical manifestations (without diarrhea/vomiting), host receptors (sialic acid versus HBGAs), infected cell types (dendritic/macrophages versus digestive epithelial cells), and pathogenesis (Tan and Jiang 2010).

Pigs share several characteristics with humans in their gastrointestinal anatomy, physiology, immune system, the presence of FUT2 gene (pigs are all secretors) and the presence of HBGAs, such as the A and H antigens on mucosal surfaces making them susceptible to HuNoV infections. In the neonatal Gn pig model, several different NoVs belonging to GII.4 and GII.12, including GII.4 HS66/2001 (Souza, Cheetham *et al.* 2007), GII.4 KU131206 (Park, Jung *et al.* 2018), GII.4 strain 766 (Craig, Dai *et al.* 2019), GII.4 2006b (Bui, Kocher *et al.* 2013, Kocher, Bui *et al.* 2014, Lei, Ramesh *et al.* 2016, Lei, Ryu *et al.* 2016, Lei, Samuel *et al.* 2016, Lei, Twitchell *et al.* 2019), GII.4 2003 (see chapters 3 and 4 of this dissertation), GII.4 HS194 (Jung, Wang *et al.* 2012), and GII.12 HS206 (Takanashi, Wang *et al.* 2011) have all resulted in diarrhea, virus shedding, seroconversion, immuno-cytopathic change in the intestinal sections, transient viremia and/or activation of innate and adaptive immune responses (Cheetham, Souza *et al.* 2006, Cheetham, Souza *et al.* 2007, Souza, Cheetham *et al.* 2007, Bui, Kocher *et al.* 2013, Kocher, Bui *et al.* 2014, Lei, Ramesh *et al.* 2016, Lei, Ryu *et al.* 2016, Lei, Samuel *et al.* 2016, Lei, Twitchell *et al.*

2019). Similar results have also been observed in Gn calves (Souza, Azevedo *et al.* 2008), making these animal models useful for studying immunology and pathogenesis, and the assessment of vaccines and antivirals against HuNoV infections prior to being tested on humans.

It is important to identify the most appropriate animal model for biomedical research. They have to be carefully determined based on their ability to recapitulate disease pathogenesis. An ideal animal model needs to reliably mimic the normal anatomy and physiology of human organs and tissues of interest, as well as accurately reflect the morphological and biochemical aspects of disease pathogenesis. Meticulous planning and organization are required for the establishment of successful Gn pig facilities (Yuan, Jobst *et al.* 2017). They are usually associated with high maintenance costs, specialized equipment and training, but prove to be a reliable tool for answering many of the questions regarding HuNoV infection and disease without using a human model (Wobus, Cunha *et al.* 2016).

### **3.6 Current HuNoV vaccine pipeline**

No commercial NoV vaccines or therapeutics are currently available, although several vaccine candidates are in various stages of human clinical trials (Lucero, Vidal *et al.* 2018). Treatment for NoV infections is centered over palliative care. This is particularly difficult in developing countries where access to healthcare is limited, and in some locations, clean water is scarce. Due to these reasons, NoV vaccines are urgently needed and they need to be safe, affordable, and efficacious, with a reasonable shelf-life.

Vaccines developed to confer protection against NoVs need to account for the genetically and antigenically diverse nature of NoVs (Bernstein, Atmar *et al.* 2015). Because of the lack of any efficient cell culture system for NoV, live attenuated NoV vaccine is out of reach at this time. VLPs have been most widely explored as a candidate for NoV vaccines. They are readily produced using various expression systems (Jiang, Wang *et al.* 1992, Tamminen, Huhti *et al.* 2012, Tan and Jiang 2012) and self-assemble to a confirmation that is structurally and antigenically similar to an infectious NoV particle.

VLPs based on GI.1 NoVs were initially developed as a monovalent vaccine (LigoCyte Pharmaceuticals, now Takeda Vaccines) candidate and evaluated for its safety, immunogenicity and efficacy in a proof-of-principle study (Atmar, Bernstein *et al.* 2011). They were administered intranasally together with monophosphoryl lipoprotein (MPL) and chitosan adjuvants. Study participants who received the vaccine had a reduced incidence rate (37%) of GI.1-associated GE compared to participants who received the placebo vaccine (69%). Infection characterized by the presence of viral RNA detected by RT-PCR was observed among 61% of vaccine recipients compared to 82% who received the placebo (Atmar, Bernstein *et al.* 2011). Protection conferred by the vaccine was synonymous with the presence of Norwalk virus-specific serum IgA and IgG levels, along with the induction of IgA ASCs and memory B cells (El-Kamary, Pasetti *et al.* 2010, Ramirez, Wahid *et al.* 2012). It was soon identified that a bivalent intramuscular (IM) vaccine (GI.1 and GII.4) adjuvanted with aluminum hydroxide elicited a stronger immune response compared to the intranasal administration (El-Kamary, Pasetti *et al.* 2010, Treanor, Atmar *et al.* 2014, Bernstein, Atmar *et al.* 2015, Sundararajan, Sangster *et al.* 2015). This bivalent IM VLP vaccine is currently under Phase III clinical evaluations and is leading the race for licensure for a NoV vaccine.

Another vaccine that is under clinical evaluations is the adenovirus-vectored GI.1 VP1 vaccine which recently concluded its Phase I clinical trials. This vaccine is orally administered in the form of a tablet and is comprised of a non-replicating adenovirus vector expressing the NoV GI.1 VP1 gene adjuvanted with a double-stranded RNA. The vaccine generated a 2-fold increase in blocking titers among 78% of the vaccinated individuals and generated strong systemic and mucosal IgA and IgG responses (Kim, Liebowitz *et al.* 2018).

P particles (Kocher *et al.*, 2014), VLPs (Cheetham, Souza *et al.* 2006) and lactic acid bacteria-based vaccine candidates (Craig, Dai *et al.* 2019) have been evaluated for their immunogenicity and protective efficacy in Gn pig model of HuNoV infection and diarrhea. Several other candidate vaccines that are still under development include: a RV-VP6 intermediate capsid expressing the NoV GI.3 and GII.4 VLPs as a trivalent vaccine (Malm, Tamminen *et al.* 2016); a bivalent GII.4 NoV and enterovirus 71 VLP-based vaccine

(Wang, Ku *et al.* 2015); and a Newcastle disease virus vector expressing a GII.4 VP1 gene (Kim, Chen *et al.* 2014).

#### **4. Concluding remarks**

Animal models have been extensively used, and have been very useful in bridging the knowledge gaps to facilitate the understanding of the viral pathogenesis and immune correlates of protective immunity against enteric viral infections (Saif, Ward *et al.* 1996). AGE caused by HRV and HuNoV is an important vaccine-preventable issue that causes severe morbidity and mortality especially among poverty-stricken countries (Mattison, Cardemil *et al.* 2018, WHO 2018). Successful vaccination campaigns that targets children at the earliest possible time of intervention will greatly benefit these communities (Bines, At Thobari *et al.* 2018, Burke, Tate *et al.* 2019). Vaccines are the most effective way of reducing morbidity and mortality and have proven in many occasions to save lives (Rappuoli, Pizza *et al.* 2014). Research focused on the development of more protective and affordable NRRVs are required in order to provide a wider coverage for RV disease while this needs to be kept in mind while developing novel HuNoV vaccines.

It remains to be seen, the success of the HuNoV candidate vaccines as they enter the human clinical trials. The success of these vaccines will help us understand NoV immunity and bring us closer to developing an effective method of defeating the burden of NoV infections worldwide.

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## Chapter 2

### **Parenterally Administered P24-VP8\* Nanoparticle Vaccine Conferred Strong Protection against Rotavirus Diarrhea and Virus Shedding in Gnotobiotic Pigs**

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## **Abstract**

Current live rotavirus vaccines are costly with increased risk of intussusception due to vaccine replication in the gut of vaccinated children. New vaccines with improved safety and cost-effectiveness are needed. In this study, we assessed the immunogenicity and protective efficacy of a novel P24-VP8\* nanoparticle vaccine using the gnotobiotic (Gn) pig model of human rotavirus infection and disease. Three doses of P24-VP8\* (200 µg/dose) intramuscular vaccine with Al(OH)<sub>3</sub> adjuvant (600 µg) conferred significant protection against infection and diarrhea after challenge

with virulent Wa strain rotavirus. This was indicated by the significant reduction in the mean duration of diarrhea, virus shedding in feces, and significantly lower fecal cumulative consistency scores in post-challenge day (PCD) 1–7 among vaccinated pigs compared to the mock immunized controls. The P24-VP8\* vaccine was highly immunogenic in Gn pigs. It induced strong VP8\*-specific serum IgG and Wa-specific virus-neutralizing antibody responses from post-inoculation day 21 to PCD 7, but did not induce serum or intestinal IgA antibody responses or a strong effector T cell response, which are consistent with the immunization route, the adjuvant used, and the nature of the non-replicating vaccine. The findings are highly translatable and thus will facilitate clinical trials of the P24-VP8\* nanoparticle vaccine.

**Keywords:** rotavirus nanoparticle vaccine; gnotobiotic pigs

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## 1. Introduction

Human rotavirus (HRV) is a leading cause of severe, dehydrating gastroenteritis in children under five years of age. Although two live-attenuated oral vaccines, RotaTeq<sup>®</sup> and Rotarix<sup>®</sup>, have been implemented as part of national vaccination programs in over 98 different countries [1], their vaccine efficacy was reported to be lower in low- and middle- income countries (LMICs [39%–70%]) compared to that in high-income countries (80%–90%) [2–7]. A combination of factors have been suggested to be responsible for the lower efficacy, which have been reviewed and discussed in detail by Arnold [8] and Desselberger [9]. Both these live vaccines have also been linked to a low risk of intussusception (1–7 cases per 100,000 vaccinated infants) as a result of the vaccine rotavirus (RV) strains replicating in the intestines [10,11], and have remained expensive even after Gavi, the Vaccine Alliance, subsidization [12], particularly in resource-deprived countries. These scenarios have increased the demand for a safer, more cost-effective, and more efficacious vaccine, especially in LMICs that can be easily administered.

Parenteral intramuscular (IM) vaccines have been preferred to oral vaccines due to their increased immunogenicity. They are also not directly affected by microbiome composition or gut enteropathy, both of which have been known to affect the efficacy of oral vaccines in LMICs [13]. Non-replicating rotavirus vaccines (NRRV) have been proposed as safer alternatives to live-attenuated vaccines as they do not lead to intussusception due to their parenteral immunization route [14].

The VP4 region of RV constitutes surface spike proteins that are cleaved by host intestinal proteases into two fragments, VP5\* and VP8\*. VP8\* forms the distal portion of the VP4 spikes, interacting with glycan receptors to facilitate viral attachment and entry [15,16]. VP8\* expressed in various culture systems has been explored as an immunogen in rotavirus vaccine development [17–

22]. VP8\*-containing vaccine candidates have been shown to induce rotavirus-specific neutralizing antibodies and/or protection in mouse, guinea pigs, and gnotobiotic (Gn) pig models [23–28]. Among those, the leading candidate is the P2-VP8 (VP8\* fused to a universal tetanus toxin CD4+ T cell epitope P2) vaccine, adsorbed with aluminum hydroxide for IM administration, which has progressed to phase 1/2 human clinical trials [19,29].

The norovirus (NoV) P particle, referred to as the P24 particle, is an octahedral nanoparticle ( $\approx 840$  kDa) composed of 24 copies of the protrusion (P) domain of the NoV capsid protein. It can be easily produced in large quantities using an *E. coli* expression system. The distal surface of each P domain, corresponding to the outermost surface of the P particle, contains three surface loops, which can tolerate large sequence insertions. Based on this concept, a nanoparticle vaccine was developed by inserting the HRV VP8\* antigen into the loop sections of the P domains. The P24-VP8\* nanoparticle consists of a 24-valent core of NoV P particle and 24 surface-displayed HRV VP8\*s. The P24-VP8\* nanoparticle shares the features of the P24 particle in self-formation, easy production, and high stability over a wide range of temperatures [30]. Efficacy studies in mice revealed that the P24-VP8\* nanoparticle vaccine is highly immunogenic and capable of inducing a significantly higher VP8\* specific antibody response as compared with free VP8\* particles even without adjuvant [30].

The main objectives of this study were to assess the immunogenicity and protective efficacy of a novel P24-VP8\* nanoparticle vaccine using the gnotobiotic (Gn) pig model of human rotavirus infection and disease. The Gn pig model of HRV (Wa, G1P [8]) infection and diarrhea has been well established and used in the pre-clinical evaluation of HRV vaccine efficacies [31]. No other conventional lab animals develop diarrhea after HRV inoculation [32]. Pigs are genetically, physiologically, anatomically, and immunologically similar to humans [33–35],

allowing data from Gn pigs to be translated to humans. The immunogenicity and protective efficacy of the P24-VP8\* nanoparticle vaccine were determined using the Gn pig model of HRV infection and disease. High serum IgA, IgG, and virus-neutralizing (VN) antibody titers, as well as HRV-specific IFN- $\gamma$  producing T cells, have been correlated with protection from HRV infection and disease, and data has been demonstrated to be comparable in Gn pigs and human studies [24,36,37].

## **2. Materials and Methods**

### **2.1. Human Rotavirus**

The virulent HRV (VirHRV) inoculum consisted of a pool composed of intestinal contents collected from the 27th passage in Gn pigs of the Wa strain HRV based on successive passages carried out in Gn pigs. A total of  $1 \times 10^5$  fluorescent focus-forming units (FFUs) of VirHRV were diluted in 5 mL of Diluent #5 [minimal essential media (MEM, ThermoFisher Scientific); 100 IU of penicillin per mL, 0.1 mg of dihydrostreptomycin per ml; and 1% HEPES] for the inoculation of each Gn pig. The median infectious dose (ID<sub>50</sub>) and median diarrhea dose (DD<sub>50</sub>) of the VirHRV in Gn pigs were determined as approximately 1 FFU [38].

The cell culture-adapted HRV Wa strain (AttHRV), derived from the 35th passage in African green monkey kidney cells (MA104, ATCC# CRL-2378.1) [38,39], were used as the positive control for the assessment of RV antigens in feces using enzyme-linked immunosorbent assay (ELISA). The origination and passage history of the VirHRV and AttHRV have been explained by Wentzel *et al.* [40].

## **2.2. Vaccine**

The P24-VP8\* vaccine was comprised of 200 µg of P24-VP8\* proteins and 600 µg Aluminum hydrogel [Al(OH)<sub>3</sub>] adjuvant. The vaccine was stored at 4 °C (up to 8 months) until administered to Gn pigs (Supplementary Figure S1). The dosage of the P24-VP8\* vaccine was selected based on a similar VP8\* molar amount of the P2-VP8 subunit vaccine used in the clinical trial [19,27,29]. The VP8\* region used in this vaccine was designed based on the sequence of Wa HRV. As the negative control, the Al(OH)<sub>3</sub> adjuvant (G-Biosciences, St. Louis, MO, USA) was diluted in sterile PBS to form a final concentration of 600 µg/mL and stored at room temperature, as per manufacturer instructions, until administered.

The purified P24-VP8\* proteins were used as the detector antigen in ELISA for the detection of serum IgA and IgG antibody responses [41] and as stimulating antigen in the intracellular IFN-γ staining assay [39,42].

## **2.3. Gn Pigs and Treatments**

Pigs (Large white cross breed) used in this study were surgically derived by hysterectomy and maintained in sterile isolators, as described previously [43]. The sterility status of the pigs housed in the gnotobiotic isolators was confirmed by culturing isolator swabs and pig rectal swabs on blood agar plates and in thioglycolate broth first at 3 days after derivation and then repeated once a week until the end of the study. Pigs were fed on a diet that solely consisted of commercial UHT sterile whole cow's milk (The Hershey Company, Hershey, PA, USA) until post-inoculation day (PID) 21, and were switched over to Similac<sup>®</sup> baby formula (Abbott Laboratories, Chicago, IL, USA) until the end of the study.

A total of 25 pigs were assigned to two groups, and a subset of pigs in each group were euthanized either pre-challenge (PID 28) or at post-challenge day (PCD) 7 (Table 1).

Pigs were administered IM with an equal volume (1 mL) of either P24-VP8\* vaccine formulated with adjuvant or adjuvant alone at 5 days of age (PID 0), followed by two booster doses at PID10 and PID21. The Phase I and Phase II clinical trials carried out to evaluate the effects of P2-VP8\* vaccine demonstrated that participants who received a 3-dose vaccination regime shed fewer attenuated rotavirus in feces as compared to trial participants who received two doses [19,29]. Based on this rationale, we opted to use the 3-dose regimen in this current study. The timing of 3 injections in Gn pigs are established in previous studies [27,37] based on the time needed to prime and boost immune responses in Gn pigs. Serum was collected at PID 0, PID 10, PID 21, PID 28, and PCD 7 for the detection of VP8\*-specific IgA, IgG, and Wa HRV-specific neutralizing antibody responses.

One subset of pigs ( $n = 3-7$ ) from each group was euthanized before the challenge at PID 28. Another subset of pigs ( $n = 7-8$ ) was orally challenged with  $1 \times 10^5$  FFU of VirHRV Wa strain and monitored from PCD 0 to PCD 7 to assess the protection against virus shedding and diarrhea conferred by the vaccine before euthanasia on PCD 7. The pathogenesis of the Wa VirHRV infection has been studied in detail in Gn pigs; diarrhea and virus shedding persisted between 4 to 7 days post infection [33,38,44,45]. Based on these observations, we limited the study duration to 7 days post-challenge in order to assess the immediate protection conferred by the vaccine against VirWa challenge. Four milliliters of 200 mM NaHCO<sub>3</sub> were given orally 15–20 min before the VirHRV challenge to reduce stomach acidity to allow for rotavirus inoculum to pass through the stomach without being degraded due to low pH in the stomach.

At euthanasia, small and large intestinal contents (SIC and LIC) were collected from all pigs and processed, as described [46], for the detection of intestinal antibody responses by ELISA.

Ileum, blood, and spleen were collected, and mononuclear cells (MNCs) were isolated from them for the detection of effector T cell responses by flow cytometry as described [42].

#### **2.4. Assessment of Diarrhea and Detection of RV Shedding in Feces by Rotavirus Antigen ELISA and CCIF**

The pigs were on a milk-based diet throughout the duration of the study, making their fecal consistency resemble that of a newborn infant. For the assessment of diarrhea, fecal consistency was recorded daily from PCD 0–7 and categorized as follows: 0: normal; 1: pasty; 2: semi-liquid; 3: liquid. The fecal scoring system used here has been well established and used for multiple Gn pigs studies [32,33,38,44,45,47,48]. Pigs were considered to be having diarrhea when their daily fecal consistency scores were recorded to be 2 or greater ( $\geq 2$ ).

Rectal swabs were collected daily to monitor virus shedding by ELISA (for the detection of RV antigens) and cell culture immunofluorescence (CCIF; for the detection of infectious virions) from PCD 0–7. Rectal swabs were processed, as reported previously [49]. ELISA and CCIF assays for the detection and titration of VirHRV antigen in rectal swabs were carried out as previously described [33,38,44,45,47,50–52]. CCIF titers [fluorescent focus units (FFU)/mL] were determined by Equation (1):

$$\frac{ffu}{mL} = \frac{\# \text{ Plaques counted}}{d \times V} \quad (1)$$

where  $d$  = dilution factor, and  $V$  = volume of virus added.

#### **2.5. RV-Specific Serum VN, and VP8\*-Specific Serum and Intestinal IgA and IgG Antibody Titration**

VN antibody titers in serum samples were determined based on methods described previously [47]. MA104 cells were cultured in 96-well plates until an even monolayer was formed ( $\approx 3$ –4 days).

Cells were washed once with sf-EMEM, and enriched with 100  $\mu$ L of sf-EMEM and incubated at 37 °C for 2 h. The media was then discarded, and the cells were inoculated with trypsin-activated AttHRV ( $4 \times 10^3$  FFU in 10  $\mu$ g/mL trypsin) in the absence or presence of 4-fold decreasing concentrations of Gn pig serum samples. The inoculum was discarded, and the plates were incubated at 37 °C for 18 h in 5% CO<sub>2</sub> containing fresh sf-EMEM. The remainder of the steps has been described in detail in a previous publication [47]. The VN antibody titer was expressed as the reciprocal of the serum dilution, which reduced the number of fluorescent cell-forming units by >80% compared to the negative control serum. VP8\*-specific IgA and IgG antibody titers in serum and intestinal contents were measured by using isotype-specific antibody ELISA with purified P24-VP8\* as detector antigen at the plate coating concentration of 6.63  $\mu$ g/mL, following methods described elsewhere [46,47,53]. When loading the testing samples on ELISA plates, four-fold serial dilutions of each sample started from 1:4 to 1:16384 for IgA, SIC, and LIC and 1:256 to 1:1048576 for IgG.

## **2.6. Flow Cytometry**

Mononuclear cells (MNCs) collected from the ileum, blood, and spleen were diluted to a concentration of  $2 \times 10^6$  cells/mL and were seeded into 12-well plates and stimulated with 12  $\mu$ g/mL of P24-VP8\* antigen for 17 h at 37 °C in 5% CO<sub>2</sub> as determined previously [42]. CD3+CD4+ and CD3+CD8+ cell surface marker staining and IFN- $\gamma$  intracellular staining have been described in previous publications [42,47,54,55]. All samples were stored in 0.05 mL of stain buffer and were maintained at 4 °C. A minimum of 100,000 events were acquired using a FACSAria flow cytometer (BD Biosciences, San Jose, CA, USA). Flow cytometry data were analyzed using FlowJo X software (Tree Star, Ashland, OR, USA).

## 2.7. Statistical Analysis

Gn pigs were randomly assigned into treatment groups upon derivation regardless of gender and body weight by animal care technicians. Student's *t*-test was used for comparisons of virus shedding and diarrhea data between the treatment groups. One-way analysis of variance (ANOVA) (General linear model) was used to compare rotavirus-specific IgA, IgG, virus-neutralizing (VN) antibody titers between the treatment groups. Tukey-Kramer HSD was used for the comparison of different time points within the same treatment group. Two-way ANOVA, followed by a Multiple *t*-test, was used for comparisons of frequencies of IFN- $\gamma$  producing T cells between treatment groups. ANOVA analyses were carried out using JMP 14.0 (SAS Institute, Kerry, NC, USA), and all other statistical analyses were performed using GraphPad Prism 7.0 (GraphPad Software, San Diego, CA, USA). A *p* value lower than 0.05 was accepted to be statistically significant.

## Results

### 3.1. Protection against Diarrhea and Virus Shedding upon Challenge with VirHRV

Vaccinated and control Gn pigs were challenged with VirHRV at PID 28 and were monitored daily for clinical signs (diarrhea) and virus shedding from PCD 1 to PCD 7. Gn pigs that were administered with P24-VP8\* vaccine had a significantly delayed onset of diarrhea (from 1.6 to 4.4 days), a significantly reduced duration of diarrhea (from 6.0 to 3.3 days), significantly lower mean diarrhea scores on PID 1 and 2, and a significantly lower cumulative fecal consistency score (from 14.3 to 9.1) as compared to the mock-vaccinated control group (Table 2 and Figure 1A). A delayed onset of virus shedding, a reduced peak titer, a reduced cumulative virus titer (presented as the area under the curve, AUC), and a significantly reduced duration (from 5.9 to 2.5 days) of virus shedding were observed in P24-VP8\* vaccinated pigs when compared to the control group (Table

2). In addition, the mean daily virus shedding titer in the vaccinated pigs was significantly reduced at PCD 2 (Figure 1B), and the reduction of total virus shed (AUC) was 2.27-fold compared to the control pigs (Table 2). However, the vaccine did not significantly reduce the incidence (%) of diarrhea and virus shedding (Table 2).

### **3.2. Strong VP8\*-Specific IgG and Virus Neutralizing, but Lack of IgA, Antibody Responses in Serum**

In order to monitor the development of VP8\* specific humoral immunity, serum samples were collected during the time of vaccine administration (PID 0, PID 10, and PID 21) at the VirHRV challenge (PID 28) and upon euthanasia (PCD 7). Serum IgG and IgA antibody responses were quantified using ELISA and depicted in Figures 2A and 2B, respectively. P24-VP8\*-specific IgG antibody titers in serum were significantly higher ( $p < 0.001$ ) in vaccinated pigs at PID 10, PID 21, PID 28, and PCD 7 when compared to pigs in the control group (Figure 2A). However, serum IgA titers were only detectable after challenge (PCD 7) with VirHRV (Figure 2B).

HRV neutralizing antibodies were detected in the serum of P24-VP8\* vaccinated pigs starting from PID 21 and were observed to increase similarly with VP8\*-specific IgG titers until euthanasia at PCD 7. In control pigs, VN antibodies were only detectable after challenge with VirHRV and were at significantly lower levels compared to the vaccinated pigs (Figure 2C).

### **3.3. Lack of P24-VP8\* Specific Antibody Responses in the Intestines**

P24-VP8\*-specific IgA and IgG antibody titers in SIC and LIC, collected at the time of euthanasia (PID 28 and PCD 7), were measured by ELISA. The P24-VP8\* vaccine did not induce any detectable intestinal IgA or IgG antibody responses before the challenge at PID 28. After the challenge, among the eight vaccinated and challenged pigs, only VP8\*-specific IgG antibodies

were detected (ELISA titers ranging from 256 to 1024) in the SIC of three pigs at PCD 7 (Supplementary Figure S2). However, the SIC IgG titers were not associated with the severity of diarrhea or the amount of virus shed in the three pigs throughout the challenge period.

### **3.4. P24-VP8\* Vaccine did not Induce Strong VP8\*-Specific Effector T Cell Responses in Intestinal and Systemic Lymphoid Tissues**

Frequencies of IFN- $\gamma$ +CD8<sup>+</sup> and IFN- $\gamma$ +CD4<sup>+</sup> T cells in ileum, peripheral blood (PBL), and spleen at PID 28, and PCD 7 are summarized in Figure 3. At PID 28, slightly higher (not statistically significant) IFN- $\gamma$  producing CD4<sup>+</sup> and CD8<sup>+</sup> T cell responses to the P24-VP8\* antigen was detected in vaccinated pigs as compared to control pigs (Figure 3A). P24-VP8\* vaccinated pigs had higher frequencies of IFN- $\gamma$ +CD4<sup>+</sup> T cells in ileum and blood and higher IFN- $\gamma$ +CD8<sup>+</sup> T cells in ileum, blood, and spleen compared to the mock-vaccinated control pigs. Upon the VirHRV challenge, there was still no significant difference in the frequencies of IFN- $\gamma$  secreting CD4<sup>+</sup> and CD8<sup>+</sup> T cells between the two groups in the intestinal (ileum) or the systemic tissues (PBL and spleen) (Figure 3B).

## **Discussion**

In this study, the immunogenicity (antibody and T cell responses) and protective efficacy of the P24-VP8\* nanoparticle vaccine were evaluated in Gn pigs. We first demonstrated that the IM P24-VP8\* vaccine conferred significant protection against infection and diarrhea when challenged with the homotypic virulent strain Wa of HRV. This was indicated by the significant reduction in the mean duration of diarrhea, virus shedding in feces, and significantly lower fecal cumulative consistency scores recorded from PCD 1–7 in vaccinated pigs compared to the controls. However, the vaccine did not significantly reduce the incidence (%) of diarrhea and virus shedding,

indicating that there was a lack of protective immune effectors at the site of infection (small intestine) at the time of challenge, which is consistent with the observed intestinal immune responses. The IM P24-VP8\* vaccine with Al(OH)<sub>3</sub> adjuvant was highly immunogenic in Gn pigs. It induced strong VP8\*-specific serum IgG and virus-neutralizing antibody responses from PID 21 to PCD 7 but did not induce serum or intestinal IgA antibody responses or a strong effector T cell response. These results are consistent with the IM immunization route, the Al(OH)<sub>3</sub> adjuvant, and the nature of the non-replicating vaccine. Non-replicating vaccines are typically ineffective in inducing effector T cell responses. The Al(OH)<sub>3</sub> adjuvant is characteristic for its ability to enhance a Th2 type immune response, promoting strong humoral responses and suppressing effector T cell responses [56].

The observed protection and immune responses data together suggest that the protection conferred by the P24-VP8\* vaccine against diarrhea and virus shedding upon challenge with the virulent Wa HRV was mediated by the vaccine-induced antibodies in the serum. Although there were no antibodies present at the lumen of the small intestine, the site of HRV infection, at the time of challenge to totally prevent the initiation of RV infection, the viruses disseminated into blood from the infected small intestinal epithelial cells could have been neutralized by the high titers of VP8\*-specific IgG and virus-neutralizing antibodies during the phase of viremia. Such mechanisms can reduce the chance of infection of more epithelial cells by the virus from the basolateral side [45]. Studies showing that passively transferred serum antibodies can suppress or delay viral infection in RV-challenged pigtailed macaques [57], and an inactivated IM HRV vaccine (CDC-9) reduced virus shedding in Gn pigs upon challenge with Wa VirHRV [48] likely share the same protection mechanism with the P24-VP8\* vaccine. The serum IgG and virus-neutralizing antibody responses induced by the P24-VP8\* IM nanoparticle vaccine had similar

dynamics and magnitude as the aluminum phosphate adjuvanted inactivated CDC-9 and P2-VP8\* IM vaccines in Gn pigs [27,48]. The P24-VP8\* vaccine demonstrated a similar degree of protection against diarrhea but a stronger protection against virus shedding in Gn pigs as compared to the P2-VP8\* vaccine [27].

There was a trend of inverse correlation between serum VP8\*-specific IgG titers at PID 28 and cumulative diarrhea scores post-challenge in the vaccinated pigs (Pearson's rank correlation,  $r = -0.6699$  and  $p = 0.0691$ ), suggesting that vaccinated pigs with higher serum VP8\*-specific IgG responses are more likely to be protected against severe diarrhea, which is in agreement with the study of serum IgG antibody in human adults showing that VP4-specific IgG titer was correlated with resistance to HRV infection [58]. The presence of high preexisting IgG titers was also correlated with less severe or shorter duration of diarrhea among children under three years of age [59]. As reviewed by Jiang *et al.*, serum antibodies, if present at critical levels, are either protective themselves or are an important and powerful correlate of protection against rotavirus disease [60].

Additional investigations are required to explore the full potential of P24-VP8\* vaccine efficacy. First, P24-VP8\* is a candidate dual-vaccine against both NoV and RV, but we only examined the immune responses and protection against HRV, not human norovirus (HuNoV). Further studies in the Gn pig model of HuNoV infection are needed to evaluate its efficacy against NoV. Second, we only examined the protection against challenge with a homotypic HRV, and it remains to be determined whether the P24-VP8\* vaccine would be effective in protecting against heterotypic HRV, as the monovalent P[8] HRV vaccine Rotarix showed significant efficacy against P[4] (70.9%) and P[6] (55.2%) HRV associated gastroenteritis in African infants [61]. One of the important potential advantages of the novel P24-VP8\* nanoparticle dual vaccine is that the vaccine can be formulated as a cocktail vaccine to cover multiple types of RVs and NoVs for broad

protection. Thus far, the Gn pig model of HRV infection and diarrhea has only been evaluated using the P [8] Wa HRV, requiring the need to test the effectiveness of Gn pigs as a suitable model for additional HRV P types to evaluate the broadness of protection of the novel P24-VP8\* nanoparticle vaccine.

## **Conclusion**

The P24-VP8\* vaccine candidate is a typical nanoparticle vaccine with 24 copies of the major RV surface neutralizing antigen VP8\* displayed on the self-assembled norovirus P24 particles. The P24-VP8\* nanoparticles are easily produced in *E. coli* with a high yield and simple purification procedures at a low cost. Significant enhancement of the immunogenicity of both VP8\* and P domain backbone have been demonstrated in mouse immunization studies. In this current study, the usefulness of the P24-VP8\* vaccine was assessed in a Gn pig model, followed by the challenge of HRV. Three doses of IM immunization of Gn pigs demonstrated the nanoparticle vaccine's effectiveness to significantly shorten the duration of HRV diarrhea and virus shedding, reduce the severity of diarrhea, and lower the amount of virus shed when challenged. Immune responses associated with protection include high titers of VP8\*-specific serum IgG antibodies and virus-neutralizing antibodies induced by the vaccine after the second and third booster doses. These findings will facilitate clinical trials of this vaccine candidate into a useful, safe, non-replicating, parental vaccine against RVs.

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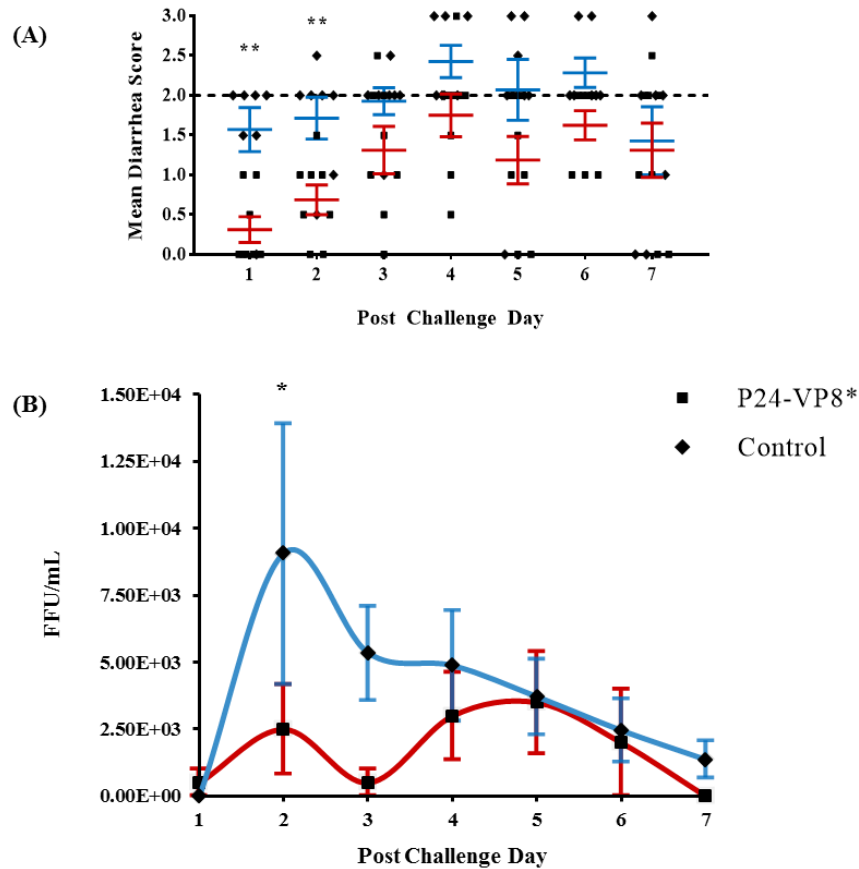
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*BMC Infect. Dis.* **2012**, *12*, 213.

**Table 1.** Assignment of treatment groups for gnotobiotic (Gn) pigs.

Group	Number of Pigs	Challenge	Time of Euthanasia
Control	3	No	PID 28
Control	7	Yes	PCD 7
P24-VP8* Vaccine	7	No	PID 28
P24-VP8* Vaccine	8	Yes	PCD 7

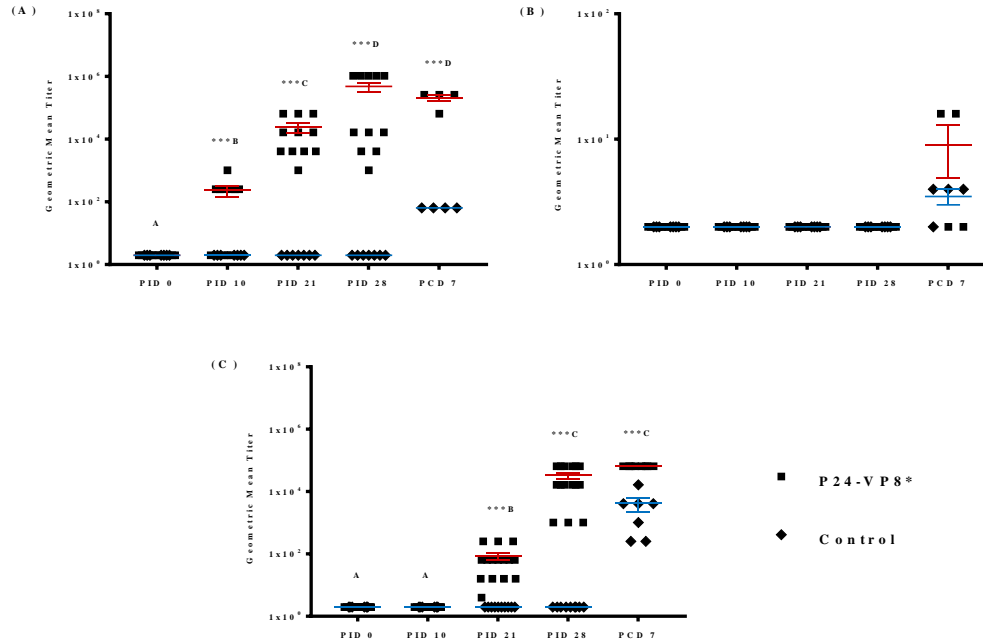


**Figure 1.** P24-VP8\* vaccine protected against VirHRV diarrhea and reduced overall virus shed among vaccinated pigs. Fecal consistency (A) and virus shedding (B) were monitored daily from post challenge day (PCD) 1 to PCD 7 after the challenge with VirHRV. Fecal consistency scores  $\geq 2$  were considered to be diarrheic (dashed line indicates the threshold of diarrhea). Statistical significance between vaccinated and control groups, determined by multiple t tests, are indicated by asterisks (\*,  $p < 0.05$ ; \*\*,  $p < 0.01$ ).

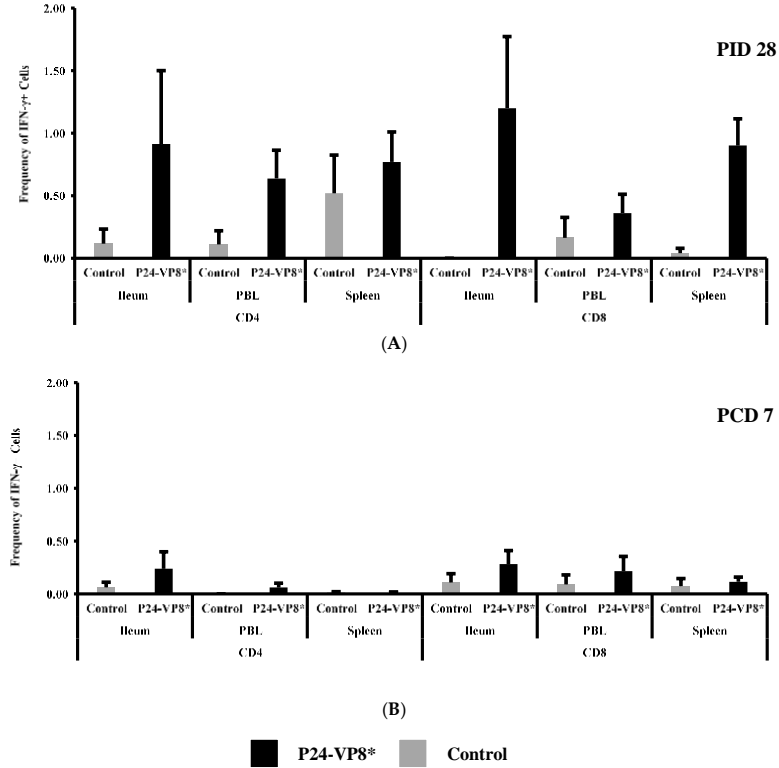
**Table 2.** Diarrhea and rotavirus fecal virus shedding in Gn pigs after the VirHRV challenge.

Treatment	<i>n</i>	Diarrhea				Fecal Virus Shedding				AUC
		% with Diarrhea <sup>a</sup>	Mean Days to Onset <sup>b</sup>	Mean Duration Days <sup>c,§</sup>	Mean Cumulative Fecal Score <sup>c</sup>	% Shedding Virus <sup>a</sup>	Mean Days to Onset <sup>b</sup>	Mean Duration Days <sup>c</sup>	Mean Peak Titer (FFU/mL)	
P24-VP8*	8	87.5	4.4 (0.5) <sup>d,*</sup>	3.3 (0.75) *	9.1 (1.23) *	75	4.8 (1.0)	2.5 (0.89) *	8500 (2196) *	11,750 (3172)
Control	7	100	1.6 (0.3)	6.0 (0)	14.3 (0.44)	85.7	1.9 (0.14)	5.9 (0.14)	11,492 (4300)	26,664 (10,489)

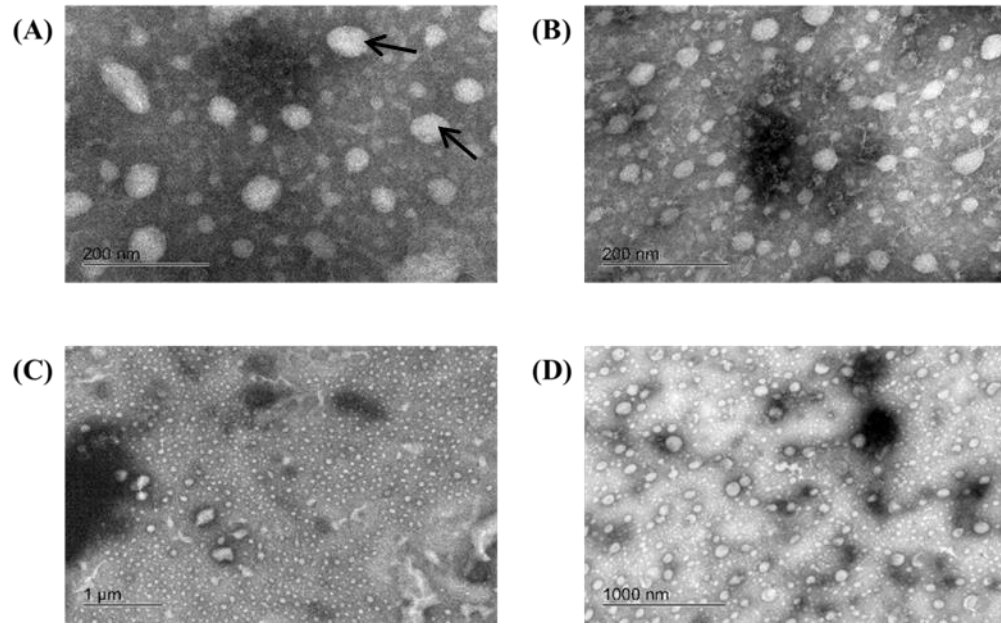
<sup>a</sup> Gn pigs were orally inoculated with  $1 \times 10^5$  FFU/mL of VirHRV at post-innoculation day (PID) 28. Rectal swabs were collected daily after the challenge from PCD 1 to PCD 7 to monitor for clinical signs and virus shedding. Pigs with daily fecal scores of  $\geq 2$  were considered diarrheic. Fecal consistency was scored as follows: 0, normal; 1, pasty; 2, semi-liquid; and 3, liquid. Fecal virus shedding data was determined by ELISA and/or CCIF. <sup>b</sup> An arbitrary designation of Day 8 was assigned to pigs that did not develop diarrhea or shed virus in feces for calculating the mean days to onset. <sup>c</sup> For the purposes of calculating diarrhea and virus shedding duration, if no diarrhea or virus shedding was observed in pigs until euthanasia day (PCD 7), the duration days were recorded as 0. <sup>d</sup> Standard error of the mean. <sup>§</sup> Student's *t*-test was used for comparison between vaccine and control groups. Asterisk indicates statistical significance between the groups ( $n = 7-8$ ; \*,  $p < 0.05$ ).



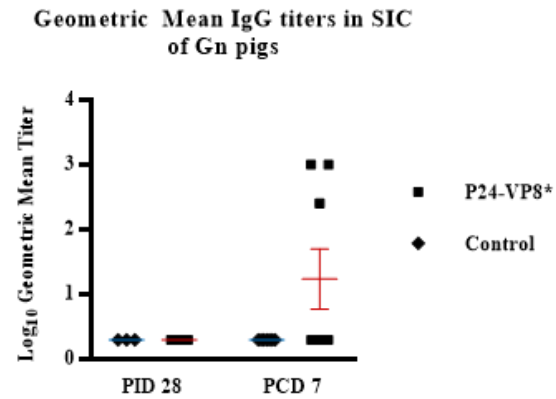
**Figure 2.** Geometric mean VP8\*-specific IgG (A) and IgA (B) and Wa-HRV neutralizing (C) antibody titers in serum collected from Gn pigs at PID 0, 10, 21, 28, and PCD 7. Pigs were vaccinated with P24-VP8\* vaccine or Al(OH)<sub>3</sub> adjuvant only. Each serum specimen was tested at an initial dilution of 1:4. Negative samples were assigned an arbitrary value of 2 for calculation and graphical illustration purposes. Comparisons between groups at the same time points were carried out using Student's *t*-test and significant differences are identified by \*\*\* ( $n = 10-15$ ;  $p < 0.001$ ). Tukey-Kramer HSD was used for the comparison of different time points within the same group, where different capital letters (A, B, C, D) indicate a significant difference,  $p < 0.01$ , and shared letters indicate no significant difference.



**Figure 3.** Frequencies of IFN- $\gamma$ +CD8<sup>+</sup> and IFN- $\gamma$ +CD4<sup>+</sup> T cells in ileum, peripheral blood (PBL), and spleen at PID 28 (A) and PCD 7 (B). Two-way ANOVA followed by Multiple t-tests were carried out for comparisons. (n = 3–8; p < 0.05). There were no significant differences.



**Figure S1.** Negative stain TEM images of P24-VP8\* particles (indicated by black arrow) taken over two different time points. Panels (A) and (C) were taken 3 months after vaccine preparation and panels (B) and (D) were imaged 8 months after vaccine preparation.



**Figure S2.** Geometric mean VP8\*-specific IgG titers in SIC samples collected upon euthanasia at PID 28 and PCD 7. Negative samples were assigned an arbitrary value of 2 for statistical calculations and graphical illustration. Three out of 8 pigs were observed to be positive for VP8\*-specific IgG antibodies. There were no significant differences.

## Chapter 3

### **Evaluation of different dose-response models for the calculation of 50% infectious dose of human norovirus Cin-1 in gnotobiotic pigs**

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Key words: median infection dose, norovirus, gnotobiotic pigs, dose-response models

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*Manuscript in preparation*

## Abstract

Human noroviruses (HuNoVs) are the leading causative agents of epidemic and sporadic acute gastroenteritis that affect people of all ages worldwide. However, very few dose-response studies have been carried out to determine the median infectious dose of HuNoVs. In this study, we determined the median infectious ( $ID_{50}$ ) and diarrhea ( $DD_{50}$ ) dose of GII.4/2003 variant of HuNoV (Cin-1) in the gnotobiotic (Gn) pig model of HuNoV infection and disease. Gn pigs were inoculated with 7 different doses (ranging from  $8 \times 10^2$  to  $2 \times 10^6$  genomic RNA copies) of Cin-1 at 33-34 days of age. Pigs were monitored daily from post-inoculation day (PID) 1 to 7, for fecal virus shedding and fecal consistency to evaluate the virus infectiousness and associated diarrhea. Using various mathematical models, we estimated the  $\text{Log}_{10} ID_{50}$  and  $DD_{50}$  to be between 3.11 to 3.76, and 3.37 to 4.87 RNA copies, respectively. Of the different models used in this study, the exponential and Beta-Poisson model were most extensively used by other dose-response studies carried out for enteric pathogens such as rotavirus and *E. coli*. Comparison of Akaike information criterion values showed that Beta-Poisson is the best-fitting mathematical model to estimate both the  $ID_{50}$  and  $DD_{50}$  of Cin-1 when using the rate of animals with virus shedding and diarrhea in each dose group. Adjusting a 3-parameter log logistic regression model to area under the curve values of virus shedding and fecal consistency scores resulted in the  $\text{Log}_{10}$  of  $ID_{50}$  to be 3.89 and the  $\text{Log}_{10} DD_{50}$  to be 5.03 RNA copies, within the range obtained from the counting data. Determining the  $ID_{50}$  of the challenge virus strain is crucial for identifying the true infectiousness of HuNoVs and for accurate evaluation of protective efficacies in pre-clinical studies of therapeutics, vaccines and other prophylactics using this reliable animal model.

# 1. Introduction

Human noroviruses (HuNoVs) are non-enveloped RNA viruses with a positive-sense single-stranded genome in the *Caliciviridae* family. They are the most common etiological agents of epidemic and sporadic acute gastroenteritis in people of all age groups (Payne, Vinjé *et al.* 2013, Pringle, Lopman *et al.* 2015, Rouhani, Peñataro Yori *et al.* 2016) and are responsible for around 125 million cases of foodborne illnesses worldwide each year (Kirk, Pires *et al.* 2015). There are currently no licensed vaccines available for HuNoVs, but several virus-like particle (VLP) vaccine candidates are currently undergoing various stages of clinical trials and have thus far shown some promise in both immunogenicity and protective efficacy studies, although the correlates of protection to norovirus infections are yet to be fully determined (Treanor, Atmar *et al.* 2014, Bernstein, Atmar *et al.* 2015, Sundararajan, Sangster *et al.* 2015, Atmar, Baehner *et al.* 2019). The lack of a widely available animal model has made it difficult for the study of viral pathogenesis, as well as the underlying immune mechanisms of protection against HuNoV infections (Ernst 2016, Wobus, Cunha *et al.* 2016). Although the stem cell-derived, human intestinal enteroid (HIE) monolayer culture system has been successful in cultivating several HuNoV strains (Ettayebi, Crawford *et al.* 2016, Ramani, Crawford *et al.* 2018), the magnitude of virus amplification is low and large quantities of infectious viral particles still can only be acquired from stool samples of infected human patients.

The ideal animal model to study HuNoV infection and disease would be one that is capable of replicating the biological and clinical features associated with human disease. Among the different models used in HuNoV research (Cheetham, Souza *et al.* 2007, Souza, Azevedo *et al.* 2008, Bok, Parra *et al.* 2011, Taube, Kolawole *et al.* 2013, Todd and Tripp 2019), gnotobiotic (Gn) pig models provide a suitable solution for studying HuNoV infection and disease due to the close similarities

in physiology, immune development, virus binding patterns, histo-blood group antigens (HBGA) phenotypes between pigs and humans (Cheetham, Souza *et al.* 2007). Since their introduction into research in the early 1960s, Gn pigs have been utilized extensively for the study of enteric virus and bacteria (Yuan, Jobst *et al.* 2017, Lei, Twitchell *et al.* 2018). Gn pig infection model for two different HuNoV GII.4 variants (GII.4/HS66 and GII.4/2006b) have been established for evaluating HuNoV vaccines (Cheetham, Souza *et al.* 2006, Souza, Costantini *et al.* 2007, Bui, Kocher *et al.* 2013, Kocher, Bui *et al.* 2014), displaying similar levels of infectivity compared to HuNoV GI.1/Norwalk and GII.4/2003 Cin-1 in human challenge studies and vaccine trials (Atmar, Bernstein *et al.* 2011, Treanor, Atmar *et al.* 2014, Bernstein, Atmar *et al.* 2015).

HuNoVs are believed to be highly infectious. A few studies have explored the infection risk (Le Guyader, Neill *et al.* 2003, Le Guyader, Krol *et al.* 2010, Lowther, Gustar *et al.* 2012) and calculated the median infectious dose (ID<sub>50</sub>) (Teunis, Moe *et al.* 2008, Atmar, Opekun *et al.* 2014) for Norwalk virus in humans. It was identified that around 2800 RNA copy numbers were sufficient to successfully infect an adult human volunteer (Treanor, Atmar *et al.* 2014). A previous study of the ID<sub>50</sub> of a GII.4/2006b variant in newborn (4-5 days of age) and older (33-34 days of age) Gn pigs was the only ID<sub>50</sub> study of HuNoV in Gn pigs (Bui, Kocher *et al.* 2013). Dose-response data provide valuable information that are used to make the most informed risk assessments for viral infections in humans and is critically important for the standardization of the animal challenge model used in pre-clinical efficacy evaluation of vaccines and anti-viral agents.

The current study uses a different HuNoV, a GII.4/2003 variant Cin-1. The Cin-1 inoculum has been well characterized and used in human volunteer challenge studies with  $5 \times 10^4$  RT-PCR units (viral RNA copies) per dose (Frenck, Bernstein *et al.* 2012, Bernstein, Atmar *et al.* 2015). The objectives of this study are to determine the median infectious and diarrhea doses, that is, the

dilution of virus inoculum at which 50% of the Gn pigs are infected (i.e., the ID<sub>50</sub>) or developed diarrhea (i.e., DD<sub>50</sub>) for the GII.4/2003 variant. The significance of this study includes: i). Identifying the most appropriate Cin-1 challenge dose in 33-34 day old Gn pigs to standardize the model for HuNoV vaccine evaluation; ii) Comparing different dose-response models used for estimating the ID<sub>50</sub> and DD<sub>50</sub> of Cin-1 in Gn pigs to determine the best fit model to the outcome variables expressed as a counting variable (using the rate or frequencies of animals affected) or as a continuous variable (the area under the curve of virus shed/diarrhea score) and; iii) To compare the obtained value with the dose used in human volunteers. These statistical analyses will maximize the internal validity and reproducibility of this animal model of HuNoV infection and disease. Comparing the infectiousness of the same GII.4 variant challenge pool in Gn pigs and humans (objective iii) will lead to a better understanding of the zoonotic potential of NoVs between different species and further validate the Gn pig model of HuNoV infection as a proper predictive tool of the future efficacy of vaccines and other antiviral strategies to control NoV diarrhea in humans.

## **2. Materials and Methods**

### ***2.1 Virus inoculum***

A pool of human stool specimens containing GII.4 strain, Cin-1 (Hu/GII.4/Cin-1/2003/US), a 2002 Farmington Hills-like variant, was isolated by Xi Jiang's laboratory at Cincinnati Children's Hospital Medical Center collected from a man who developed a 3-day illness characterized by diarrhea, vomiting, nausea, abdominal cramps, and fever in 2003. This sample underwent extensive quality control prior to being used as a challenge pool in various human studies (Frenck, Bernstein *et al.* 2012, Bernstein, Atmar *et al.* 2015). The HuNoV concentration of the challenge

pool was determined by quantitative real-time RT-PCR (RT-qPCR) and as approximately  $2 \times 10^6$  viral genomic RNA copies/mL of stool. The challenge pool was stored at  $-80^{\circ}\text{C}$  in individual 1 mL aliquots until the day of Gn pig inoculation.

## ***2.2 Gnotobiotic pigs and treatments***

Near-term pigs (Large white cross breed) were derived by aseptic hysterectomy and maintained in sterile isolator units as described previously (Yuan, Jobst *et al.* 2017). To determine the sterility status of the isolators that the pigs were housed in, rectal swabs collected from pigs were cultured on blood agar plates (Hardy Diagnostics) and in Thioglycollate media (Hardy Diagnostics) 3 days after derivation and repeated once a week until the end of the study. Pigs were fed commercial ultra-high temperature-treated sterile cow milk throughout the study. A total of 28 pigs were assigned to seven groups. Pigs were randomly divided into groups upon derivation regardless of gender and body weight. Each group of pigs received a different dose of Cin-1 inoculum at postpartum day (PPD) 33 or 34. Prior to inoculation with HuNoV, 4 ml of 200 mM sodium bicarbonate was given orally 15 min to neutralize stomach acids. The Cin-1 inoculum was mixed with 5 ml of Diluent #5 (minimal essential medium with 1% penicillin-streptomycin and 1% HEPES) on the day of inoculation. All pigs received oral doses of Cin-1 ranging from  $8 \times 10^2$  to  $2 \times 10^6$  genomic RNA copies at PID (post-inoculation day) 0. Clinical signs and fecal virus shedding were monitored daily until euthanasia. All pigs were euthanized on PID 7. All experiments involving the use of Gn pigs were approved by the Institutional Animal Care and Use Committee at Virginia Tech (IACUC protocol: 17-110-CVM). All experimental procedures were carried out in compliance with federal and university regulations.

### ***2.3 HBGA-typing of Gn pigs by immunofluorescence assay***

Prior to inoculation, all Gn pigs were screened for their HBGA type by immunofluorescence assay. Epithelial cells collected from the cheeks were prepared as described previously (Bui, Kocher *et al.* 2013). HBGA phenotypes were detected from these cells using fluorescent labeled antibodies described elsewhere (Lei, Ryu *et al.* 2016). All slides were prepared with VECTASHIELD® Antifade Mounting Medium with 4,6-diamidino-2-phenylindole (DAPI) which was used as a nuclear counterstain (Vector Laboratories) for fluorescent microscopy. Based on this screening technique, HBGA type A<sup>-</sup> and H<sup>-</sup> pigs were excluded from this study because A<sup>-</sup> or H<sup>-</sup> pigs are less susceptible to NoV infection than A<sup>+</sup> or H<sup>+</sup> pigs (Cheetham, Souza *et al.* 2007, Bui, Kocher *et al.* 2013).

### ***2.4 Detection of fecal consistency and HuNoV shedding by RT-qPCR***

Fecal consistency and virus shedding were monitored at 24-hour intervals at the same time daily, after HuNoV inoculation at PID 0, by rectal swab sampling. The following scoring system was used to assess fecal consistency: 0, solid; 1, pasty; 2, semiliquid; 3, liquid. Pigs with fecal consistency scores of 2 or greater were considered to be diarrheic. Presence of HuNoV genomes in rectal swab samples collected after inoculation with different doses of Cin-1 were evaluated using RT-qPCR protocol as described previously (Lei, Ryu *et al.* 2016). Briefly, once collected, swabs were swirled in 1 ml PBS to release the feces and centrifuged at 10000 g for 5 min. 250 µl of the supernatant collected was mixed with 750 µl TRIzol (Invitrogen) following manufacturer's instructions for viral RNA extraction. The extracted RNA was then dissolved in 40 µl autoclaved dd-H<sub>2</sub>O. Five microliters of RNA were used in 20 µl RT-qPCR reaction with a SensiFAST Probe No-ROX One-Step Kit (Bioline) to detect HuNoV genomes. Primers COG2F, COG2R, and probe

RING2 were used with cycling conditions as described in a previous study (Kageyama, Kojima *et al.* 2003). A standard curve was generated using COG2 amplicon-containing cDNA expression plasmids in serially diluted tenfold from  $2 \times 10^6$  to 2 genomic RNA copies. Amplification was performed on CFX96 Real-Time System (Bio-Rad), and data were collected and analyzed with Bio-Rad CFX Manager 2.0.

## ***2.5 Electron Microscopy***

Negative-stain electron microscopy (EM) was carried out to determine the aggregation status of Cin-1 inoculum. Briefly, TEM grids were treated with 1% aqueous Alcian blue (Sigma-Aldrich) solution for 5 min and washed with a few drops of distilled water until the dye is removed. Samples were diluted as mentioned in Section 2.2 to ensure that the visualized particles correspond to the dilution administered to Gn pigs. A droplet of sample was added to each grid and allowed to sit for 1 minute to ensure adsorption onto the grid. 3% Sodium (K) phosphotungstate (PTA; Sigma-Aldrich) were then added and allowed to stain for 1 min. Upon removing the treatment solution using filter paper, the grids were allowed to air dry. Zeiss 10A transmission electron microscope was then used to visualize and image the stained Cin-1 NoV particles at 200 k to 250 k magnitudes.

## ***2.6 Statistical analysis***

### ***2.6.1 Analysis of variance among challenge doses***

The analyses of variances were carried out using Infostat<sup>®</sup> connected to R (<https://www.infostat.com.ar/index.php?mod=page&id=46>) and further confirmed using scripts from the R software (R Core Team) in R Studio. The variables related to virus shedding were analyzed using a general linear model (GLM), considering the treatment (pigs receiving different doses of HuNoV) as a fixed factor and the Gn pigs within the groups as a random factor. The

variance was modeled using a varIdent structure for the variance-covariance matrix. The variables associated to diarrhea were analyzed by one-way ANOVA prior to testing the normality and homoscedasticity assumptions. In all cases, multiple post ANOVA comparisons were carried out using the Tukey method for comparisons between the 7 different doses. Statistical significance was considered at  $p < 0.05$  for all comparisons.

### ***2.6.2 ID<sub>50</sub> and DD<sub>50</sub> calculations using different dose-response models***

For a specific pathogen, in a specific host, using a specific exposure route for a particular endpoint (response or outcome: in this case virus shedding and diarrhea), there is a unique dose response relationship that can be described using different mathematical functions that allows for selecting the model with the best fit.

#### ***i. Reed-Muench, Dragstedt-Behrens and Spearman-Kärber method***

The Reed-Muench (RM) method, first described in 1938 (Reed and Muench 1938), is an old fashion method that has been widely used for the calculation of 50% end point in experimental biology. The RM method employs a two-step equation that involves the calculation of the proportionate distance (PD) between dilutions above and below the 50% end point as calculated using Equation (1).

$$\text{Proportionate distance (PD)} = \frac{\text{Percentage infected at dilution next above 50\%} - 50\%}{(\text{Percentage infected at dilution next above 50\%} - \text{Percentage infected at dilution next below 50\%})} \quad (1)$$

$$\log 50 \% \text{ end point} = (\log \text{dilution above 50\%}) - (PD * \log \text{dilution factor}) \quad (2)$$

The dilution factor used in this equation describes the fold difference between the two inoculum titers above and below 50% response rate. The median dose was then calculated based on Equation

(2). The RM method has been used previously for the determination of the ID<sub>50</sub> of a different HuNoV variant (GII.4/2006b) in Gn pigs (Bui, Kocher *et al.* 2013).

The Dragstedt-Behrens (DB) method (Dragstedt and Lang 1928, James 1959) is very similar to the RM method but instead of working with the cumulative sums directly, it uses the fraction of the cumulative sums that are positive at each dose. The ID<sub>50</sub> is estimated by interpolating the line that connects the hypothetical fractions of the bracketing doses (Siev 2018).

Both methods rely on data to be equally-spaced, with each group containing equal “n” numbers, and the overall data to be symmetric in nature for an accurate estimate of the dose-response. Although primarily used for their historical relevance, the RM and DB methods are still used extensively in modern scientific research as the primary model for calculating the end-point dilution dose (Bui, Kocher *et al.* 2013, Ramakrishnan 2016, Elikaei, Hosseini *et al.* 2017, Zhao, Xie *et al.* 2017, Han, Chen *et al.* 2018, Spackman, Malladi *et al.* 2019, Sudeep, Vyas *et al.* 2019).

Spearman-Kärber is another method that is widely used and specially suggested by the regulatory agencies for the calculation of virus titers and mean infectious doses. These non-parametric methods produce accurate estimates of the mean but not the median. An important criteria for being able to use this method would be the presence of dose response data with 0% and 100% response in order to generate a symmetrical distribution of data with well-defined upper and lower plateaus (Siev 2018).

***ii. Exponential dose-response model and Beta-Poisson generalized linear model (GLM)***

Both Exponential and Beta-Poisson models have been identified to be the best-fit models for the calculation of ID<sub>50</sub> of various viral infections in humans and other animal models.

The exponential dose response model is derived by assuming that the parameter  $r$  representing the survival of the pathogen in the host is a constant parameter. The mechanistic microbial dose response model is the exponential equation (3) from which there is a binomial likelihood of  $r$  pathogens that survive to initiate an infection. This means that either the pathogen survives or does not to initiate an infection.

$$P(r) = 1 - \exp(-r \cdot \text{dose}) \quad (3)$$

The Beta Poisson dose response model is an expansion from the exponential model. In this case, it is assumed that the survival of the pathogen in the host is a random variable with a Beta Poisson distribution for the average of the bolus dose. This allows for an increased level of realism in modeling the dose response relationship in the host.

$$P(r) = 1 - \left[ 1 + \frac{\text{dose} \cdot 2^{1/\alpha} - 1}{N_{50}} \right]^{-\alpha} \quad (4)$$

In equation (4),  $N_{50}$  is an estimate of the median infectious/diarrhea dose with units of counts (i.e. genome copy numbers) and  $\alpha$  is a unitless model parameter. Equation (4) represents an approximation of the exact form of the Beta Poisson model (Weir, Mitchell *et al.* 2017). This approximated form retains the linearity at low doses, a fundamental characteristic of microbial dose response models (Haas, Rose *et al.* 2014, Weir, Mitchell *et al.* 2017).

Assumptions of the model:

a. *The number of aggregates in the virus suspension are random Poisson-distributed.*

This assumes that a Poisson distribution of NoV aggregated among Gn pigs (replicates) receiving the same challenge doses. This assumption helps to explain that some pigs are highly infected and others do not in the same dose group due to this random chance to receive one or several aggregates.

b. *Aggregates size vary according to a log-series distribution but it is not a problem*

c. *The dilution procedure do not modify the aggregation condition of the sample*

d. *One organism is capable of producing an infection if it arrives at an appropriate site.*

Once the viruses enter the host, the viruses become disaggregated and act (infect) independently. Organisms have independent and identical probability  $P(r)$  of surviving to reach and infect at an appropriate site.

Survival probabilities  $P(r)$  are given by the beta distribution.

Online tools are available for both models and can be found here:

1. Exponential Model: AATBioquest® - <https://www.aatbio.com/tools/ed50-calculator>
2. Beta-Poisson Model: NCBI Statistical Computational Biology Infectious Dose or Dilution (ID<sub>50</sub>) Server - [https://www.ncbi.nlm.nih.gov/CBBresearch/Spouge/html\\_ncbi/html/id50/id50.cgi](https://www.ncbi.nlm.nih.gov/CBBresearch/Spouge/html_ncbi/html/id50/id50.cgi) (Spouge 2015). This tool was based on VACMAN, a computational program that calculates statistics for *in vitro* and *in vivo* infectivity data (Spouge 1992).

Calculations of ID<sub>50</sub> and DD<sub>50</sub> were also carried out using the R scripts published by Weir 2017 (Weir, Mitchell *et al.* 2017) for Exponential and Beta Poisson (R Core Team). Briefly, the script uses the maximum likelihood estimation (MLE) to fit the counting data (rate of animals with virus

shedding/diarrhea) to both theoretical distributions, either Exponential or Beta-Poisson due to their biologic plausibility. The process calculates the probability of obtaining the observed data given a theoretical distribution by minimizing the deviance (Y) and the Akaike information criterion (AIC) of each of these fitted models are defined by equations (5) and (6) respectively.

$$\text{Deviance} = Y = -2 [\ln M2 - \ln M1] \quad (5)$$

Where  $\ln M1$ ,  $\ln M2$  are the MLE for the full (M2) and restricted (M1) models. Optimized deviance follows a Chi-squared distribution with  $k - p$  degrees of freedom, where  $k$  is the number of doses and  $p$  is the number of dose-response parameters of a given model. The model is rejected if  $Y > X^2(k-p, \alpha)$ .

$$\text{AIC} = 2p + Y \quad (6)$$

Where  $p$  is the value of the parameter of the model and  $Y$  is the deviance. The AIC adds a penalty for adding parameters to the model to avoid model overfitting (increasing the number of parameters in the model almost always improves the goodness of the fit). If two or more models are significant, the model with the lowest deviance (and AIC) is chosen. Bootstrapping is performed to characterize the uncertainty of parameter estimates of the distribution, most commonly by generating confidence intervals. The estimates from this approach approximate the uncertainty associated with the “true” distribution by repeatedly sampling the data and re-computing a statistic (Weir, Mitchell *et al.* 2017).

***iii. ID<sub>50</sub> and DD<sub>50</sub> estimated by the adjustment of a three-parameter log logistic (3PLL) dose-response model on the shedding and diarrhea AUC values***

Area under the curves (AUC) of virus shedding (Log<sub>10</sub> genomic copies) and diarrhea severity (fecal score) for each individual pig were calculated. These two continuous variables were based

on a 3PLL model and the ID<sub>50</sub> and DD<sub>50</sub> estimated using the “dr package” in R described previously (Ritz, Baty *et al.* 2016).

### **3. Results**

#### ***3.1 Assessment of infection status in Gn pigs***

Infection caused by HuNoV Cin-1 was defined by the presence of viral RNA quantified using RT-qPCR carried out on samples isolated from rectal swabs on any day from PID 1 to 7. The percentage of affected animals, mean days to onset, duration, peak titer and AUC of fecal virus shedding, in pigs in each of 7 dose groups are summarized in Table 1. An increase in inoculation dose was positively associated with a shorter incubation period, which coincided with the observed increased duration (Figure 1A), as well as an increased overall virus shed in feces measured by AUC (Figure 1B). All pigs belonging to dose groups 1 to 4 shed detectable titers of virus in their feces, while 67% of pigs shed virus when inoculated at doses between  $3.2 \times 10^3$  to  $2 \times 10^4$  RNA copies. Only 25% of the pigs that were inoculated with  $8 \times 10^2$  RNA shed virus. Important to note, pigs that were administered a dose of  $2 \times 10^5$  RNA copies shed significantly higher amount of virus in their feces ( $p < 0.0001$ ) and shed virus for a significantly longer duration than pigs in the other groups ( $p < 0.0001$ ) (Figure 1A and 1B).

#### ***3.2 Assessment of diarrhea status in Gn pigs***

After inoculation, pigs were monitored daily for diarrhea status. Fecal consistency scores were determined based on previous studies carried out by our group (Lei, Ramesh *et al.* 2016, Lei, Ryu *et al.* 2016, Lei, Samuel *et al.* 2016): 0 solid; 1 pasty; 2 semi-liquid; or 3 liquid. A score of 2 or greater ( $\geq 2$ ) was considered to be diarrheic. The percentage of pigs with diarrhea, the mean duration, the AUC and mean onset day of diarrhea from Cin-1 inoculated pigs are summarized in

Table 1. A longer duration of diarrhea (Figure 1C) and a higher cumulative diarrhea score (Figure 1D) were observed in Gn pigs that were inoculated with higher doses of Cin-1. Pigs that were inoculated with  $2 \times 10^5$  RNA copies of Cin-1 that had the highest virus titers shed in their feces also experienced diarrhea for a longer duration of time than the pigs inoculated with the other doses. Pigs belonging to dose group 1 experienced diarrhea for the longest duration of time (5 out of 7 days) and had the quickest onset (within 1.5 days after inoculation), indicating severe clinical onset mimicking that in humans (Cheetham, Souza *et al.* 2006, Cheetham, Souza *et al.* 2007), while HuNoV-associated gastroenteritis typically lasts for 3-5 days after infection among susceptible populations (Green 2013). Pigs in dose groups 5 and 6 had a delayed onset to diarrhea together with lower cumulative fecal consistency scores, demonstrating a milder diarrhea burden. No diarrhea was observed among pigs in dose group 7. In summary, the third dose with  $2 \times 10^5$  RNA copies of Cin-1 was also the optimal dose in terms of severity and mean duration of diarrhea.

### ***3.3 Determination of ID<sub>50</sub> and DD<sub>50</sub> using various dose-response models***

The parameters used for conventional RM method is displayed in supplementary material Supplementary Table S1. The cumulative frequencies (%) of pigs shedding virus and experiencing diarrhea were used to calculate the ID<sub>50</sub> and DD<sub>50</sub> doses in conventional RM method. The ID<sub>50</sub> and DD<sub>50</sub> of Cin-1 were calculated to be log dose 3.11 and 4.86, respectively. The ID<sub>50</sub> and DD<sub>50</sub> calculated using the exponential and the beta-Poisson dose-response models are presented in Table 2. AUC-based estimates of ID<sub>50</sub> and DD<sub>50</sub> using the 3PLL model were log 3.89 and 5.02 respectively (Table 2 and Figure 3). From the estimates calculated using the Spearman-Kärber (SK) method, only the DD<sub>50</sub> can be considered reliable, while the ID<sub>50</sub> even within the range of the estimates obtained by the other method is not reliable due to the lack of sufficient dose-response data in the lower limit.

### ***3.4 Comparison of infectiousness of HuNoV Cin-1 in humans and Gn pigs.***

We compared the percentage, mean duration and peak day of virus shedding between humans and Gn pigs after inoculation with the same HuNoV Cin-1 inoculum (Table 3). In the human adult challenge study (Frenck, Bernstein *et al.* 2012), after oral inoculation with  $5 \times 10^4$  RNA copies of HuNoV Cin-1, 16 out of 23 secretors (70%) were infected, which was defined by the detection of HuNoV in stool samples by RT-qPCR same as in the Gn pig study. In Gn pigs, an inoculation dose of  $2 \times 10^4$  infected 67% of pigs, whereas  $8 \times 10^4$  and  $2 \times 10^5$  RNA copies infected 100% pigs (Table 1). Among pigs inoculated with  $2 \times 10^5$  RNA copies, the duration and range of days of virus shedding are comparable to those of humans and the peak day of virus shedding is almost identical (PID 3). These data indicate that the infectiousness of HuNoV Cin-1 in Gn pigs and humans are very similar and the Gn pig model when inoculated with the optimal virus dose ( $2 \times 10^5$  RNA copies) accurately replicates the course of HuNoV infection in humans.

### ***3.5 Identification of best-fitting method for dose-response analysis of Cin-1***

Both Exponential and Beta-Poisson are routinely used as interchangeable logit models for the determination of median infectious- and median diarrhea- doses for different pathogens due to their biological plausibility. Comparisons of goodness of fit data demonstrated that both models are equally effective for the determination of  $ID_{50}$  (Figure 2A and 2B; and Table 4a) but the Beta-Poisson method, based on a lower deviance and AIC values, was determined to be the best-fitting model for determining the  $DD_{50}$  of Cin-1 (Figure 2C and 2D; and Table 4b). The  $ID_{50}$  and  $DD_{50}$  values determined by beta-Poisson model was  $2.57 \times 10^3$  RNA copies and  $2.09 \times 10^4$  RNA copies respectively.

### ***3.6 Determination of an optimal challenge dose***

Based on the virus shedding and diarrhea status of infected pigs, we determined the optimal challenge dose of Cin-1 to be  $2 \times 10^5$  (Table 5). Our data shows that pigs infected at this dose had a mean onset day of 1.3, with virus shed in feces in large quantities (AUC) for almost the whole duration of the infection period (6.3 days out of 7; Table 1). Moreover, pigs in this dose group also experienced the highest diarrhea burden among all dose groups, with diarrhea starting at 2.8 days after inoculation and occurring for a duration of 4 days. Pigs in this group also had the highest mean cumulative diarrhea score of 9.31 (Table 2).

### ***3.7 Aggregation of Cin-1***

The Cin-1 virus pool has been previously demonstrated to be aggregated (Messner, Berger *et al.* 2014), but no evidence was provided with regards to the size of each aggregate. In an attempt to ascertain the amount of virus particles within each aggregate, TEM micrographs were taken of Cin-1 inoculum at  $8 \times 10^4$  and at  $2 \times 10^5$  RNA copies. The average number of virus particles within each observed aggregate was determined to be 175 and 390 respectively. Figure 4 shows representative images of Cin-1 norovirus inoculum pool at  $8 \times 10^4$  and  $2 \times 10^5$  RNA copies.

## **4. Discussion**

In this study, we determined the  $ID_{50}$  and  $DD_{50}$  of HuNoV GII.4/2003 Cin-1 variant in Gn pigs, a large animal model that has proven to be capable of replicating HuNoV GII.4-associated disease in humans (Cheetham, Souza *et al.* 2006, Bui, Kocher *et al.* 2013). The  $ID_{50}$  and  $DD_{50}$  calculated with the best fitting, beta-Poisson model, are  $2.57 \times 10^3$  RNA copies and  $2.09 \times 10^4$  RNA copies, respectively. Our data was analyzed with different dose response models, and all the  $ID_{50}$  estimates were within 1 log of each of the methods, confirming the accuracy of the experiments.

The GII.4/2006b variant of HuNoV was primarily observed to cause illness among the pediatric population in day cares and hospitals (Tu, Bull *et al.* 2008, Chen, Feng *et al.* 2015, Kumazaki and Usuku 2015). Bui *et al* determined the ID<sub>50</sub> of GII.4/2006b variant in neonatal (4-5 days of age) and older (33-34 day old) Gn pigs using RM calculation method. An ID<sub>50</sub> of  $6.43 \times 10^4$  RNA copies was identified based on the infection status of older pigs (Bui, Kocher *et al.* 2013). The Farmington Hills virus was responsible for around 64% of cruise ship outbreaks and 45% of the land-based outbreaks, most of which occurred in long-term care facilities, schools, and restaurants, in the US in 2002 (Isakbaeva, Widdowson *et al.* 2005, Bull, Tu *et al.* 2006, Johnston, Qiu *et al.* 2007). In the current study, using the RM method, we determined the ID<sub>50</sub> of Cin-1, a variant of the Farmington Hills virus, to be  $1.84 \times 10^3$  RNA copies in similar aged pigs (Table 2). A 35-fold higher virus titer is required to establish infection among 50% of the pigs inoculated with the GII.4/2006b virus as compared to the Cin-1 (Table 5), indicating that Cin-1 is a more infectious strain in Gn pigs.

In a previous human clinical study, administering a dose of  $5 \times 10^4$  RNA copies of Cin-1 from the same Cin-1 challenge pool caused infection among 70% of secretor positive individuals (Frenck, Bernstein *et al.* 2012). A phase I vaccine study in human volunteers carried out by Bernstein and colleagues used a challenge dose of  $4.4 \times 10^3$  RNA copies (Bernstein, Atmar *et al.* 2015) based on a pilot study showing similar rates of infection (26/34 [76.5%]) and illness (19/34 [55.9%]) compared to the  $5 \times 10^4$  RNA copies used by Frenck (Frenck, Bernstein *et al.* 2012, Bernstein, Atmar *et al.* 2015). However, this challenge dose ( $4.4 \times 10^3$  RNA copies) was too low and caused infection only in 62.5% and disease (vomiting or diarrhea of mild or greater severity) in 37.5% of the volunteers among the placebo control group. This data compared to the slightly reduced incidence of infection (54%) and disease (20%) among the vaccine recipients, leading to the

inconclusive protective effect of the vaccine due to the lack of statistical significance (Bernstein, Atmar *et al.* 2015). Similarly, in the present study, in dose group 5 ( $2 \times 10^4$  RNA copies), only 67% of the pigs shed virus and 33% had diarrhea, whereas 100% of the pigs in dose groups 1-4 shed virus and 75% to 100% had diarrhea. This data shows an observable trend that corroborates the data from Frenck and Bernstein (Frenck, Bernstein *et al.* 2012, Bernstein, Atmar *et al.* 2015). Collectively, these data highlight the importance of identifying the optimal virus challenge dose for the evaluation of protective efficacy of vaccines in animal models and in humans.

Diarrhea status in this study was determined based on the fecal scores that are assigned by the researchers conducting the study working in blind regarding the dose administered to each group. The conditions established within the gnotobiotic lab setting are well controlled (Yuan, Jobst *et al.* 2017), preventing the interference of extraneous pathogens or dietary changes that can cause diarrhea or influence the state of infection. The presence of other pathogens/microorganisms in the environment can lead to discrepancies regarding the true cause of diarrhea (Lei, Twitchell *et al.* 2019).

Regardless of their universal usage, the RM and DB methods are heavily reliant on a sequential progression of responses, since they use only information from two points around the potential titer completely overlooking any random distribution of data (Siev 2018). Nonetheless, there has been continued debate, among the research community, on the reliability of RM and DB and their use (particularly due to the ease of methodology) for equally spaced dose levels, making them valuable tools for a rapid and/or rough calculation of  $ID_{50}$  and  $DD_{50}$  for non-statisticians. When handling sequentially spaced dose levels such as the ones in this study, RM and DB have been described to be highly reliable and have been known to provide a high coverage rate ( $> 95\%$  CI), but on the other hand when data is more randomly distributed, carrying out RM and DB method

could complicate the inference due to inaccuracies, questioning the internal validity of the data and results.

The Spearman-Kärber (SK) method is another non-parametric method that can be easily calculated by hand with more accurate estimates of the mean dose (Miller 1973, Miller and Ulrich 2001). It relies on the symmetric nature of dose response data to calculate the median dose, meaning that it requires a dose with 0% and 100% responses to calculate the median dose. Some dose-response studies are not capable of generating data fulfilling the criterion. In this study, this is observable with the ID<sub>50</sub> data where all the dose groups had animals that shed virus. On the other hand, the SK method would be applicable for calculating the DD<sub>50</sub>, since dose groups contained all (100%) or none (0%) of the pigs infected.

With the increasing availability of powerful statistical tools, logistic regression-based models have been more heavily relied on for dose-response calculations for their accuracy and robustness compared to non-parametric methods (Spackman, Malladi *et al.* 2019). Both the exponential and Beta-Poisson are routinely used for the quantitative determination of dose-response relationships (Haas 2002). The exponential equation takes the symmetric nature of the curve around the inflection point into account when calculating the median dose, while reducing the effects of variability, due to large differences between the doses used. Using a logistic regression model (exponential model), the ID<sub>50</sub> of the original Norwalk virus (GI.1, 8fIIa isolate) challenge pool was predicted to be around  $2.8 \times 10^3$  RNA copies in all secretor positive individuals (Atmar, Opekun *et al.* 2014). Similarly, in the current study, we determined the ID<sub>50</sub> of Cin-1 to be around  $2.57 \times 10^3$  RNA copies. These data show a similar infection potential between the prototypic GI.1 Norwalk virus and the Cin-1. With the availability of more dose-response studies and the relatability between human studies and Gn pig studies, it could eventually be possible to compare

the pathogenesis of different HuNoV genogroups to help further identify similarities and/or differences between different HuNoVs.

More than generating an ID<sub>50</sub>, Beta-Poisson dose-response models, can describe the full range of probability of response (ID<sub>20</sub> or ID<sub>80</sub>), and it is accurate at low doses as well (Roederer 2015). It allows for greater flexibility and a wider range of understanding in the estimated probability of infection. AIC is an estimate of the expected relative distance between the fitted model and the unknown true mechanism that actually generated the observed data (Korner-Nievergelt, Roth *et al.* 2015). Comparing both these models using AIC showed the closeness of the two models for calculating the ID<sub>50</sub> while the beta-Poisson model was the ideal model for DD<sub>50</sub> estimation.

Using the 3PLL model, it allows for the estimation of the ID<sub>50</sub> and DD<sub>50</sub> based on cumulative data (AUC), a continuous variable. The closeness of these ID<sub>50</sub> and DD<sub>50</sub> estimates demonstrates the reliability of the model for calculating accurate dose response. Overall, both approaches prove their value to dose-response studies and can be used separately to simply determine the median infectious doses, or together for a more concrete understanding of the infectious potential of the pathogen. AIC was used to identify the most reliable model that can be used for calculating the ID<sub>50</sub> and DD<sub>50</sub> based on the data collected. We showed that Beta-Poisson model is the one for the counting variable while 3PLL is suitable for the AUC continuous variable, reinforcing the validity of the estimated ID<sub>50</sub> and DD<sub>50</sub> in Gn pigs.

Interestingly, there were three values of AUC of virus shedding in the two lower doses that are very high, this result could be due to aggregation effect that was confirmed by EM. Since the very first visualization of HuNoV, samples isolated from stool filtrates without extensive processing have always been identified as aggregates (Kapikian, Wyatt *et al.* 1972, Teunis, Moe *et al.* 2008, Otto, Clarke *et al.* 2011). A recent study showed that a large fraction of norovirus shed into stool

reside inside membrane-bound vesicles and such vesicles increase virus stability within the gastrointestinal tract and enhance the virus infectivity (Santiana, Ghosh *et al.* 2018). Although EM is not routinely used for laboratory diagnosis of HuNoV infections, they provide a good understanding whether the virus retains its natural qualities as an aggregate which defines its natural state of existence. As demonstrated here (Figure 4), determining the aggregation status of HuNoV at different inoculum doses allow for the understanding of HuNoV infectivity as a single virion compared to an aggregate. As shown by Teunis, *et.al*, the difference in the infectivity of 8ffa and 8ffb strains of HuNoV is hypothesized due to the aggregation status of the viruses (Teunis, Moe *et al.* 2008). Based on this calculation method, we estimated here that, a dose of  $2 \times 10^5$  RNA copies contained around 512.8 infectious virus particles in 100  $\mu$ l of Cin-1 inoculum, translating to  $5.128 \times 10^3$  infectious particles / mL.

Our studies have demonstrated that Gn pigs are a well-suited model for studying the infectivity of GII.4 HuNoV strains. We have showed its closeness to humans regarding their susceptibility to HuNoV infection. Gn pigs are capable of exhibiting the full course of HuNoV infection and develop disease very similar to the one presented in humans. In conclusion, we have established a reliable model that can be used to test candidate prophylactics and therapeutics prior to clinical trials in humans, and the model is ready to be used for the evaluation of immunogenicity and protective efficacy of candidate HuNoV vaccines.

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**Table 1:** HuNoV fecal shedding and diarrhea after inoculation of Gn pigs with different doses of Cin-1

Dose group	# of viral genome copies	n	Virus shedding				Diarrhea			
			(%) <sup>a</sup>	Mean duration days (SEM) <sup>c,d</sup>	AUC <sup>c,d</sup>	Mean onset day (SEM)	(%) <sup>b</sup>	Mean duration days (SEM) <sup>c,d</sup>	AUC <sup>c,d</sup>	Mean onset day (SEM)
1	2.00E+06	4	4 (100%)	2.5 (0.6) <sup>BC</sup>	9506 <sup>B</sup>	2 (0.4) <sup>B</sup>	4 (100%)	5.0 (0.3) <sup>A</sup>	9.06 <sup>A</sup>	1.5 (0.5) <sup>D</sup>
2	4.00E+05	4	4 (100%)	1.3 (0.3) <sup>CD</sup>	5232 <sup>B</sup>	4 (1.2) <sup>AB</sup>	3 (75%)	1.3 (0.9) <sup>ABC</sup>	7.04 <sup>A</sup>	5.5 (1.2) <sup>ABC</sup>
3	2.00E+05	4	4 (100%)	6.3 (0.5) <sup>A</sup>	126774 <sup>A</sup>	1.3 (0.3) <sup>B</sup>	4 (100%)	4.0 (0.9) <sup>AB</sup>	9.31 <sup>A</sup>	2.8 (0.5) <sup>CD</sup>
4	8.00E+04	6	6 (100%)	2.8 (0.5) <sup>B</sup>	13495 <sup>B</sup>	1.5 (0.3) <sup>B</sup>	6 (100%)	3.8 (1) <sup>AB</sup>	7.46 <sup>A</sup>	3.2 (0.9) <sup>CD</sup>
5	2.00E+04	3	2 (67%)	1 (0.6) <sup>B</sup>	93 <sup>B</sup>	3.3 (2.3) <sup>AB</sup>	1 (33%)	3.3 (0) <sup>ABC</sup>	1.50 <sup>B</sup>	6.3 (1.7) <sup>AB</sup>
6	3.20E+03	3	2 (67%)	1.3 (0.9) <sup>BCD</sup>	2667 <sup>B</sup>	4 (2.1) <sup>AB</sup>	3 (100%)	1.0 (0) <sup>BC</sup>	3.17 <sup>AB</sup>	5 (2.1) <sup>BC</sup>
7	8.00E+02	4	1 (25%)	0.5 (0.5) <sup>D</sup>	2972 <sup>B</sup>	6.8 (1.3) <sup>A</sup>	0 (0%)	0.0 (0) <sup>C</sup>	2.75 <sup>AB</sup>	8 (0) <sup>A</sup>

a. Gn pigs were orally inoculated with HuNoV GI.4/2003 variant (Cin-1) at 6–7 days of age. Rectal swabs were collected daily after inoculation from PID 1-7 to determine virus shedding by qRT-PCR.

b. Fecal consistency was assessed from PID 1-7 as 0, solid; 1, pasty; 2, semiliquid; 3, liquid. Pigs with daily fecal consistency scores of 2 or greater were considered to be diarrheic.

c. SEM, standard error of the mean; AUC, area under the curve.

d. Numbers in the same column followed by different capital letters (A, B, C, D) differ significantly (one-way ANOVA, P<0.05); while shared letters indicate no significant difference.

**Table 2:** Log ID<sub>50</sub> and DD<sub>50</sub> calculations of Cin-1

Calculations based on the % of affected Gn pigs		
Method	Log ID <sub>50</sub>	Log DD <sub>50</sub>
Reed-Muench		
<i>Conventional</i>	3.11	4.86
<i>"skrmdb" package R</i>	3.39	4.58
Dragstedt-Behrens		
<i>"skrmdb" package R</i>	3.39	4.58
Spearman-Karber		
On line tool/	3.51	4.49
<i>"skrmdb" package R</i>		
Exponential ( <i>Weir, 2017</i> )	3.76	4.76
Beta-Poisson ( <i>Weir, 2017</i> )	3.41	4.32
Beta-Poisson <i>on line tool</i>	3.76	3.90
Calculation based on AUC		
Method	Log ID <sub>50</sub>	Log DD <sub>50</sub>
3PLL <i>drc package</i>		
/ <i>AATBioquest</i>	3.89	5.02
<i>online tool</i>		

**Table 3:** Comparison of virus shedding in unvaccinated Gn pigs and humans after inoculation with the same Cin-1 inoculum

Host	Age	Cin-1 Dose	n	Virus shedding (%)	Mean duration days (range) <sup>c</sup>	Peak virus shedding day (PID)
Human <sup>a</sup>	19-48 years	5.00E+04	23	70	5.2 (2-30)	3
Human <sup>b</sup>	18-50 years	4.40E+03	34	76.5	-	-
Human <sup>b</sup>	18-50 years	4.40E+03	48	62.5	-	-
Gn pig	33-34 days	2.00E+04	3	67	1.0 (1-2)	2
Gn pig	33-34 days	8.00E+04	6	100	2.8 (2-4)	3
Gn pig	33-34 days	2.00E+05	4	100	6.3 (5-7)	4

a. Data reported by Frenck et al. 2012.

b. Date reported by Bernstein et al. 2015.

c. Virus shedding in human stools were monitored for up to 30 days; in Gn pigs for 7 days post-inoculation.

**Table 4a:** Comparison of goodness of fit for the determination of best-fitting ID<sub>50</sub> model for Cin-1

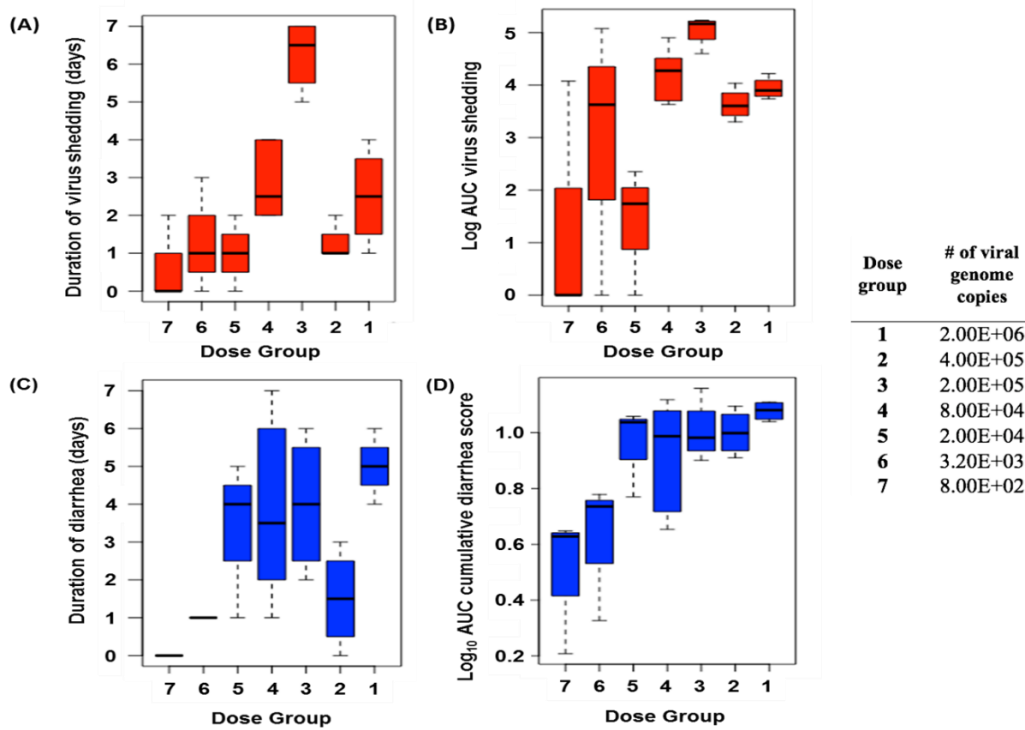
Model	Minimized Deviance	AIC	Chi-Squared p-value	Conclusion
Exponential	3.7423	5.742	0.7115	Shows a good fit to the data
Beta Poisson	1.713	5.713	0.8873	Shows a good fit to the data

**Table 4b:** Comparison of goodness of fit for the determination of best-fitting DD<sub>50</sub> model for Cin-1

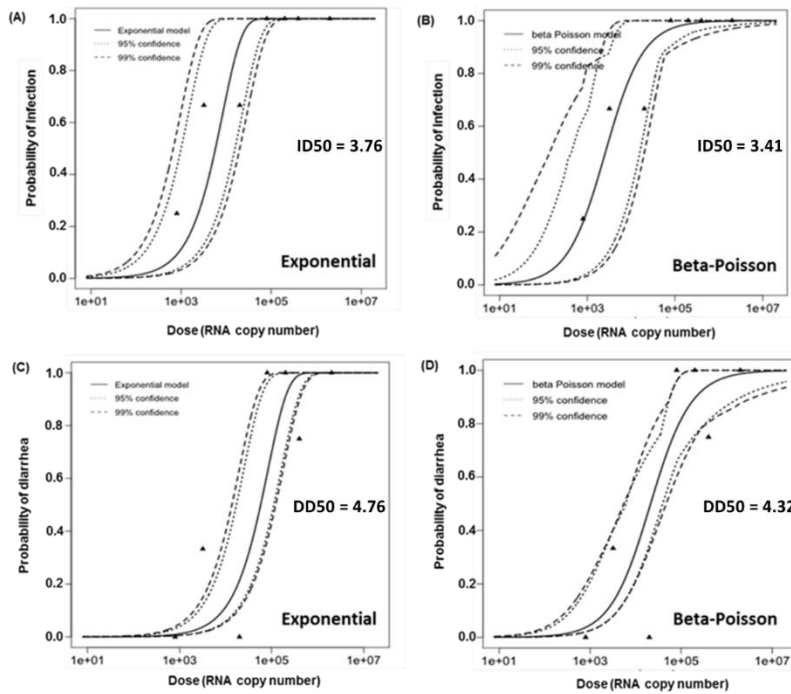
Model	Minimized Deviance	AIC	Chi-Squared p-value	Conclusion
Exponential	16.094	18.1	0.0133	Does not show a good fit to the data
Beta-Poisson	10.4989	14.5	0.0623	Shows a good fit to the data

**Table 5:** Comparison of Cin-1 to GII.4/2006b 092895 challenge pool used in previous studies.

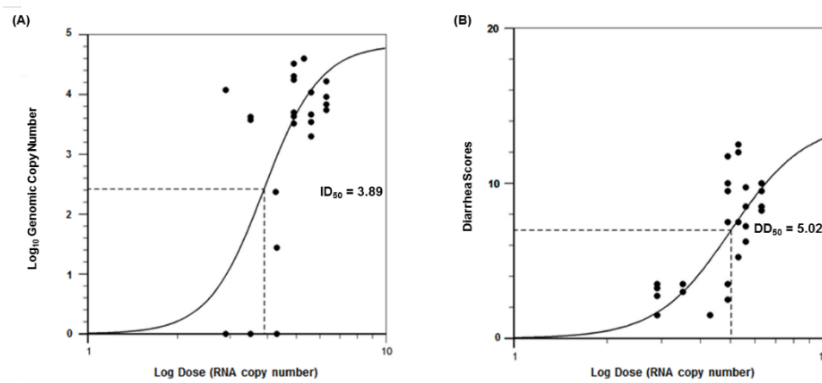
Norovirus Variant	Optimal challenge dose (viral genome copy)	ID <sub>50</sub> dose	Method of ID <sub>50</sub> determination
GII.4/2003 Cin-1	2.0 x 10 <sup>5</sup>	This study	Beta-Poisson
GII.4/2006b 092895	6.43 x 10 <sup>5</sup>	Kocher et al 2014; Lei et al 2016	Reed-Muench



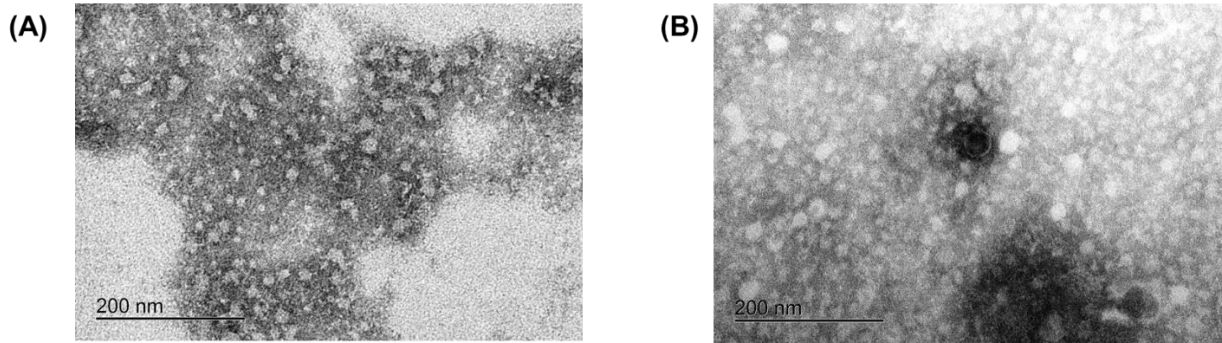
**Figure 1.** Box plots showing (A) duration of virus shedding, (B) Log<sub>10</sub> AUC of virus shedding, (C) duration of diarrhea and (D) Log<sub>10</sub> cumulative diarrhea scores, among each dose group.



**Figure 2.** Dose-response curves extrapolated for the exponential model (A and C) showing the probability of infection and the probability of diarrhea, compared with the beta-Poisson model (B and D). Dotted lines show the 95% and 99% credible bands.



**Figure 3.** Estimates of (A) ID<sub>50</sub> and (B) DD<sub>50</sub> based on a 3PLL curve using AUC values.



**Figure 4:** Electron micrograph of Cin-1 inoculum showing aggregate sizes in (A)  $8 \times 10^4$  RNA copies and (B)  $2 \times 10^5$  RNA copies.

**Supplementary Table S1A:** Parameters used for ID<sub>50</sub> calculation using conventional RM method

Dose group	# of viral genome copies	Log <sub>10</sub> Dose	No. of pigs shedding virus	No. of pigs not shedding virus	Shedding Accumulate	Non-shedding accumulate	Cumulative Shedding	Cumulative % of pigs shedding virus
1	2.00E+06	6.3	4	0	23	0	23/23	100
2	4.00E+05	5.6	4	0	19	0	19/19	100
3	2.00E+05	5.3	4	0	15	0	15/15	100
4	8.00E+04	4.9	6	0	11	0	11/11	100
5	2.00E+04	4.3	2	1	5	1	5/6	83.3
6	3.20E+03	3.5	2	1	3	2	3/5	60
7	8.00E+02	2.9	1	3	1	5	1/6	16.7

**Supplementary Table S1B:** Parameters used for DD<sub>50</sub> calculation using conventional RM method

Dose group	# of viral genome copies	Log <sub>10</sub> Dose	No. of pigs with diarrhea	No. of pigs without diarrhea	Diarrhea Accumulate	Non-diarrheic accumulate	Cumulative Diarrhea Rate	Cumulative % of pigs shedding virus
1	2.00E+06	6.3	4	0	18	0	18/18	100
2	4.00E+05	5.6	3	1	14	1	14/15	93.3
3	2.00E+05	5.3	4	0	11	1	11/12	91.7
4	8.00E+04	4.9	6	0	7	1	7/8	87.5
5	2.00E+04	4.3	0	3	1	4	1/5	20
6	3.20E+03	3.5	1	2	1	6	1/7	14.3
7	8.00E+02	2.9	0	4	0	10	0/10	0

## Chapter 4

### **Parenterally-administered tetravalent VLP-based vaccine evaluated in Gn pig mode of GII.4 human norovirus infection and diarrhea**

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*Manuscript in preparation*

## Abstract

Human norovirus (HuNoVs) are responsible for causing more than 20% of all viral gastroenteritis among people of all age groups. There are no vaccines available. HuNoV are highly contagious and they are genetically very diverse with continuously emerging new genotypes and variants that lead to fast spreading within the human population through immune escape. Vaccine development has been limited to the use of bioengineering technologies to produce virus-like particles (VLPs) and other sub-viral particles of HuNoV. In this study, we tested the immunogenicity and protective efficacy of a novel intramuscular (IM) tetravalent VLP (VP1 of GI.1, GII.3, GII.4, GII.17) vaccine candidate in the gnotobiotic (Gn) pig model of HuNoV infection and disease. Three doses of the VLP vaccine with an alum adjuvant were administered to Gn pigs at 5 days of age (PID 0), PID 10 and PID 21. At PID 28, subsets pigs were challenged with one of three doses of GII.4/2003 Cin-1 HuNoV ( $2 \times 10^5$ ,  $8 \times 10^4$ , or  $2 \times 10^4$  genome copies), and monitored for 7 days for HuNoV infection and diarrhea. The IM VLP vaccine did not confer any protection against Cin-1-induced infection or diarrhea even when pigs were challenged with the lowest Cin-1 dose, although it was able to induce strong genotype-specific IgA and IgG responses in the serum of vaccinated pigs. Hemagglutination inhibition (HAI) antibody titers were detected at both pre-challenge and post-challenge. VLP-specific IFN- $\gamma$  producing CD4<sup>+</sup> and CD8<sup>+</sup> T cells were observed to be elevated among vaccinated pigs at post-challenge day (PCD) 7 in the spleen and blood but not in the ileum. These results indicate that the IM tetravalent VLP vaccine was highly immunogenic, but the presence of high levels of immune effectors induced by the vaccine were not sufficient for protecting the Gn pigs from Cin-1 challenge. This study demonstrated the lack of cross-variant protection of HuNoV vaccine due to immune evasion because GII.4 VLP in the vaccine is derived

from the Sydney 2012 strain, a different variant from the GII.4/2003 Cin-1, the Farmington Hills strain. There are 23 amino acid substitutions in the major receptor binding domain (P2) of the capsid protein VP1 between the two variants. This finding has important implications in HuNoV vaccine development. With the highly variable antigenic diversity observed among emerging and re-emerging variants of HuNoV, vaccines have to include multiple variants and have to be routinely updated in order to ensure protection among the population.

# 1. Introduction

Human noroviruses (HuNoV) are the leading causative agents of acute gastroenteritis (AGE) among all age groups (Hall, Glass *et al.* 2016, Mattison, Cardemil *et al.* 2018). HuNoV are responsible for over 20% of all AGE epidemics annually (Ahmed, Hall *et al.* 2014). In the US, HuNoV-associated gastroenteritis accounts for ~21 million cases, ~2 million hospital visits, ~71,000 hospitalizations and ~800 deaths, with a vast majority (90%) of deaths occurring among the elderly ( $\geq 65$  years of age) (Aliabadi, Lopman *et al.* 2015). GII.4 HuNoVs are responsible for >80% of all HuNoV-associated GE and is the most diverse of NoV genotypes (Chhabra, de Graaf *et al.* 2019). Other genotypes including GI.1, GII.3, and GII.17 are also known to cause HuNoV epidemics among different ranges of the world (Boon, Mahar *et al.* 2011, van Beek, de Graaf *et al.* 2018), with GII.17 predominating in Asia in more recent years (de Graaf, van Beek *et al.* 2015).

NoVs are transmitted through a fecal-oral route and epidemics often occur in healthcare facilities, restaurants, and schools among other settings where people are in close proximity of one another (CDC 2011, Brennan, Cavallo *et al.* 2018, Free, Buss *et al.* 2019). A vaccine against HuNoV disease is urgently needed. However, with cellular tropisms for HuNoVs only recently being identified (Estes, Ettayebi *et al.* 2019, Green, Kaufman *et al.* 2019), and the lack of an effective cell culture system, the development of cell-culture based vaccines are still out of reach at this time. Due to this reason, development of candidate norovirus (NoV) vaccines have been based on the generation of virus-like particles (VLPs) taking advantage of various recombinant protein expression systems, which has paved the path for the development of the first generation of HuNoV VLP vaccine (Jiang, Wang *et al.* 1992, Ramirez, Wahid *et al.* 2012, Tamminen, Huhti *et al.* 2012, Tan and Jiang 2012, Tan and Jiang 2019).

The aims of this study were: (i) to evaluate the protective efficacy, and (ii) to determine the immunogenic potential of an intramuscular (IM) administered tetravalent VLP vaccine composed of GI.1, GII.3, GII.4 and GII.17 HuNoV VP1 derived VLPs and aluminum hydroxide adjuvant in the Gn pig challenge model of GII.4 infection and diarrhea. At the time this study was carried out, the optimal Cin-1 challenge dose had not been established. In order to avoid a high virus challenge dose that overwhelmed the vaccine induced immunity, we challenged Gn pigs with three different Cin-1 doses, based on previous human challenge studies (Frenck, Bernstein *et al.* 2012, Bernstein, Atmar *et al.* 2015).

## **2. Materials and Methods**

### ***2.1 Vaccine***

The vaccine mixture was formulated using equal concentrations (50 µg each) of GI.1, GII.3, GII.4 and GII.17 VLPs (total concentration of 200 µg of VLP) combined with 600 µg Aluminum hydrogel [Al(OH)<sub>3</sub>] adjuvant. The vaccine was stored at 4 °C until administration.

Each of the purified VLPs were used as the detector antigen in ELISA for the detection of serum and intestinal genotype-specific IgA and IgG antibody responses (Liu, Wen *et al.* 2013) and, as the stimulating antigen in the intracellular IFN-γ staining and flow cytometry assay (Yuan, Wen *et al.* 2008, Wen, Tin *et al.* 2014). GI.1 and GII.4 VLPs were also used in the hemagglutination inhibition assay (HAI) assay.

### ***2.2 Challenge virus inoculum***

A pool of human stool specimens containing GII.4 strain, Cin-1 (Hu/GII.4/Cin-1/2003/US), a 2002 Farmington Hills-like variant, was collected by Xi Jiang's laboratory at Cincinnati Children's

Hospital Medical Center collected from a man who developed a 3-day illness characterized by diarrhea, vomiting, nausea, abdominal cramps, and fever in 2003. This sample underwent extensive quality control prior to being used as a challenge pool in various human studies (Frenck, Bernstein *et al.* 2012, Bernstein, Atmar *et al.* 2015). The HuNoV concentration of the challenge pool was quantified by using RT-qPCR and contained approximately  $2 \times 10^6$  viral genomic RNA copies/mL of stool. The challenge pool was stored at  $<-70^{\circ}\text{C}$  in individual 1 mL aliquots until the day of Gn pig inoculation.

### ***2.3 Gnotobiotic pigs and treatments***

Near-term pigs (Large white cross breed) were derived by aseptic hysterectomy and maintained in sterile isolator units as described previously (Yuan, Jobst *et al.* 2017). Rectal swabs collected from pigs were cultured on blood agar plates (Hardy Diagnostics) and in Thioglycollate media (Hardy Diagnostics) 3 days after derivation and repeated once a week until the end of the study in order to determine the sterility status of the isolators that the pigs were housed in. Pigs were fed commercial ultra-high temperature-treated sterile cow milk throughout the study until post inoculation day (PID) 21, after which they were switched over to Similac<sup>®</sup> (Abbott Laboratories) baby formula until the end of the study. A total of 23 pigs were assigned to two groups (VLP Vaccine and Control). Pigs were randomly divided into the groups upon derivation regardless of gender and body weight. One group of pigs received the tetravalent VLP vaccine starting at 5 days of age or PID 0, followed by two booster doses at PID10 and PID21. The pigs in control group received the adjuvant only at the same time points. The timing of 3 injections in Gn pigs are established in a previous study (Kocher, Bui *et al.* 2014), based on the time needed to prime and

boost immune responses in Gn pigs. At PID 28 or post-challenge day (PCD) 0, pigs in each group were further split into 3 groups each based on the virus challenge dose they received (Table 1).

Serum was collected at PID 28, and PCD 7 for the detection of pre-challenge and post challenge VLP-specific IgA and IgG antibody responses and for GII.4-specific hemagglutination inhibition assay.

Prior to inoculation with HuNoV, 4ml of 200 mM sodium bicarbonate was given orally 15 min to neutralize stomach acids. The Cin-1 inoculum was mixed with 5 ml of Diluent #5 (minimal essential medium with 1 % penicillin-streptomycin and 1 % HEPES) on the day of inoculation. All pigs received oral doses of Cin-1 ranging from  $2 \times 10^4$  to  $2 \times 10^5$  genomic RNA copies at PID 28 / post-challenge day (PCD) 0 (Table 1). Clinical signs and fecal virus shedding were monitored daily until euthanasia. All pigs were euthanized 7 days post inoculation. At euthanasia, small and large intestinal contents (SIC and LIC) were collected from all pigs and processed, as described (Parreno, Hodgins *et al.* 1999), for the detection of intestinal antibody responses by ELISA. Ileum, spleen and blood were collected, and mononuclear cells (MNCs) were isolated from them for the detection of effector T cell responses by flow cytometry as described (Yuan, Wen *et al.* 2008, Kocher, Bui *et al.* 2014). All experiments involving the use of Gn pigs were approved by the Institutional Animal Care and Use Committee at Virginia Tech (IACUC protocol: 17-110-CVM). All experimental procedures were carried out in compliance with federal and university regulations.

#### ***2.4 HBGA-typing of Gn pigs by immunofluorescence assay***

Prior to vaccination, all Gn pigs were screened for their HBGA type by immunofluorescence assay. Epithelial cells collected from the cheeks were prepared as described previously (Bui, Kocher *et*

*al.* 2013). HBGA phenotypes were detected from these cells using fluorescent labeled antibodies described elsewhere (Lei, Ryu *et al.* 2016). All slides were prepared with VECTASHIELD® Antifade Mounting Medium with 4,6-diamidino-2-phenylindole (DAPI) which was used as a nuclear counterstain (Vector Laboratories) for fluorescent microscopy. Based on this screening technique, HBGA type A<sup>-</sup> and H<sup>-</sup> pigs were excluded from this study because A<sup>-</sup> or H<sup>-</sup> pigs are less susceptible to NoV infection than A<sup>+</sup> or H<sup>+</sup> pigs (Cheetham, Souza *et al.* 2007, Bui, Kocher *et al.* 2013).

### ***2.5 Detection of fecal consistency and HuNoV shedding by RT-qPCR***

Fecal consistency and virus shedding were monitored at 24-hour time points at the same time daily, after HuNoV inoculation at PID 0, by rectal swab sampling. The following scoring system was used to assess fecal consistency: 0, solid; 1, pasty; 2, semiliquid; 3, liquid. Pigs with fecal consistency scores of 2 or greater were considered to be diarrheic.

Presence of HuNoV genomes in rectal swab samples collected after inoculation with different doses of Cin-1 were evaluated using RT-qPCR protocol as described previously (Lei, Ryu *et al.* 2016). Briefly, once collected, swabs, were swirled in 1 ml PBS to release the feces and centrifuged at 10000g for 5 min. 250 µl of the supernatant collected was mixed with 750 µl TRIzol (Invitrogen) following manufacturer's instructions for viral RNA extraction. The extracted RNA was then dissolved in 40 µl autoclaved dd-H<sub>2</sub>O. Five microliters of RNA were used in 20 µl RT-qPCR reaction with a SensiFAST Probe No-ROX One-Step Kit (Bioline) to detect HuNoV genomes. Primers COG2F, COG2R, and probe RING2 were used with cycling conditions as described in a previous study (Kageyama, Kojima *et al.* 2003). A standard curve was generated using COG2 amplicon-containing cDNA expression plasmids in serially diluted tenfold from 2 x 10<sup>6</sup> to 2

genomic RNA copies. Amplification was performed on CFX96 Real-Time System (Bio-Rad), and data were collected and analyzed with Bio-Rad CFX Manager 2.0.

### ***2.6 ELISA for the detection of serum IgA and IgG VLP-specific antibody responses***

ELISA was carried out on heat-inactivated serum samples to identify the presence of genotype-specific IgA and IgG responses as previously described (Graham, Jiang *et al.* 1994). Briefly, 96-well microtiter plates (Falcon) were coated with purified VLPs at 0.32 µg/mL diluted in PBST + 2% non-fat dry milk (pH 7.4) and incubated overnight at 4 °C. The plates were then washed with washing buffer (PBS pH 7.4 + 0.05% Tween 20) three times and blocked with 300 µL/well of blocking buffer (PBS pH 7.4 + 5% non-fat dry milk) for two hours at room temperature. After the plates were washed two times with washing buffer and 100 µL of serially diluted test serum (1:2 to 1:65536) were added to each well and incubated for one hour at 37 °C. After washing the plates three times, 100 µL of HRP-conjugated anti-pig IgG or IgA diluted 1:5000 in PBST + 2% non-fat dry milk (pH 7.4) was added. The plates were then incubated for 1 hour at 37°C. After washing, the plates three times, 100 µL of SureBlue™ (Seracare) was added and the plate was incubated for ten minutes room temperature, in the dark for the color to develop. The development of color was inhibited by 100 µL of TMB stop solution (Seracare) and the absorbance was measured at 450 nm.

### ***2.7 Hemagglutination inhibition assay***

Hemagglutination inhibition assay was performed as described previously (Czako, Atmar *et al.* 2012). Briefly, commercially available (BioIVT) human type O erythrocytes (RBCs) were collected from healthy adult volunteers in Alsever buffer, and washed three times with PBS without Ca<sub>2</sub> and Mg<sub>2</sub>. After each wash step, the blood samples were centrifuged for 10 min at 3000 RPM at 4°C and the supernatant discarded. The pellet was resuspended in 50 mL of PBS. In the

last wash step, the cells were centrifuged 10 min at 4500 RPM and then the pellet was stored at 4°C until used. The RBC working suspension was prepared using 0.75 ml of RBC pellet in 100 ml of saline buffer pH 6.2. In a V-bottomed 96-well microtiter plate, serial dilutions of the VLPs were mixed with the 10 µL RBC working solution to ensure that VLP was titrated to 4 hemagglutination units (~20 ng of GI.1 or GII.4 VLPs. Same VLPs as in the vaccine). In a separate V-bottomed 96-well microtiter plates, two-fold dilutions of the serum were made starting with an undiluted sample. GI.1 or GII.4 VLP was then added at 0.32µg/mL followed by 50ul/well of RBC working suspension was added and incubated for 2 hours at 4°C. The controls of this assay were: A) Positive Control (known serum with inhibition titer) with 3.2 µg/mL of GI.1 or GII.4 VLP, B) Negative Control (known samples with no inhibition titer) with 3.2 µg/mL of GI.1 or GII.4 VLP. C) No VLP. D) No serum. The HAI titer was defined as the reciprocal of the highest dilution of serum that completely inhibited hemagglutination by the viral antigen. Geometric mean titers (GMTs) were calculated to summarize the hemagglutination inhibition titer on PID 28 and PCD 7 for vaccinated and control pigs.

## **2.8 Flow Cytometry**

Mononuclear cells (MNCs) collected from the ileum, spleen and blood upon euthanasia and were diluted to a concentration of  $2 \times 10^6$  cells/mL and were seeded into 12-well plates and stimulated with 12 µg/mL of GI.1, GII.3, GII.4 and GII.17 antigens, mock (unstimulated negative control) and PHA (positive control) for 17 h at 37 °C in 5% CO<sub>2</sub> as determined previously (Kocher, Bui *et al.* 2014). CD3+CD4+ and CD3+CD8+ cell surface marker staining and IFN-γ intracellular staining have been described in previous publications (Yuan, Ward *et al.* 1996, Yuan, Wen *et al.* 2008, Lei, Ryu *et al.* 2016, Twitchell, Tin *et al.* 2016). All samples were stored in 0.05 mL of

staining buffer and were maintained at 4 °C. A minimum of 100,000 events were acquired using a FACSAria flow cytometer (BD Biosciences, San Jose, CA, USA). Flow cytometry data were analyzed using FlowJo X software (Tree Star, Ashland, OR, USA).

## ***2.9. Statistical Analysis***

Student's t-test was used for comparisons of virus shedding and diarrhea data between the treatment groups. One-way analysis of variance (ANOVA) (General linear model) was used to compare VLP-specific IgA and IgG antibody titers between the treatment groups. Tukey-Kramer HSD was used for the comparison of different time points within the same treatment group. Two-way ANOVA, followed by a Multiple t-test, was used for comparisons of frequencies of IFN- $\gamma$  producing T cells between treatment groups. ANOVA analyses were carried out using JMP 14.0 (SAS Institute, Kerry, NC, USA), and all other statistical analyses were performed using GraphPad Prism 7.0 (GraphPad Software, San Diego, CA, USA). A p value less than 0.05 was accepted to be statistically significant.

## **3. Results**

### ***3.1 Assessment of clinical signs and HuNoV virus shedding in vaccinated and control Gn pigs***

VLP vaccinated and mock vaccinated (control) Gn pigs were challenged orally with one of the three doses of Cin-1 (Dose 1, Dose 2 or Dose 3) at PID 28 / PCD 0 and were observed daily for clinical signs and virus shedding in feces until euthanasia at PCD 7. Fecal consistency scoring system (0 – normal; 1 – pasty; 2 – semi-liquid; and 3 – liquid) was used to determine whether Gn pigs experienced NoV-associated diarrhea. A fecal consistency score of 2 or greater ( $\geq 2$ ) were deemed to be diarrheic (Lei, Ramesh *et al.* 2016). HuNoV infection was determined by the

presence of viral RNA quantified using RT-qPCR carried out on samples isolated from rectal swabs collected from PCD 1-7. There were no differences in virus shedding and diarrhea among vaccinated and control Gn pigs over each of the challenge dose groups (Table 2). Gn pigs that received the lower challenge doses (Dose Groups 2 and 3) shed virus for an average of 2 days while Gn pigs received the higher challenge dose (Dose Group 1) shed virus for at least 6 days after virus was initially detected in their feces (Figure 1A). Pigs that were given the higher challenge dose had a greater diarrhea burden indicated by an increased duration, a faster onset of diarrhea and a longer diarrhea duration as compared to pigs that received a lower challenge dose (Table 2 and Figure 1C and 1D).

The pattern of virus shedding and diarrhea in both the vaccinated and control pig groups across the three different virus challenge doses resemble those in the ID50 and DD50 study (Table 1, Chapter 3), suggesting that the vaccine did not confer any noticeable protection against GII.4/2003 Cin-1 challenge.

### ***3.2 IM VLP vaccine induced strong VLP-specific IgG and IgA antibodies in serum but not in the intestines of Gn pigs***

The VLP vaccinated Gn pigs had significantly higher titers of serum IgA and IgG antibodies specific to each of the four VLPs as measured by ELISA using each VLP as the detector antigen on PID 28 and PCD 7 compared to control pigs irrespective of virus challenge dose (Figure 2). All four VLPs in the vaccine were able to induce equally high levels of VLP-specific IgA and IgG titers. No significant differences in IgA and IgG responses in the serum were observed before and after challenge, or among different virus challenge dose groups. This shows that high titers of

serum VLP-specific IgA and IgG antibodies induced by the vaccine were not influenced by the infection status.

Upon euthanasia at PCD 7, SIC and LIC were collected from pigs to determine the presence of VLP-specific IgA and IgG intestinal antibodies. Antibody titers in vaccinated and control pigs were equally low. Interestingly, 1 out of 7 vaccinated pigs in Dose Group 1 had high VLP-specific IgA titers in LIC, and higher IgG in its SIC and LIC. However, this pig had similar overall severity of virus shedding and diarrhea compared to other pigs in the same group who did not develop intestinal antibody responses.

### ***3.3 HAI antibody titers in Gn pig serum***

Surrogate assays such as HBGA blocking assay, and HAI assay have been routinely used in place of a virus neutralization assay for functional NoV antibody detection (Czako, Atmar *et al.* 2012, Garaicoechea, Aguilar *et al.* 2015, Atmar, Ettayebi *et al.* 2019). In this study, HAI assay was used to assess the ability of the VLP vaccine to induce GI.1 and GII.4 VLP-specific functional antibodies in serum (Figure 3). High titers of GI.1-specific HAI antibodies were present in the serum of all VLP vaccinated pigs at both PID 28 and PCD7 regardless challenge dose group (Figure 3A), suggesting the induction of HAI antibody responses by the VLP vaccine. In control pigs, GI.1-specific HAI titers were only detected at PCD 7 among the two higher challenge dose groups (Figure 3A), suggesting that the Cin-1 infection primed for the cross-genogroup HAI antibody responses. GII.4-specific HAI antibody responses were also detected in all VLP vaccinated pigs at both PID 28 and PCD7 regardless challenge dose group (Figure 3B). However, it is unexpected that control pigs had similar titers of GII.4-specific HAI titers as the vaccinated pigs at PID 28 in two challenge dose groups (Groups 1 and 3).

An increase in the GI.1 and GII.4 HAI titers were observed post-challenge among all vaccinated and control pigs regardless the challenge dose group, suggesting that Cin-1 infection either primed (in control pigs) or boosted (in vaccinated pigs) HAI antibody responses.

### ***3.4 VLP-specific IFN- $\gamma$ producing CD4 and CD8 T cells were detected among all Gn pigs in systemic lymphoid tissues at PCD 7.***

Upon euthanasia at PCD 7, MNCs isolated from ileum, spleen and peripheral blood were stimulated with VLPs derived from HuNoV GI.1, GII.3, GII.4 and GII.17, and stained with antibodies specific to CD3, CD4, CD8 and IFN- $\gamma$  for the quantification of IFN- $\gamma$  producing T cells. The IM VLP vaccine primed IFN- $\gamma$  producing T cell responses specific to all 4 genotypes of HuNoV antigens. Among the pigs that were challenged with the highest virus dose (Dose 1), higher frequencies of GII.4 and GII.17 specific IFN- $\gamma$  producing CD4 and CD8 T cells were present in spleen and blood of the vaccinated pigs compared to the control pigs (Figure 4). However, the level of intestinal (ileum) T cell responses were similar between pigs in VLP vaccinated and control groups. In the pigs challenged with the two lower virus doses, overall higher frequencies of IFN- $\gamma$  producing CD4<sup>+</sup> and CD8<sup>+</sup> T cell responses were detected in the spleen and blood of vaccinated pigs than the control pigs (data not shown). These data suggest that the VLP vaccine primed for low level systemic effector T cell responses. However, the systemic effector T cells were not protective against HuNoV infection in Gn pigs.

## **4. Discussion**

In this study, Gn pigs were administered with three doses of the VLP vaccine containing equal concentrations of GI.1, GII.3, GII.4, and GII.17 formulated with Al(OH)<sub>3</sub> adjuvant, or adjuvant

only (Control) and then challenged with  $2 \times 10^4$ ,  $8 \times 10^4$  or  $2 \times 10^5$  genomic RNA copies of a Cin-1 strain of HuNoV at PID 28. Protection conferred by the vaccine was evaluated based on fecal virus shedding and fecal consistency data collected daily from PCD0 to PCD7. The serum and intestinal VLP genotype-specific IgA and IgG antibody responses induced by the vaccine were measured by ELISA, and effector T cell responses to individual VLP genotypes were measured by flow cytometry. Although the vaccine induced significant systemic antibody and IFN- $\gamma$  producing T cell immune responses specific to every VLP genotype within the vaccine, the vaccine failed to induce intestinal antibody and T cell responses, and did not confer any noticeable protection against virus shedding or diarrhea when challenged with any one of the three doses of Cin-1 in Gn pigs. These results concur with previous findings in naïve mice (Tamminen, Malm *et al.* 2016), which showed that only intranasal, not IM immunization with GII.4 VLPs induced mucosal IgA antibodies capable of blocking the VLP binding to the HBGA receptors. In orally pre-exposed individuals, such as most adult humans, IM vaccine may be able to induce anamnestic intestinal IgA responses (Sundararajan, Sangster *et al.* 2015). However, in naïve hosts such as Gn pigs (and human infants), the IM vaccine could not induce sufficient intestinal immune responses to confer any protection. In a previous study in Gn pigs, VLP derived from GII.4 VA387 variant when given intranasally with MPL and chitosan as mucosal adjuvants, conferred 60% protection rate against diarrhea upon challenge with a GII.4/2006b variant (Kocher, Bui *et al.* 2014). These data suggest that mucosal vaccination routes and mucosal adjuvants may be more effective against HuNoV infection than IM route for VLP vaccine in Gn pigs (Heinimäki, Malm *et al.* 2018).

A serum HAI titer of 40 has previously been correlated with protection in human volunteers challenged with Norwalk virus (Czako, Atmar *et al.* 2012). However, the GII.4-specific serum HAI titers of 40 and above observed in Gn pigs did not correlate with protection against Cin-1.

Further studies are needed to fully understand the reasons for the discrepancy between the strong immunogenicity and the lack of protection of the VLP vaccine. A likely reason for the ineffectiveness of the VLP vaccine against the Cin-1 challenge is the lack of cross protection between different genogroups, genotypes and even variants of HuNoV. Although a previously conducted study did demonstrate cross-variant protection induced by intranasal VLP and P particle vaccines in Gn pigs (Kocher, Bui *et al.* 2014). The many different HuNoV variants in the environment indicate an ever-changing capsid composition that allows for HuNoV immune evasion (Smith and Smith 2019). The GII.4 VLP in the tetravalent vaccine was derived from a Sydney strain (emerged in 2012), a different variant from the GII.4/2003 Cin-1, the Farmington Hills strain which was prevalent in 2002. With 10 years between circulation, there is enough antigenicity difference between the two variants to allow Cin-1 to escape neutralization by the antibodies induced by the Sydney strain VLPs in the vaccine (Motoya, Nagasawa *et al.* 2017). Emergence of new GII.4 strains have been attributed to the changes in the blockade epitopes, which allows the virus escape from protective herd immunity (Lindesmith, Beltramello *et al.* 2012, Lindesmith, Costantini *et al.* 2013).

A total of 35 substitutions (93% identity) were observed when comparing the major capsid protein amino acid sequence alignment of Cin-1 2003 (JQ965810) and Sydney 2012 (JX459908). The S domain of the major capsid protein contained 2 substitutions, P1-1 domain contained 3 substitutions, the P2 domain contained 23 substitutions, and the P1-2 domain contained 4 substitutions (Table 3). Among the GII.4 blockade epitopes (Lindesmith, Costantini *et al.* 2013), a total of 11 substitutions were observed (5 substitutions in epitope A, 1 substitution in epitope B, 1 substitution in epitope C, 2 substitutions in epitope D, and 2 substitution in epitope E; Table 4).

Pairwise sequence alignment of blockade amino acid sequences of Cin-1 and Sydney 2012 strains revealed an 80.3% sequence similarity between the two variants.

We were not able to measure the HBGA blocking antibody titers in this study, a known correlate of protection, however, it could be predicted to see a good level of HBGA blocking titers against the VLP derived from the Sydney strain (or any other 3 genotype VLPs) but lower or no HBGA blocking titers against the VLP derived from Cin-1 in the sera of the vaccinated pigs.

In Gn pig studies, the gnotobiotic condition of pigs exclude confounding factors that can influence HuNoV infectivity and diarrhea, such as gut microbiome (Lei, Twitchell *et al.* 2019). It was shown that colonization with human gut microbiome enhanced HuNoV replication and diarrhea severity. In the present study, 6 out of 14 vaccinated pigs from the different challenge dose groups were contaminated by bacteria during the immunization experiment, but all 9 control pigs remained clean. The contaminating bacteria may have negatively affected the protective effect, if any, induced by the VLP vaccine.

To avoid a high virus challenge dose that may overpower the vaccine induced immunity, we tested three different challenge doses. The lowest challenge dose  $2 \times 10^4$  genomic RNA copies only infected 67% of both vaccinated and control pigs, indicating that this challenge dose was too low. The challenge dose  $2 \times 10^5$  genomic RNA copy numbers determined as being the optimal dose in our concurrent study (described in Chapter 3) was confirmed in this study to induce infection and diarrhea in 100% of the control pigs. After challenge with this dose of Cin-1, the VLP vaccinated pigs had same incidence, duration and titers of virus shedding and same incidence, duration and severity of diarrhea as the control pigs, clearly demonstrating the lack of protection.

In conclusion, the IM VLP vaccine was highly immunogenic but was not able to provide any protection against virus shedding and diarrhea induced by a GII.4/2003 Cin-1 variant HuNoV. Although it has been suggested based on *in silico* analysis (Motoya, Nagasawa *et al.* 2017) and *in vitro* antibody and VLP binding experiments (Mallory, Lindesmith *et al.* 2019) that antigenic diversity of variants within GII.4 genotype led to evasion of herd immunity and resulted in the repeated pandemics of HuNoV gastroenteritis, our study provides the very first *in vivo* experimental evidence for the total lack of cross-variant protection between the Sydney and Farmington Hills GII.4 strains due to immune evasion. This finding has important implications in HuNoV vaccine development. It could be foreseen that with the amount of antigenic diversity observed among emerging and re-emerging variants of HuNoV, vaccines would have to include multiple variants and have to be routinely updated in order to ensure sustained protection among the population. It remains to be seen whether this vaccine can confer protection from GII.4/2012 Sydney variant infection and diarrhea.

***Author Contributions:***

Conceptualization, L.Y., Validation, A.R. and L.Y.; Formal Analysis, A.R.; Investigation, A.R., J.M., E.G., S.L., E.T., T.B., and L.Y.; Resources, L.Y.; Writing – Original Draft Preparation, A.R., and L.Y.; Writing – Review & Editing, A.R., J.M., E.G., S.L., E.T., T.B., and L.Y.; Visualization, A.R., and L.Y.; Supervision, L.Y.; Project Administration, A.R. and L.Y.; Funding Acquisition, L.Y.

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***Conflicts of Interest:***

The authors declare that there are no conflicts of interest. The funders had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, or in the decision to publish the results.

***Ethical Approval:***

All animal experiments were conducted in accordance with protocols approved by the Institutional Animal Care and Use Committee at Virginia Tech (IACUC protocol: 17-110-CVM).

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**Table 1. Assignment of treatment groups for gnotobiotic (Gn) pigs**

<b>Virus Dose Group</b>	<b>Challenge Virus Dose</b>	<b>Vaccine Group</b>	<b>Number of Pigs</b>
1	2x10 <sup>5</sup> Genomic RNA Copies	Control	4
		VLP Vaccine	7
2	8x10 <sup>4</sup> Genomic RNA Copies	Control	2
		VLP Vaccine	4
3	2x10 <sup>4</sup> Genomic RNA Copies	Control	3
		VLP Vaccine	3

**Table 2a. HuNoV fecal shedding and diarrhea data after inoculation with  $2 \times 10^5$  Genomic RNA copies of Cin-1**

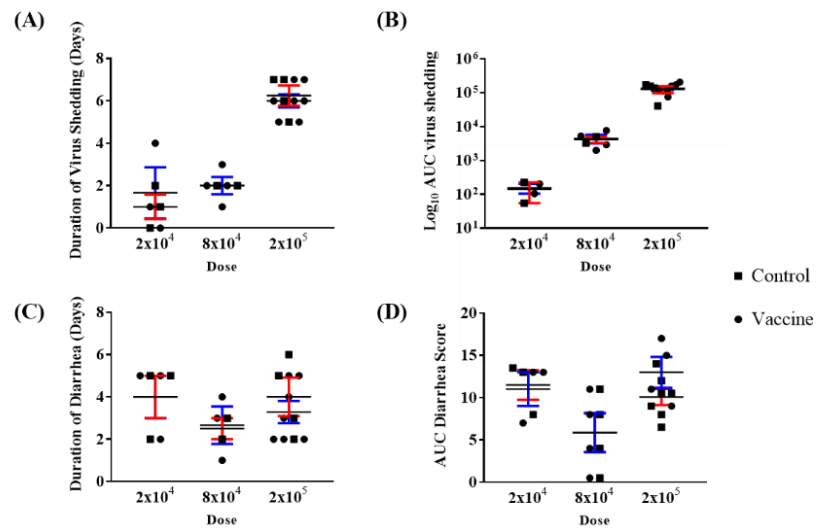
Dose	Group	n	Virus Shedding					Diarrhea				
			Shedding (%)	Mean onset days (SEM)	Mean days with shedding	Geometric mean peak titre shed (RNA copies/g of feces)	AUC	Diarrhea (%)	Mean onset days (SEM)	Mean days with Diarrhea	Mean cumulative score	
$2 \times 10^5$ RNA Copies	VLP Vaccine	7	100 (7/7)	2 (0.31)	6.0 (0.31)	4.53E+04	136094 (16669)	100 (7/7)	2.29 (0.47)	3.29 (0.52)	10.1 (0.95)	
	Control	4	100 (4/4)	1.25 (0.25)	6.25 (0.48)	4.12E+04	127063 (29653)	100 (4/4)	2.75 (0.48)	4 (0.91)	13.0 (1.8)	

**Table 2b. HuNoV fecal shedding and diarrhea data after inoculation with  $8 \times 10^4$  Genomic RNA copies of Cin-1**

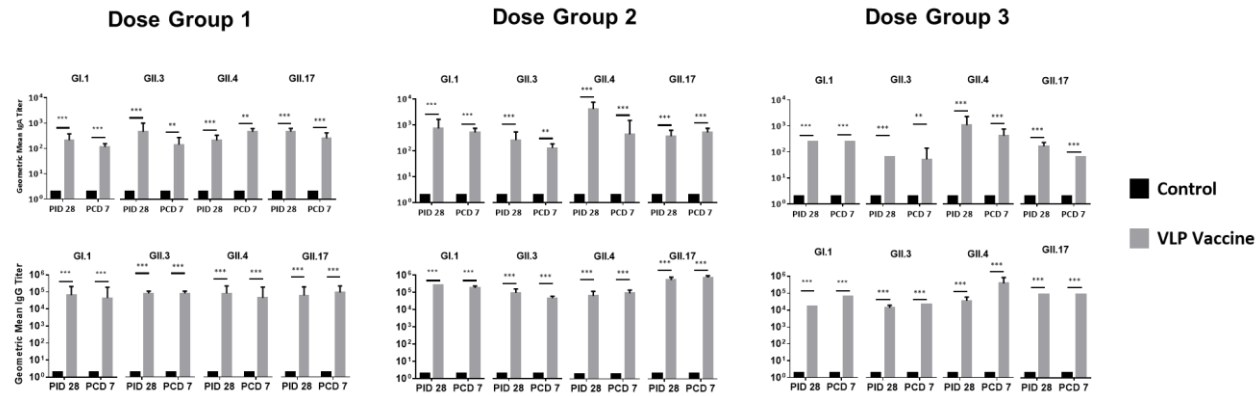
Dose	Group	n	Virus Shedding					Diarrhea				
			Shedding (%)	Mean onset days (SEM)	Mean days with shedding	Geometric mean peak titer shed (RNA copies/g of feces)	AUC	Diarrhea (%)	Mean onset days (SEM)	Mean days with Diarrhea	Mean cumulative score	
$8 \times 10^4$ RNA Copies	VLP Vaccine	4	100 (4/4)	1.75 (0.48)	2.0 (0.41)	3.77E+03	4478 (1272)	75 (3/4)	5.75 (0.75)	1.75 (0.85)	7.13 (2.9)	
	Control	2	100 (2/2)	1 (0)	2 (0)	5.45E+03	4151 (863)	100 (2/2)	6 (0.0)	2.5 (0.35)	7.5 (0)	

**Table 2c. HuNoV fecal shedding and diarrhea data after inoculation with  $2 \times 10^4$  Genomic RNA copies of Cin-1**

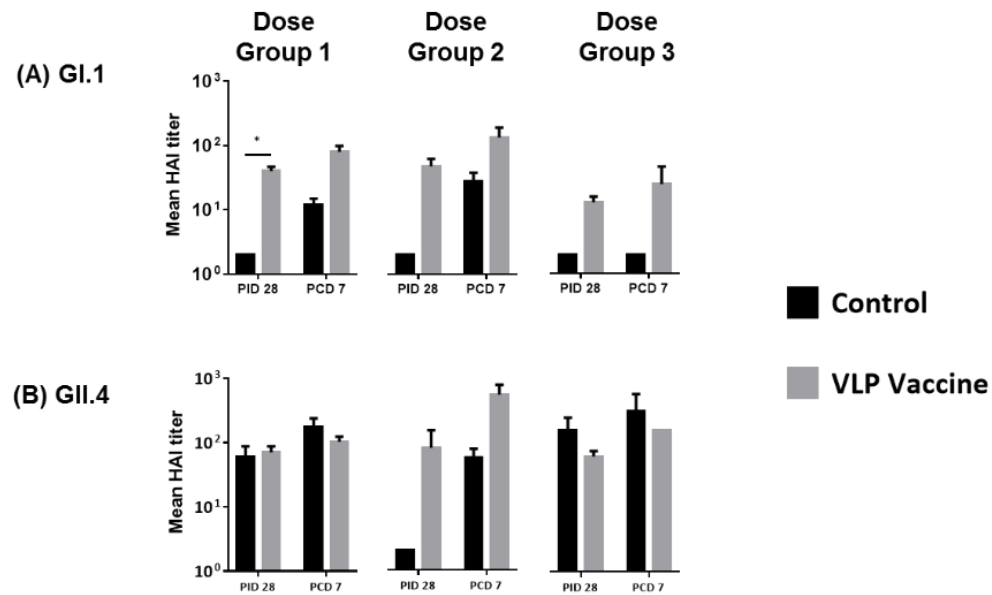
Dose	Group	n	Virus Shedding					Diarrhea				
			Shedding (%)	Mean onset days (SEM)	Mean days with shedding	Geometric mean peak titer shed (RNA copies/g of feces)	AUC	Diarrhea (%)	Mean onset days (SEM)	Mean days with Diarrhea	Mean cumulative score	
$2 \times 10^4$ RNA Copies	VLP Vaccine	3	66 (2/3)	5 (2)	3 (1)	1.09E+02	155 (41)	100 (3/3)	1 (0)	4 (1)	11.5 (1.76)	
	Control	3	66 (2/3)	3 (2)	2 (0)	1.07E+02	140 (70)	100 (3/3)	2.3 (0.33)	4 (1)	11.0 (2.0)	



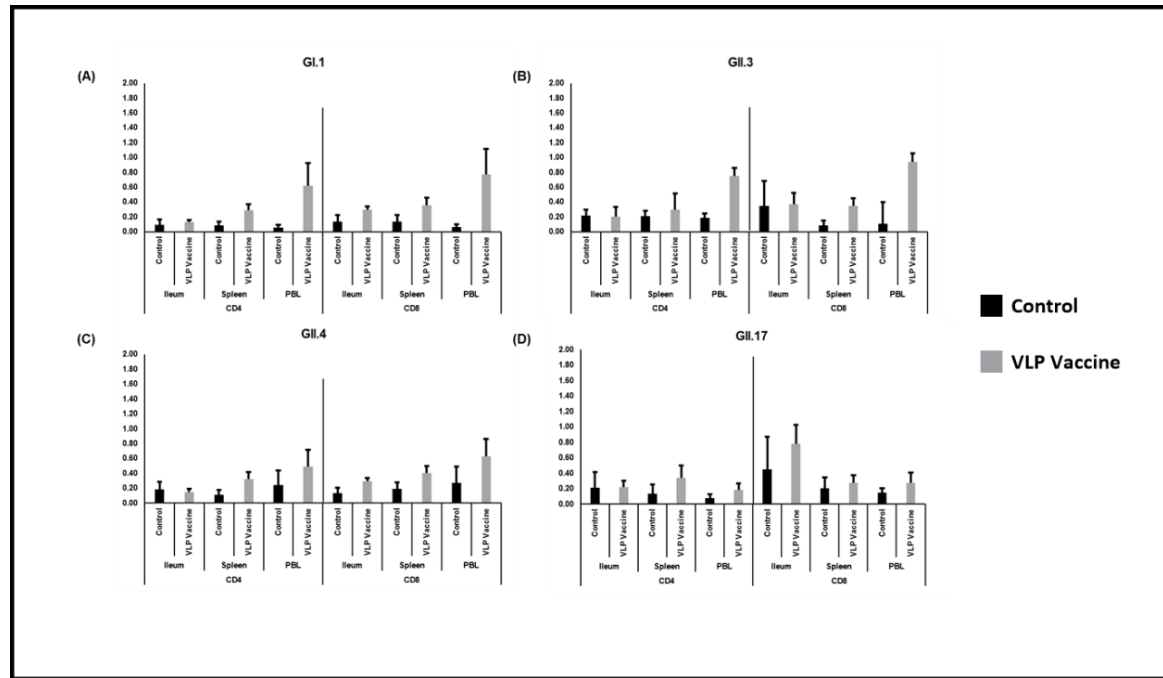
**Figure 1.** Virus shedding and diarrhea in vaccinated and control pigs. Daily virus shedding and diarrhea were monitored from PCD 0 – PCD 7 with (A) duration of virus shedding, (B) cumulative virus shedding shown as AUC, (C) duration of diarrhea and (D) cumulative diarrhea scores, of vaccinated and control Gn pigs among three virus challenge dose groups. There were no significant differences between the vaccine and control groups for any of the data.



**Figure 2.** VLP-specific IgA (top) and IgG (bottom) serum antibodies against GI.1, GII.3, GII.4 and GII.17 HuNoV at PID 28 and PCD 7 in vaccinated and control Gn pigs among three virus challenge dose groups. Student T-test was used to compare antibody titers between the vaccine and control groups on each time point. \*\* p<0.01; \*\*\*p<0.001).



**Figure 3.** Serum HAI titers against GI.1 (A) and GII.4 (B) HuNoV VLP at PID 28 and PCD 7 in vaccinated and control Gn pigs among three virus challenge dose groups. ANOVA was used to compare HAI titers. There were no significant differences between the vaccine and control groups at any time point.



**Figure 4.** IFN- $\gamma$  producing CD4<sup>+</sup> and CD8<sup>+</sup> T-cell responses in the intestinal (ileum) and systemic (spleen and peripheral blood lymphocyte, PBL) lymphoid tissues of VLP vaccinated (n=7) and Mock (n=4) vaccinated Gn pigs. Pigs were challenged with  $2 \times 10^5$  genomic RNA copies at PID 28 and euthanized at PCD 7. Frequencies were subtracted by unstimulated background numbers. Data presented are mean frequencies of IFN- $\gamma$  producing T-cells. Error bars are standard error of means.

**Table 3. Amino acid sequence substitutions within S, P1-1, P1-2 and P2 domains observed between Cin-1 2003 and Sydney 2012 strains**

<b>Domain</b>	<b>Amino acid substitution (total)</b>	<b>Amino acid substitution within one group</b>	<b>Amino acid substitution between different group</b>	<b>Amino acid substitution which potentially influence the protein folding</b>	<b>Amino acid location</b>
<b>S</b>	2	1	1	-	50–225
<b>P1-1</b>	3	3	-	-	226–278
<b>P2</b>	23	17	6	-	279–405
<b>P1-2</b>	4	3	1	-	406–520

**Table 4. Observed amino acid substitutions among identified GIL4 blockade domains**

<b>VLP</b>	<b>Epitope</b>															
	<b>A</b>						<b>B</b>		<b>C</b>		<b>D</b>			<b>E</b>		
	<b>294</b>	<b>296</b>	<b>297</b>	<b>298</b>	<b>368</b>	<b>372</b>	<b>333</b>	<b>382</b>	<b>340</b>	<b>376</b>	<b>393</b>	<b>394</b>	<b>395</b>	<b>407</b>	<b>412</b>	<b>413</b>
<b>Cin-1 (2003)</b>	A	T	H	N	N	N	M	K	G	E	N	G	T	S	T	G
<b>Sydney (2012)</b>	T	S	R	N	E	D	V	K	T	E	G	T	T	S	N	T

## **Chapter 5**

### **General discussion and future directions**

Ashwin Ramesh

Vaccination is one of the most successful medical practices that has played a significant role in positively impacting our longevity (Rappuoli, Pizza *et al.* 2014, Kim and Jang 2017). Novel vaccines that enter the pipeline require stringent testing and repeated quality control in order to ensure their safety, immunogenicity and efficacy before they are rolled out to the targeted population (Crowcroft and Klein 2018). Diarrhea is responsible for 9% of childhood deaths globally (Liu, Oza *et al.* 2015), a rate which has been only recently reduced due to the introduction of rotavirus (RV) vaccines as part of national immunization programs (Burnett, Jonesteller *et al.* 2017). The impact that gastroenteritis (GE) diseases have on communities especially in developing countries is evidenced by the steady burden of outbreaks and their associated mortalities (Graves 2013). Lower vaccine effectiveness against RV infection and disease in resource-limited settings has been identified to be multi-factorial (Clarke and Desselberger 2015).

The two main concepts discussed in my thesis include: (1) To determine whether intramuscularly (IM) administered vaccines are effective in priming the immune system against human-RV and human norovirus (HuNoV) infection and disease using a gnotobiotic (Gn) pig model, and (2) To determine the median infectious dose ( $ID_{50}$ ) and median diarrhea dose ( $DD_{50}$ ) of HuNoV GII.4 Cin-1 variant in order to establish Gn pigs as an effective animal model to study HuNoV infections, and to assist with the standardization of dose-response models used to determine an optimal infectious dose for the accurate evaluation of vaccines and therapeutics for use in future studies.

Currently, a P2-VP8\* RV vaccine is in its advanced (Phase II) stages of clinical trials and is the front runner of non-replicating RV vaccines (NRRV) for vaccine licensure (Groome, Koen *et al.* 2017). Pre-clinical trials of this vaccine have been carried out in Gn pig models and have shown to be effective in protection against RV diarrhea before progressing towards human clinical trials

(Wen, Wen *et al.* 2014). As part of this thesis, we first explored the IM route of vaccine administration to test a novel nanoparticle RV vaccine in order to determine its immunogenicity and protective efficacy against RV infection and disease using the Gn pig model. This vaccine was developed based on the concept that NoV P particles (a 24-mer nanoparticle) can tolerate large sequence insertions within their P domain surface loop in order to display foreign epitopes (Tan and Jiang 2012). This vaccine can easily be synthesized and expressed using *E. coli* expression vectors. Three IM doses of this vaccine primed the Gn pig immune system and ensured the production of sufficient adaptive immune responses to provide strong protection against RV infection and diarrhea. Protection was indicated by the significant reduction in the mean duration of diarrhea, virus shedding in feces, and significantly lower fecal cumulative consistency scores in post-challenge day (PCD) 1-7 among vaccinated pigs compared to the mock immunized controls. (Ramesh, Mao *et al.* 2019). While this study only evaluated the protective efficacy against RV, further studies need to be carried out to determine whether the P particles are able to retain their immunogenicity (Kocher, Bui *et al.* 2014) against HuNoV infection and disease. Our study provided the preclinical evaluation data needed for IND application by the company, Anhui Zhifei Longcom Biopharmaceutical Co., Ltd., China, to start human clinical trials of this vaccine and helped to generate a strong case for P particle-based vaccines (Tan and Jiang 2019) encouraging further research to be carried out in this field for the development of P particle-based vaccines.

GII.4 HuNoVs belong to the most diverse genotype of NoV strains and are responsible for over 80% of all NoV-related GE in the world today. Immune responses to NoV infections have been attributed to drive the selection of emerging pandemic strains of NoV through both antigenic and genetic drifts and shifts (White 2014). Gn pigs have previously been used to determine the ID<sub>50</sub> of GII.4/2006b HuNoV strain (Bui, Kocher *et al.* 2013). In Chapter 3 we estimated the Log<sub>10</sub> ID<sub>50</sub>

and DD<sub>50</sub> to be between 3.11 to 3.76, and 3.37 to 4.87 RNA copies, respectively. Furthermore, of the different routinely used dose-response models for quantitative microbial risk-assessment, we identified that the beta-Poisson model to be the best-fitting model for determining both the ID<sub>50</sub> and DD<sub>50</sub>. By comparing the ID<sub>50</sub> values of GII.4/2003 to GII.4/2006b strain, the GII.4/2006b variant required 35-fold higher genomic copy numbers in order to establish infection among 50% of the 33-34-day old Gn pigs. The GII.4/2003 strain is a Farmington Hills variant which was responsible for causing around 64% of cruise ship outbreaks and 45% of the land-based outbreaks, most of which occurred in long-term care facilities, schools, and restaurants, in the US in 2002 (Isakbaeva, Widdowson *et al.* 2005, Bull, Tu *et al.* 2006, Johnston, Qiu *et al.* 2007). Standardizing dose-response data from different circulating variants will help expedite HuNoV vaccine development.

VLP vaccine have been the main focus of subunit-based vaccines since they are able to replicate the morphological confirmation of HuNoVs. The advantages of using VLP vaccines as candidates is that they can easily be synthesized using different expression systems (Herbst-Kralovetz, Mason *et al.* 2010) and large amounts of VLPs can be produced very quickly to target new emerging strains. In Chapter 4, we evaluated immunogenicity and protective efficacy of a novel tetravalent VLP vaccine containing GI.1, GII.3, GII.4 and GII.17 VLPs in the Gn pig model of GII.4 infection and diarrhea. The vaccine was highly immunogenic, and was able to induce very strong VLP-specific IgA and IgG antibody responses against all 4 genotypes as well as HAI antibodies in the serum and primed for VLP-specific IFN- $\gamma$  producing CD4<sup>+</sup> and CD8<sup>+</sup> T cell responses in the spleen and blood. However, the abundance of immune effectors did not confer any protection against the Cin-1 variant, likely due to the antigenic difference between the GII.4 variant in the vaccine and the challenge GII.4 variant. It remains to be seen if the vaccine is capable of conferring

protection when challenged with the same GII.4 variant. Findings from this study suggests that for any HuNoV VLP vaccine to confer broad protection, it has to include all major currently circulating genogroups, genotypes and multiple variants with in the genotypes.

In summary, these studies demonstrate the benefits of Gn pigs as a large animal model that is capable of recapitulating both the RV and GII.4 HuNoV infection and disease. It is very exciting times for the prospect of HuNoV research. With recent identification of cellular tropisms, easily-reproducible cell culture models will be the main focus for researchers. Research efforts focusing on the mechanisms of NoV infection, pathogenesis and immunity using cell culture and animal models will answer many questions including the one raised in Chapter 4 regarding immune evasion. In order to be able to truly test the immunogenic potential of novel vaccines and their ability to confer protection among a completely naïve population, Gn pigs provide the solution. It has to be recognized that having these powerful research tools is truly a privilege and it needs to be used more often to create significant groundbreaking advancements in enteric viral research.

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