



[논문]A hybrid DNA sequencing approach is needed to properly link genotype to phenotype in multi-drug resistant bacteria

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초록(Abstract)	<p>Antibiotic resistance genes (ARGs) are now viewed as emerging contaminants posing a potential worldwide human health risk. The degree to which ARGs are transferred to other bacteria via mobile genetic elements (MGEs), including insertion sequences (ISs), plasmids, and phages, has a strong association with their likelihood to function as resistance transfer determinants. Consequently, understanding the structure and function of MGEs is paramount to assessing future health risks associated with ARGs in an environment subjected to strong antibiotic pressure. In this study we used whole genome sequencing, done using MinION and HiSeq platforms, to examine antibiotic resistance determinants among four multidrug resistant bacteria isolated from fish farm effluent in Jeju, South Korea. The combined data was used to ascertain the association between ARGs and MGEs. Hybrid assembly using HiSeq and MinION reads revealed the presence of IncFIB(K) and pVPH2 plasmids, whose sizes were verified using pulsed field gel electrophoresis. Twenty four ARGs and 95 MGEs were identified among the 955 coding sequences annotated on these plasmids. More importantly, 22 of 24 ARGs conferring resistance to</p>



various antibiotics were found to be located near MGEs, whereas about a half of the ARGs (11 out of 21) were so in chromosomes. Our results also suggest that the total phenotypic resistance exhibited by the isolates was mainly contributed by these putatively mobilizable ARGs. The study gives genomic insights into the origins of putatively mobilizable ARGs in bacteria subjected to selection pressure.

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