



GENETIC CHARACTERIZATION OF FUNGI ISOLATED

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Abstract

A multistate fungal meningitis outbreak started in September of 2012 which spread in 20 states of the United States. The outbreak has been fatal so far, and has affected 751 individuals with 64 deaths among those who received contaminated spinal injections manufactured by a Compounding Center located in Massachusetts. In a preliminary study, Food and Drug Administration (FDA) investigated the outbreak in collaboration with Centers for Disease Control and Prevention (CDC), state and local health departments, and identified four fungal and several bacterial contaminations in the recalled unopened injection vials.



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INTRODUCTION:

A multistate fungal meningitis outbreak started in mid-September of 2012. This outbreak affected individuals who had received contaminated injections (that included betamethasone, cardioplegia, and triamcinolone solutions), manufactured and distributed by a Compounding Center located in Massachusetts to outpatient facilities in 20 states of the United States. The firm voluntarily terminated all operations, surrendered its license, and announced a recall of all their products on October 3, 2012. In the beginning, FDA investigated this outbreak in collaboration with U.S. Centers for Disease Control and Prevention (CDC), state and local health departments, and analyzed the unopened vials of spinal injections [8-12]. Four fungal (including *Aspergillus tubingensis*, *Aspergillus fumigatus*, *Cladosporium* sp., and *Penicillium* sp.) and several bacterial contaminations (*Bacillus circulans*, *Bacillus firmus*, *Bacillus flexus*, *Bacillus halmapalus/horikoshii*, *Bacillus idriensis*, *Bacillus lentus*, *Bacillus niabensis*, *Bacillus niacini*, *Bacillus nealsonii*, *Bacillus pumilus*, *Bacillus simplex*, *Bacillus subtilis* group, *Brevibacillus choshinensis*, *Kocuriarosea*, *Lysinibacillus* sp., *Paenibacillus barengoltzii/timonensis*, *Paenibacillus pabuli/amolyticus*.) were identified in the recalled unopened vials shipped by this Compounding Center [2-4]. Later, while analyzing the tissue and human fluids of patients infected with above contaminated injections CDC confirmed *Exserohilum rostratum* as the predominant fungal infection in this outbreak, and identified 22 additional fungal species. Furthermore, CDC was able to isolate four more fungal species (*Cladosporium cladosporioides*, *Exserohilum rostratum*, *Rhodotorula aryngris*

and *Rhizopusstolonifer*) from some of the unopened vials examined. The outbreak was deadly and affected a total of 751 individuals resulting in 64 deaths, as of October 23, 2013 [4-7].

STATEMENT OF RESEARCH ARGUMENT:

This follow-up study was carried out to assess DNA sequencing of the ITS1 region of rRNA gene for rapid identification of fungal pathogens during public health outbreak investigations. A total of 26 environmental swabs were collected from several locations at the manufacturing premises of the Compounding Center known to have caused the outbreak. The swab samples were initially examined by conventional microbiologic protocols and a wide range of fungal species were recovered. Species-identification of these microorganisms was accomplished by nucleotide sequencing of ITS1 region of rRNA gene. Analysis of data confirmed 14 additional fungal species in the swabs analyzed.

OBJECTIVE OF THE STUDY:

- To study the Genetic Diversity of Recovered Fungal Species from Environmental.
- To study the Public Health Significance of the Presence of Fungi in Environment.
- To study the Population Genetics of Fungi.
- To study the High genetic variability and low local diversity in a population of arbuscular mycorrhizal fungi.

CONCLUSION:

Sequence characterization of the ITS1 locus can be used for the detection and differentiation of fungi from the environmental swab samples. This communication also reports for the first time the presence of 14 indicator fungal species isolated from the environmental swabs collected from the Compounding Center who previously manufactured the methylprednisolone injections contaminated with molds. DNA sequencing of the ITS1 region of rRNA gene can be used for rapid identification of fungal pathogens during outbreak investigations of public health importance.

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