

6th International Conference on

Genomics & Pharmacogenomics

September 12-14, 2016 Berlin, Germany

High throughput identification of novel conotoxins from cone snails by multi-transcriptomic sequencing

Qiong Shi^{1,2,3}, Chao Peng¹, Chao Bian^{1,2}, Jia Li¹ and Junming Xu^{1,2}¹Shenzhen Key Lab of Marine Genomics, China²BGI-Zhenjiang Institute of Hydrobiology, China³Shenzhen University, China

With an estimation of over 500 species, cone snails are classified into *Conus*, the biggest genus among marine invertebrates. Cone snails apply a complex cocktail of venom components to capture and digest prey. According to variation in diet, cone snails are divided into piscivorous, molluscivorous and vermivorous groups. In the past few years, our lab has successfully performed transcriptomic sequencing of around 10 species. Here, we summarize our recent data about a special species, Chinese tubular cone snail (*C. betulinus*), which is the dominant conus species inhabiting the South China Sea. The transcriptomes of venom ducts and venom bulbs from a variety of specimens of this species were sequenced using both next-generation sequencing and traditional Sanger sequencing technologies, resulting in identification of a total of 215 distinct conopeptides. Among these, 183 were novel conopeptides, including 9 new super families. It appears that most of the identified conopeptides are synthesized in the venom duct, while a handful of conopeptides are identified only in the venom bulb and at very low levels. Variation in conopeptides from different specimens of *C. betulinus* was observed, which suggested the presence of intraspecific variability in toxin production at the genetic level. These novel conopeptides provide a potentially fertile resource for development of new pharmaceuticals and a pathway for discovery of new conotoxins.

Biography

Qiong Shi has completed his PhD from China Zhongshan University and Postdoctoral studies from Beijing Normal University and Japan Hokkaido University. Before joining BGI in 2011, he has worked at USA National Institutes of Health, University of Maryland and OriGene Technologies Inc. He is the Dean of BGI Academy of Marine Sciences, VP and Chief Scientist of BGI Fisheries, a Genomics Professor at University of Chinese Academy of Sciences and Shenzhen University and the Chief of Shenzhen Key Lab of Marine Genomics. He has published over 60 academic papers and 6 monographs and acquired 12 Chinese patents.

shiqiong@genomics.cn

Notes: