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Journal Name:	British Microbiology Research Journal
Manuscript Number:	2015_BMRJ_18071
Title of the Manuscript:	Diversity of Rotavirus VP7 and VP4 Genotypes Associated with Severe Childhood Diarrhea in North West Cameroon: Detection of Unusual strains G1P[6], G2P[6], G2P[8] and G3P[6]
Type of the Article	Original Research Article

General guideline for Peer Review process:

This journal's peer review policy states that **NO** manuscript should be rejected only on the basis of '**lack of Novelty**', provided the manuscript is scientifically robust and technically sound.

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(<http://www.sciencedomain.org/page.php?id=sdi-general-editorial-policy#Peer-Review-Guideline>)



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PART 1: Review Comments

	Reviewer's comment	Author's comment (if agreed with reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)
Compulsory REVISION comments	The manuscript BMRJ_18071 entitled "Diversity of Rotavirus VP7 and VP4 Genotypes Associated with Severe Childhood Diarrhea in North West Cameroon: Detection of Unusual strains G1P[6], G2P[6], G2P[8] and G3P[6]", describes the rotavirus genotypes and distribution among children in Cameroon. After reading the manuscript some issues have arisen: 1. The time of sample collection was January and December 2004. The sample is too old since many new Genotypes and serotypes have been found. Infection status in local place (North West Cameroon) has likely varied. Many references are out-of-date. A lot of documents published in the last years are not cited in the manuscript. Such as followings: Iyoha O;Abiodun PO. Human rotavirus genotypes causing acute watery diarrhea among under-five children in Benin City, Nigeria. Niger J Clin Pract, 2015, vol.18, No.1, 48-51 Suzuki T;Hasebe A;Miyazaki A;Tsunemitsu H. Analysis of genetic divergence among strains of	1. Aged data: We disagree that our data is too old since it reflects the status of rotavirus in the year of study. It should be noted that work published by Esona et al (2010) was based on data collected "during 1999-2000" which ironically showed that rotavirus was more common in older children (24 – 60 months Vs <24 months old). This contrasts with our study which found the disease to be more common in younger children, and we detected new strains, hence the relevance of our data. Old references Current and old literature relevant to this study were cited where necessary. 2. Methods: Methods for polyacrylamide gel electrophoresis (PAGE) and RT-PCR were revised. Line 55 – 59: Statement beginning from line 55 – 59 was deleted. 3. Unusual strains: We explained that "Common environmental factors such as overcrowding, mass movement and poor living conditions that are prevalent in many developing countries could also facilitate disease transmission leading to mixed



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	porcine rotavirus C, with focus on VP4 and VP7 genotypes in Japan. Virus Res. 2014. Hyun Ju Oh;Hyun-Sik Kang;Ki Soo Kang; et al. Distribution of Disease Severity and Group A Rotavirus Genotypes (VP7 & VP4) in Children with Acute Rotavirus Gastroenteritis. Pediatric Gastroenterology, Hepatology & Nutrition, 2011, Vol.14(2):148-154. Ahmed SF;Mansour AM;Klena JD;Husain TS;Hassan KA;Mohamed F;Steele D. Rotavirus genotypes associated with acute diarrhea in egyptian infants.Pediatr Infect Dis J. 2014, 33(Suppl 1):S62-S68. Early similar report was published by Esona et al. (Esona MD, Armah GE, Steele AD. Rotavirus VP4 And VP7 Genotypes Circulating In 273 Cameroon: Identification of unusual types. J Infect Dis 2010;202(Suppl):205-11). Probably, the article has a basic significance for the North West Cameroon. There is little meaning for general rotavirus characteristics in other places over the world. 2. The methodology for viral RNA extractionn, enzyme Immunoassay (EIA), polyacrylamide gel electrophoresis (PAGE) and double-stranded RNA (dsRNA) extraction , especially Genotyping of Rotavirus isolates, are common.	infections" (lines 99 -102), and that " The segmented nature of the rotavirus genome and high rate of mutation [17] suggest that during a mixed infection with different rotavirus strains genetic reassortment (substitution of RNA segments between different RNA strands) could occur" giving rise to mosaic strains and unusual genotypes, lines 160 -162 (section in red added) Vaccine efficacy: This will be addressed in our future study. Others: Line 58: [12]. Accepted. Spaces deleted. Others: 1. Authors and affiliations: The second author's name was corrected for spelling and affiliation 2. Other errors identified by authors were corrected. 3. Reference 16 was moved to position 8 and subsequent references were renumbered accordingly including three new ones. 4. Subsections were renumbered to reflect the changes made under materials and methods and results and discussion sections 6. Line 185 – 189 was moved to line 160 for flow. 5. All corrections appear in red in the draft revised manuscript.
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	3. The manuscript did not explain why there was such high incidence of unusual rotavirus strains circulating in the NWR Cameroon. What's difference with the previous documents? How to assess vaccine efficacy under this condition? What is practical significance? Others Line 58 Delete a space before 12 in the square brackets [12]. And so on.	
<u>Minor</u> REVISION comments		
<u>Optional/General</u> comments		