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Genomics & New Drug Discovery

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The widespread and excessive use of antibiotic was mainly responsible for the selective pressure that acts as a driving force for the development of antibiotic resistance. This was exemplified with nosocomial infections and resistant acquired infections. This problem has to be addressed and to find new drugs via the application of the new technologies especially genomics and proteomics [1].

The technology development in area of new drug discovery as a result of the microbial genome sequencing for unusual microorganisms (e.g. extremophilic microorganisms) may open avenues to new drug discovery and provide a great help for the treatment of serious diseases and to identifying novel molecular targets for high throughput screening. The high precision application of new molecular technologies recognized and the use of data-rich bioinformatics would strengthens the microbial biodiversity and in turn lead to an increase the natural product diversity [2]. This will ensure continuing role that microbial secondary metabolites may play in the new drug discovery to address the problem in the years ahead.

Molecular biologists have developed toolbox of techniques, both computational (bioinformatics) and experimental, to squeeze biological information from DNA sequences: this is functional genomics. To exploit opportunities for drug discovery arising from large-scale microbial genome sequencing projects, computational and bioinformatics' methods are required in the initial identification and selection of molecular targets, followed by a series of post-genome approaches [3,4] to validate and characterise the targets, devise screens and pursue structure-based drug design. Together, genomics and functional genomics provide a precise molecular blueprint of a cell or organism.

For example, Tuberculosis (TB) offers an attractive target for new antibiotics because of the huge numbers of sufferers and the long period of treatment compared with other bacterial infections. On the other hand, *Mycobacterium* genomics promises came to illuminate the basis for its pathogenicity pattern and how to control it.

The decline in discovery of natural products does not imply that all the useful compounds have been found. It will be a challenge to bring some of the untouched biosynthetic potential revealed by genome sequencing to light. The Filamentous soil bacteria of the genus *Streptomyces* are remarkable, and merit special consideration with regard to the metabolic differentiation. The way they are reflected in their biosynthetic potential to produce novel, bioactive compounds that could significantly influence strategies for search and discovery, screening, and bioprocess development for a new drug discovery [1,5]. To extend whole-genome studies to more streptomycetes would reveal these relationships in a comprehensive way, which would enable validation of current methodologies (from 16S rDNA phylogenies to DNA-DNA pairing) and lead to new understanding of speciation, phylogenetic relationships, and genome function in secondary metabolism [6,7].

The availability of a variety of molecular technologies helped to assess genetic diversity at the DNA level. Interestingly, the current extraction and analysis of DNA directly from the environment confirms the presence of a large number of microorganisms that are not identified using the conventional cultivation methods. Recently, several start-up industries have been formed which aim to isolate secondary metabolic gene-clusters from these uncultivable organisms.

The combination of microbial resistance and lack of progress in the discovery of novel drugs may necessitates a reassessment of future research and development approaches to antibiotic discovery [8,9]. The only realistic solution is to find new research avenues to identify novel, or unexploited, bacterial gene products that can serve as targets for antibiotics and kill bacteria by completely different mechanisms from existing drugs [10-12]. The ability to search for novel bacterial drug targets, or validate known potential targets, has been revolutionized by the advent of total genome sequence analysis and associated genetic techniques, which are rapidly advancing the knowledge of numerous infectious agents.

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