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GENOMIC STUDY OF SOME THERAPEUTIC FUNGI IN GAYA DISTRICT, BIHAR, INDIA

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ABSTRACT

The present paper deals with genomic study in some therapeutic fungi in Gaya District. Fungal genomes are among the smallest genomes of eukaryotes. Some therapeutic fungus i.e *Aspergillus fumigatum,Candida albicans, and Cryptococcus neoformans* were collected in addjoinig area of Gaya and Bodh Gaya. Fungal sample 5 mL of collection solution was poured on the culture plate, and the fungal mycelium was pelleted in a microcentrifuge tube by centrifugation at 14,000 rpm for 1 min. the supernatant was transferred to a fresh microcentrifuge tube with equal volume of ethanol and vortexed. The lysate was placed in the Spin column and centrifuged at 10,000 rpm for 1 min followed by two washes with 500 µL of wash buffer. The DNA was eluted in 100 µL of elution buffer by spinning at 10,000 rpm for 2 min and was stored at −20 °C till further processing. approximate base pair (Mb)size of band on gel electroforosis in fungus *Aspergillus fumigatum,* no of chromosome 8 and30Mb, *Candida albicans* no of chromosome 8 and 16Mb and *Cryptococcus neoformans* no of chromosome 14 and 19Mb. High levels of fungal DNA *with candida albicans* but low levels of fungal DNA with *Aspergillus fumigagatum.*

Kew words: Genomics,Ethanol *A. fumigatum,C albicans, and C neoformans.*

INRODUCTION

Genomics is an interdisciplinary field of biology focusing on the structure, function, evolution, mapping, and editing of genomes. A genome is an organism's complete set of DNA, including all of its genes as well as its hierarchical, three-dimensional structural configuration. In contrast to genetics, which refers to the study of *individual* genes and their roles in inheritance, genomics aims at the collective characterization and quantification of *all* of an organism's genes, their interrelations and influence on the organism**.**

Fungal genomes are among the smallest genomes of eukaryotes. The sizes of fungal genomes range from less than 10 Mbp to hundreds of Mbp. The average genome size is approximately 37 Mbp in Ascomycota, 47 Mbp in Basidiomycota and 75 Mbp in Oomycota. Due to their compact size fungal genomes can be sequenced with less resources than most other eukaryotic genomes and are thus important models for research. Some fungi exist as stable haploid, diploid, or polyploid cells, others change ploidy in response to environmental conditions and aneuploidy is also observed in novel environments or during periods of stress.

Genomics also involves the sequencing and analysis of genomes through uses of high throughput DNA sequencing and bioinformatics to assemble and analyze the function and structure of entire genomes. Advances in genomics have triggered a revolution in discovery-based research and systems biology to facilitate understanding of even the most complex biological systems such as the brain**.** Fungal genomics that has greatly expanded our view of the genetic and physiological diversity of these organisms. We provide here an overview of available fungal genomes and highlight some of the biological insights that have been derived through their analysis.

MATERIAL AND METHODS

Genomic sample 5 mL of collection solution was poured on the culture plate, and the fungal mycelium was pelleted in a microcentrifuge tube by centrifugation at 14,000 rpm for 1 min. Two hundred fifty microlitres of Resuspension Solution A, *200 units of lyticase* enzyme and 150 µL of proteinase K were added to the cell pellet and incubated for 45 min at 37 °C. Five hundred microlitres of lysis buffer was added, and the mixture was vortexed in a bead tube on a vortexer for 10 min at maximum speed followed by incubation at 90 °C for 2 h with intermittent vortexing. *The bead tube was sonicated for 20 min in an ultrasonicator water bath* .After centrifugation for 2 min at 14,000 rpm, the supernatant was transferred to a fresh microcentrifuge tube with equal volume of ethanol and vortexed. The lysate was placed in the Spin column and centrifuged at 10,000 rpm for 1 min followed by two washes with 500 µL of wash buffer. The DNA was eluted in 100 µL of elution buffer by spinning at 10,000 rpm for 2 min and was stored at −20 °C till further processing. The extracted DNA was run on a 1% gel to assess the quality . PCR was carried out to amplify the fungal DNA using forward primer. The amplified products were electrophoresed in a 2% agarose gel and visualized on an Ultra Violet transilluminator using a 100 bp molecular marker for marking of approximate base pair sizes.

RESULT AND DISCUSSION

Generally, obtaining DNA from fungi is more difficult than from bacteria or from mammalian cells as the fungal cell wall is tough to break using the conventional extraction methods. This is attributed to fungi possessing a thick and complex cell wall resulting in poor release of DNA. Poor efficiency of DNA extraction, low numbers of fungal cells. Therefore, in addition to using specific primers and probes, suitable for the detection of low level of fungal DNA, it is extremely important to use the most efficient method of DNA extraction. Additional procedures leading to disruption of the fungal cell wall .

Our result reveled that approximate base pair (Mb)size of band on gel electroforosis in fungus *Aspergillus fumigatum,* no of chromosome 8 and30Mb, *Candida albicans* no of chromosome 8 and 16Mb and *Cryptococcus neoformans* no of chromosome 14 and 19Mb. High levels of fungal DNA *with candida albicans* but low levels of fungal DNA with *Aspergillus fumigagatum*.

Table :Genomic study of some fungus.

S N	Fungus organism	Chromosome no	Approximate base pair (Mb)size of band on gel electroforosis
1	*Aspergillus fumigatum*	8	30
2	*Candida albicans*	8	16
3	*Cryptococcus neoformans*	14	19

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