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Whole Genome Sequence and Multidrug Resistant in Fungi

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Abstract

The comparative genomic study of fungal pathogens allows the detection of genes and variations linked to virulence and antibiotic resistance. The methods, tools, and developments used to study clinically significant fungal pathogens utilizing whole genome sequencing are discussed in this article. It provides the resolution needed to compare closely related strains like in outbreak analysis or to compare multidrug resistant isolate from the same host over time. In addition to basic research, genomic analysis of fungal pathogens can have a positive impact on diagnostics. New metagenomic techniques will enable direct analysis of complex data as sequencing scales rise.

Keywords: Whole Genome Sequencing; Multidrug Resistant; Pathogenic Fungi

Introduction

During the early 1940s, penicillin was developed as the first widely used antibiotic targeted against microorganisms as a modern medicine. Managing infections caused by pathogenic fungi is difficult because of antibiotic resistance. Mutant fungi are also easily isolated, both in the laboratory and in the clinic, that are resistant to a variety of antibiotics beyond those initially used as a treatment [1].

The diagnosis and treatment of systemic fungal infections can be challenging for clinicians. It is a broad concept that describes the failure of a fungal infection to respond to antifungal treatment [2]. There is a problem of multidrug resistance in chemotherapy for bacterial infections as well as cancer treatments. A limited number of antifungal compounds contribute to fungus drug resistance [1,2].

Whole Genome Sequencing (WGS)

In order to study fungal pathogens, whole genome sequencing is an invaluable tool. Genomic studies of human pathogenic fungal species have revealed the repertoire of proteins that contribute to host interactions by providing a comprehensive picture of gene content and functional potential [3]. High-resolution whole genome sequencing promises to revolutionize surveillance and diagnosis of infectious diseases [4]. Not only does the genome of provide genetic resources for comparative genomics, evolutionary studies, and alleviating the bottlenecks in molecular breeding like in edible mushroom [5].

The final determinant of characteristics such virulent as well as antibiotic resistance is genetic material. In order to identify the genetic components of these features, it appears to be promising to analyze genome sequences of species or isolates with different virulence or resistance profiles. The genomes of fungal pathogens are really quite dynamic, with significant differences across and within species [6,7].

The genetic changes have been associated with rapid adaptation to the environment, which is likely what led to the evolution of viral and antifungal resistance [8]. Identifying Single Nucleotide Polymorphisms (SNPs) and small insertions/deletions (INDELs) between specimens of a particular fungal pathogen strain is the primary focus of research examining the relationship between genetic variants and treatment resistance or virulence. These strains

could represent various population isolates [9].

Regarding analyzing fungal infections' genomes, there are commonly two main methods. First one involves a genome assembly de novo for example, for a species that has not yet sequenced and assembled. The other method, known as re-sequencing, employs sequence read alignment to find differences between a sequenced isolate and an existing reference assembly [10].

In medical mycology laboratory, molecular technologies of detection and identification have developed. Through to create molecular tools that can detect and identify various pathogens, in addition to the occurrence of mutations associated to antifungal resistance high-quality genome data is therefore required [11].

Outbreaks and Emerging Species

A huge outbreak of infection has been attributed to a variety of fungus species. Contrasting to the dominating species that lead to human pathogens, several outbreaks have been driven by pathogens organisms that are not frequently the source of infection; as a result some of these strains have not been extensively investigated or sequenced. In these situations, the main objective of WGS has been to provide a reference genome that can be used for subsequent genomic or transcriptome investigations of pathogenesis. The origin and patterns of transmission of an outbreak can be traced by comparing the genomes of clinical samples with the environmental isolates from populations of these fungi [12].

Among the fungi isolates, Candida auris can readily spread in health care settings, resulting in outbreaks. Its ability to colonies skin and body sites. It causes invasive infections with high crude mortality and is often multidrug resistant, with some isolates showing resistance to all three major classes of antifungals. Candida auris has become one of the most dangerous yeasts on earth [13].

Candida auris isolates from specific geographical regions are highly similar according to genomic analysis of resistance to drugs. Candida auris is an emerging, multidrug resistant fungus causing fungemiain humans. The findings suggest that its actual global distribution remains obscure due to the fact that current clinical diagnosis methods misidentified it as Candidahaemulonii [6].

Evolution of fungi in patients

Patients who have chronic fungal infections exhibit genomic modifications and survival adaptations. The whole genome re-sequencing technique used to see how C. albicans isolates alter after infection. It was observed that during clinic transfer, isolates picked up additional mutations, particularly those connected to host adaptability as well as genome regions showing loss of heterozygosis during passage which contain genes that are related to drug resistance [14,15].

Antifungal Resistance

Genome sequence can identify known antibiotic resistance mutations, sometimes providing an indication of whether specific medications will control the infection. In the identification of point mutations in certain therapeutic targets which strongly linked with resistance, whole genome variants could be searched. For instance, particular mutations in the azole drugs target [16]. Over expression of genes that encode multi drug efflux pump lead to drug resistance, which is widely used antifungal agent fluconazole and other toxic substances in the fungal pathogen *Candida albicans* [17].

Conclusion

Microbial Genome sequencing is a method that is being used, becoming more frequently, to examine human fungi infections in clinical laboratory. The available genome sequence data allows for the examination of the microevolution of isolates.

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