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Antibiotic resistance characteristic and genes analysis of a marine water sourced *Klebsiella pneumoniae*

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ABSTRACT Objective: Both antibiotic resistant bacteria (ARBs) and antibiotic resistant genes (ARGs) are considered as one of the most dangerous environmental pollutants in the 21st century by the WHO. This study aims to understand the ARGs of *Klebsiella pneumoniae* (*K. pneumoniae*) with multiple drug resistance bacterium from the marine water collected from a beach at Sanya Bay, and to explore the antibiotic resistance mechanism of the *K. pneumoniae*, providing a basis for exploring the transfer of drug resistance genes of beach, and preventing and controlling the health risk of entertainment population. **Methods:** The sample of marine water were collected and screened by Mcconkey plate. The drug sensitive test was detected by Merieux VITEK2, The DNA was extracted and one strain of 16srDNA was sequenced and identified as *K. pneumoniae*. Whole-genome resequencing was performed using Illumina HiseqXten platform, and the obtained sequences were compared with NCBI blasting. The reference bacterium were multi-resistant *K. pneumoniae* HS11286. Plasmids were extracted and the resistant genes were identified. **Results:** The ARGs encoding protein was 117/4801 (identity > 40%) and the carrying rate was 2.436 9%. The identity of following ARGs of OKPB, sul1, rpoB, ef-tu, phoP, sul2, AAC(6)-ib-cr, QnrB, floR, aadA16 were more than 99%. The strain showed resistance to ampicillin, ticacillin/clavulanic acid and chloramphenicol, and was intermediate to ampicillin/sulbactam, compound sulfamethoxazole, ciprofloxacin, minocycline. Preliminary positioning showed that Qnrs, sul1, tetA, cat, QacE were carried on plasmid. **Conclusion:** The multiple drug resistant bacteria strain has a variety of different resistant phenotypes, some ARGs can be easily spread by plasmid. It probably will bring exposure risk to people for entertainment. Sensibility of some antibiotics were on the brink of resistance, It is necessary to tracking corresponding antibiotics pollution and strengthening monitoring of ARBs and mobile resistant elements of bacteria.

Keywords: Antibiotic resistant bacterium; Antibiotic resistant genes; *Klebsiella pneumoniae*; Marine water

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