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An uncommon case of subcutaneous basidioleiomycosis in a young adult — a case report

Athi Ekumakoe, Johnny Aye, David Livingstone, Mmemy George, Shashikala Nair
Pondicherry Institute of Medical sciences, Pondicherry, India

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Basidioleiomycosis is an uncommon fungal infection of the subcutaneous tissue of the lower limbs caused by Basidiole- ium ranarum. It presents as discrete granulomatous inflammation of the skin and subcutaneous tissue affecting the immature component young adults. We report a 13-year-old male who presented with soft tissue swelling of the left lower limb for the past 4 months. He had consulted a private hospital previously where he underwent incision and drainage and was prescribed multiple antibiotics. As there were no resolution of the symptoms, he presented to us with swelling of the thigh and 1 x 1 cm size non-healing ulcer over the posterior aspect at the site of incision with inflammation of the surrounding tissue. On examination, the surrounding tissues also showed induration and warmth. The routine blood investigations were normal and serology for HIV was also negative. The pus aspirate was cultured in Sabouraud’s Dextrose agar and incubated at 25°C showed growth of aspergillus, glabrata, and aspergillus, raciborskii, usually found in culture. Basidioleiomycosis is caused by the inhalation of fungal spores, especially in patients with suppressed immune systems. Basidioleiomycosis affected human populations after COVID-19. Accord- ing to searches, many cases of basidioleiomycosis to COVID-19 has been widely reported from Europe, and India. Of course, it seems that the underlying disease and most importantly uncontrolled diabetes or immunocompromised disease are the conditions for the development of black fungi. In one study, breast cancer patients receiving chemotherapy for breast cancer showed 10/23 tissue samples of malignant melanin pigment (necrotic melanin pigment) and 1/23 tissue samples had 10/23 soft tissue samples of COVID-19. The effective factors and challenges to overcome this black mold infection are.

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The effect of COVID-19 and immunosuppressive drugs on the spread of mucormycosis

Maryam Esfandi
Iran University of Medical science, Tehran, Iran

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Mucormycosis is a serious but rare opportunistic fungal infection that spreads rapidly, so prompt diagnosis and treatment are essential to prevent high morbidity rates and complications. Mucormycosis is caused by the inhalation of fungal spores, especially in patients with suppressed immune systems. Mucormycosis affected human populations after COVID-19. According to searches, many cases of mucormycosis to COVID-19 has been widely reported from Europe, and India. Of course, it seems that the underlying disease and most importantly uncontrolled diabetes or immunocompromised disease are the conditions for the development of black fungi. In one study, breast cancer patients receiving chemotherapy for breast cancer showed 10/23 tissue samples of malignant melanin pigment (necrotic melanin pigment) and 1/23 tissue samples had 10/23 soft tissue samples of COVID-19. The effective factors and challenges to overcome this black mold infection are.

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Investigating the link between pleomorphism and virulence in Cryptococcus

Kenya Fernandez, James Fraser, Dave Carter
University Of Sydney, Sydney, Australia

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Objective: Fungal pathogen Cryptococcus neoformans and C. gattii are responsible for hundreds of thousands of annual deaths in immunocompromised individuals. Considerable phenotypic variation is exhibited by strains in response to stress encountered during host infection, including increased capsule and cell size, the release of cell capsules, and the production of granules (1–15 μm) and irregular cells. We aimed to investigate whether the production of these morphological variants is associated with virulence in two strains of rats. The first is a collection of diverse clinical isolates obtained from HIV/AIDS patients in Botswana with accompanying clinical data. The second is a collection of lines derived from the C. neoformans type strain H99 with high genetic similarity but differing levels of virulence. Some lines in this set possess a mutation in SGR29, which encodes a component of the SAGA histone acetyltransferase complex that has previously been implicated in the hyper-variation of C. neoformans. Methods: Isolates were cultured under conditions that simulate stress encountered in vitro (DMM, 3% CO2, 37°C) as these are known to enhance capsule production and induce cell size changes. Cells were concomitant with hila, vacuolar, and vacuolar, and phenotypes were scored. For clinical isolates, MLSF analysis was performed to determine their virulence. For H99 strains, Galleria mellonella larval infection assays, growth curves, and antifungal susceptibility testing was performed to determine their virulence and growth profiles. Serial Black frost and regular scanning electron microscopy were used to investigate the internal morphology of the giant, micro, and irregular cells to confirm that they possess attributes of functional cells. Results: Substantial phenotypic variation was seen across both collections. In the clinical strain set, phenotypic variants fell into two groups associated with differing symptoms. The production of ‘large’ phenotypes was associated with a higher C24 count and was negatively correlated with antifungal pressure indicators, suggesting that these are induced in early-stage infection. Small ‘small’ phenotypes were associated with lower C24 counts, negatively correlated with monopodial inflammation indicators, and positively correlated with intracranial pressure indicators, suggesting that they are produced later during infection and may promote proliferation and dissemination. Isolates possessing giant cells, microcells, and cell capsule were rare, but strikingly, they were associated with patient death. In the H99 set, strains from hyperparasite lines had larger average capsule size, larger capsule cell size, and increased production of microcaps and cell capsule. Deletion of SGR29 in an intermediate virulence line substantially increased its production of microcaps and released capsule, consistent with a switch to hyperparasitism. SGR29 loss-of-function mutations were subsequently identified in clinical isolates and were found to be significantly correlated with patient death. Expansion of a TA repeat in the second inversion of SGR29 in clinical isolates was positively correlated with cell and capsule size, suggesting an affect on SGR29 function. Conclusion: Our results extend the evidence for a link between pleomorphism and virulence, with a likely role for epigenetic mechanisms mediated by SAGA-induced histone acetylation.