Review of: "Genomic analysis of virulence factors and antimicrobial resistance of group B Streptococcus isolated from pregnant women in northeastern Mexico"

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Potential competing interests: The author(s) declared that no potential competing interests exist.

Palacios-Saucedo et al investigated virulence factors and antimicrobial resistance patterns of GBS isolated from preterm pregnant women (35-37 weeks of gestation) in northeastern Mexico. The study included important populations i.e. both pregnant mothers and their newborns. Using genomic analysis, they found ten principal virulence genes and also they determined the resistance pattern of GBS. They isolated only 17 GBS among 1154 pregnant women. The main conclusion is that GBS colonization is low in pregnant women and absent in newborns where the isolated bacteria exhibited growing resistance to antimicrobials. The very low number of GBS (17) isolated from a huge number of pregnant women (1154) entails the authors didn't investigate possible risk factors before the study (i.e. their objective is not a significant burden to be investigated) and/or their population is not representative and/or there were problems in specimen handling and processing. And the problem in specimen handling and/or processing could be a reason for the absence of GBS in the newborns of colonized mothers. The 1.47% prevalence of GBS in their study is quite incomparable with different studies in different countries and with other studies conducted in Mexico which reported a high rate of GBS colonization.

Our concerns with this study are the following;

1. Methods: - The methods section is vague as it is too shallow and there are no explanations on the important aspects of socio-demographic data collection, specimen collection, and processing, quality control, sample size determination, sampling technique, and procedure. It is not mentioned when and how the specimen was collected from mothers and their newborns. In addition, they didn't mention inclusion criteria i.e. which pregnant women and/or newborns were included and/or excluded from the study. One of the reasons for the low GBS colonization rate could be the absence of exclusion criteria. If all pregnant women are included, prevalence could be hindered since they might use antibiotics within a short period of enrollment. Regarding newborns; only newborns of colonized mothers with normal vaginal delivery (but authors included newborns with another way of delivery than normal one like cesarian section), babies that are not wiped and bathed should be enrolled in the study. Additionally, the specimen should be collected from the ear, nose, and umbilicus of newborns of each enrolled woman immediately after birth. The number of newborns sampled is too small i.e. 6 which is difficult to conclude. The sample size determination and sampling technique (probable or non-probable) is also not mentioned. If this is not set well, the study population is not representative. Moreover, there should be a logical and scientific way of sample size determination; otherwise, reporting the prevalence of GBS in a cross-sectional study is not justified. Besides, the way how the quality of quantitative data, specimen handling, transporting, storage, processing, and reagents/equipment is controlled is not mentioned. The

quality, efficiency, and sterility of the culture media are not mentioned at all. Antibiotic susceptibility testing would better be following CLSI guidelines. Determining the strength of association between predictors and outcome variables using an adjusted odds ratio could be more explanatory. Overall, the absence of brief data on these entire issues makes the method awkward and readers may not be justified for the low prevalence of GBS in pregnant women and the absence of GBS in newborns.

2. Results: - the clinical and/or other characteristics of the included newborns are not mentioned. The inclusion of both newborns and mothers is vague. Any data on the genetic variability (mutation) of virulent and drug resistance genes are not reported. This makes it hard to predict the emergence of future genetic alterations in GBS with the probability of escaping potent drugs like vancomycin. The authors better screened the susceptibility pattern of GBS to many recommended drugs. The multidrug resistance patterns of GBS are also not mentioned.

Generally, the methodology of this study is vague and limited. Therefore, it is difficult to interpret and discuss the results having this impaired methodology. Maybe only genomic analysis data in the study are worth mentioning. Otherwise, inferring and discussing the GBS colonization rate in both mothers and newborns in this study does not scientifically sound.