



SDI Review Form 1.6

PART 1:

Journal Name:	<u>British Microbiology Research Journal</u>
Manuscript Number:	2013_BMRJ_4896
Title of the Manuscript:	Multiple Antimicrobial Resistance in Vibrio sp isolated from River and Aquaculture Water Sources in Imo State, Nigeria
Type of the Article	Research Paper

General guideline for Peer Review process is available in this link:

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

- This form has total 7 parts. Kindly note that you should use all the parts of this review form.



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PART 2: 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)
<u>Compulsory</u> REVISION comments	• 50 rivers and an unknown number of aquaculture sites have been tested. There is no Nigeria map to help us understand what sites they are talking about. Please add info and map. • What kind of aquaculture sources? Is there a direct correlation with the river waters? Are the sites close? Is there a cross-contamination of the two types of waters? This is crucial to understand the discussion and to draw any conclusion. • What were the criteria behind the choice of the antibiotics to be tested? Why not screening sulphamethoxazole, trimethoprim, chloramphenicol, tetracycline? These are all very common antibiotic resistances in Vibrios. As for the ESBL, why not ceftriaxone, ceftazidime, cefotaxime, aztreonam? I'm not saying they need to screen all these antibiotics but they have at least to explain why they chose the ones they tested. Is there any epidemiological data about this Nigerian region and strains we are missing? • 5 figures and 2 tables is definitely too much for such a short amount of data. Please reduce the number of figures, they are redundant, and figure 4 and 5 do not need to be there, they can just be explained in the text (as already done). • Results and discussion section can be tricky if not used properly like in this case. Data are not explained clearly and need to be reorganized. Maybe the use of paragraphs (separating river and aquaculture results) in this section will help. • Lines 104-107. The authors isolated 157 Vibrio strains and then said that the Api test identified VC, VP and VV. How many of each species? All the 157	50 samples were collected at different times from the river and aquaculture sources sampled. 50 rivers and aquaculture sites were not sampled. The aquaculture samples were collected from private and commercial fish ponds. The sites are not close to the river that was sampled and so no cross contamination. The antibiotics were chosen because they are the ones most commonly used around here. Noted and taken care of. Okay, noted. API test was used for as much as the panel could take care of. All 157 isolates could not be tested,



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strains where only these 3 species? Was there any other non-confirmed strain? Api worked for every strain? Why in tables 1 and 2 as well as all the figures the authors refer only to *Vibrio* spp? If they have identified the species they should refer to it as such. This would add to the value of the manuscript. Please revise tables 1 and 2 and give us the exact numbers of the VC, VP and VV strains as well as of those that are not identified at the species level (if any).

- The above confusion is a main issue in all the paper. Tables 1 and 2 refer to what exactly? PLEASE CHANGE THE FORMAT (see below for an example).
- Figure 3. When referring to *Vibrio* spp here, do the authors refer to all the *Vibrio* species isolated (including VC) or is all *Vibrio* spp without VC (like in tables 1 and 2)?
- The discussion section is interesting but too speculative and long. Lots of information given here would better fit the introduction. The authors have not enough data to speculate about possible circulation of R plasmids in their strains (lines 170-176), nor is of any interest the analysis of someone else's results (lines 178-182).
- The real interesting finding of the paper, the identification of TEM in *Vibrio* spp is kind of lost in the entire manuscript (lines 184-195). Is this a VC, VP or VV strain? Where was it isolated? What is its resistance profile?
- Conclusion, lines 327-328. "genes encoding ESBL s". Did I get it wrong or only one strain was TEM positive?

Species	Number of isolates	Amp	Te	Do	Car	Mez	K
VC	Xxx	%	%	%	%	%	%
VP	Yyy						
VV	Zzz						
<i>Vibrio</i> spp	www						

but among the isolates that were isolated the species listed in the text were the ones identified.

The format used for the table is okay as it is.

Results of fig 3 refers to the total resistance rates for all the *Vibrio* spp including VC

Okay, noted

Okay, noted



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<u>Minor</u> REVISION comments	- English revision is needed. Abstract is not clear at all. This is a consequence of how the data are described in the text. Introduction needs a major revision. It is confusing in terms of references (i.e. ref 19, line 59 refers to Aeromonas not Vibrios); there are references missing (lines 48, 54, 67, 100); ref 22, line 64 is a general ref to antibiotic resistance surveillance in Vibrios, not specific to beta-lactams as the authors use it for; they are missing the main references to Vibrio cholerae ESBL papers (Mandel 2012 EID, Darley 2012 The Lancet, Ismail 2008 J Clin Microb). - Throughout the paper there are several mistakes for the scientific names of the species: V. cholerae not cholera, V. parahaemolyticus not parahaemolyticus, V. vulnificus not fulnicus. - I'm not familiar with the reference style of the journal but I don't think that a sentence like "According to [22]" is acceptable. This is widespread in the text (lines 22, 38, 41 and so on).	Noted and taken care of. Noted and taken care of Noted and taken care of. This is the reference style prescribed by the journal.
<u>Optional/General</u> comments	THE AUTHORS DESCRIBED THE ANTIBIOTIC RESISTANCE PROFILE OF A WIDE COLLECTION OF VIBRIO STRAINS COLLECTED FROM THE ENVIRONMENT, EITHER FROM RIVER OR AQUACULTURE WATER SOURCE IN NIGERIA. THEY ANALYSED 10 DIFFERENT ANTIBIOTICS AND PERFORMED EXTENDE BETA-LACTAMASE PHENOTYPIC TESTS. OVERALL STRAIN COLLECTION SHOWS A CERTAIN DEGREE OF RESISTANCE TO SEVERAL ANTIBIOTICS.	