1163-34-400      **Eric Ngang Che\*** (`ericngangche@yahoo.com`), Washington, DC, and **Yeona Kang** (`yeona.kang@howard.edu`) and **Abdul-Aziz Yakubu** (`ayakubu@howard.edu`). *Risk Structured Model of Cholera Infections In Cameroon.*

In this talk, we introduce a risk-structured ODE cholera model of Cameroon with no spatial structure [1]. We use a "fitted" demographic equation (disease-free equation) to capture the total population of Cameroon, and then use a fitted low-high risk structured cholera differential equation model to study reported cholera cases in Cameroon from 1987-2004. The basic reproduction number of our fitted cholera model, $\mathcal{R}_0$, is bigger than 1 and our model predicted cholera endemicity in Cameroon. In addition, the fitted risk structured model predicted a decreasing trend from 1987 to 1994 and an increasing trend from 1995 to 2004 in the pre-intervention reported number of cholera cases in Cameroon from 1987 to 2004. Using the fitted risk structured cholera model, we study the impact of vaccination, treatment and improved sanitation on the number of cholera infections in Cameroon from 2004 to 2022. Furthermore, we use our fitted model to predict future cholera cases.

## Reference

[1] E. Che, Y. Kang and A. Yakubu, *Risk structured model of cholera infections in Cameroon*, Mathematical Biosciences **320** (2020), 108303.

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