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Commentary

PCR-Based Vector for Antibiotic Resistance

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DESCRIPTION

Antimicrobial Resistance (AMR) is an important health issue in the world. Unlike known genes, unknown genes are difficult to detect. To evaluate and predict, known and unknown resistance genes that are responsible for AMR should be identified and characterized. World Health Organization declared Antimicrobial Resistance is one of the most important health problems in the world and more than 7,50,000 people die because of AMR each year. It is predicted the number can reach 10 million in 2050 if necessary and effective steps are not taken to prevent AMR. The treatment options for infections with antimicrobial-resistant pathogens are decreasing due to the increase of newly emergent resistance genes and the spreading of resistant strains. One of the reasons for the spreading of AMR can be the usage of antibiotics for the treatment of infections in animals besides humans, even they are used as a food additive to promote the growth of livestock. They accumulated in the environment because of both prevalent usage and no disappears activity after usage. The antibiotic resistance genes can emerge naturally or in the presence of antibiotic pressure. However, antibiotic pressure in the environment accelerates the dissemination of them even the resistance genes occur naturally. Improvement of new and efficient techniques for detection of known/unknown antibiotic resistance genes from various environments is important to foresee the potency of antibiotic resistance problem and overcome this issue. It allows cloning of resistance genes at all orientations just by changing restriction enzymes for primers and fragmentation.

Investigation of antibiotic resistance genes was begun with the emergence of antibiotic-resistant strains in clinical isolates and insufficient treatment of infectious diseases. Phenotypic methods like antibiogram and microdilution and genotypic methods like PCR have been used for a long time. Phenotypic methods are not enough to detect antibiotic resistance caused by which gene and dominant resistance gene mechanism and it need a culture of microorganisms. Some genotypic methods like PCR cannot be used to detect unknown resistance genes and the presence of a part of the gene could not be clear evidence of antibiotic resistance. Cloning of antibiotic resistance genes is a more reliable method and it has been used to clone them from different sources by using cloning vector. Functional metagenomics is another molecular option for cloning antibiotic resistance genes from different sources. The disadvantages of the method are the presence of a resistance gene in the vector that prevents cloning of all resistance genes and obtaining of vector need efforts and significant cost.

In this commentary, we construct an extraordinary vector, is PCR based vector named as K vector and developed a cloning method. The constructed vector proved that PCR amplicon containing plasmid origin of replication sequence can enable cloning of antibiotic resistance genes. The ability of K fragment for resistance gene cloning from genomic DNA was tested and it was successful. The utility of K fragment for resistance gene cloning and functional metagenomics from different sources like wastewater, faeces, and the soil may be tested. The vector and method can contribute to the fight against antibiotic resistance problem by detecting, describing and characterizing them.

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