

## **A comprehensive look at *Xenopus* gut microbiota: effects of feed, developmental stages and parental transmission**

It is well established that the gut microbiota play an important role in the overall health of their hosts [1]. To date, there are still a limited number of studies on the complex microbial communities inhabiting vertebrate digestive systems, especially the ones that also explored the functional diversity of the microbial community [2]. This manuscript reports a comprehensive study on the phylogenetic and metabolic profiles of the *Xenopus* gut microbiota. The author describes significant changes in the gut microbiome communities at different developmental stages and demonstrates different microbial community composition across organs. In addition, the study also investigates the impact of diet on the *Xenopus* tadpole gut microbiome communities as well as how the bacterial communities are transmitted from parents to the next generation. This is one of the first studies that addresses the interactions between gut bacteria and tadpoles during the development. The authors observe the dynamics of gut microbiome communities during tadpole growth and metamorphosis. They also explore host-gut microbial community metabolic interactions and demonstrate the capacity of the microbiome to complement the metabolic pathways of the *Xenopus* genome. Although this study is limited by the use of *Xenopus* tadpoles in a laboratory, which are probably different from those in nature, I believe it still provides important and valuable information for the research community working on vertebrate's microbiota and their interaction with the host.

1. Jandhyala SM, Talukdar R, Subramanyam C, Vuyyuru H, Sasikala M, Nageshwar Reddy D. Role of the normal gut microbiota. *World J Gastroenterol*. 2015;21(29):8787-803. doi: 10.3748/wjg.v21.i29.8787. PubMed PMID: 26269668.
2. Bletz MC, Goedbloed DJ, Sanchez E, Reinhardt T, Tebbe CC, Bhujju S, et al. Amphibian gut microbiota shifts differentially in community structure but converges on habitat-specific predicted functions. *Nature Communications*. 2016;7(1):13699. doi: 10.1038/ncomms13699.