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Poster presentation

Fungal volatile fingerprints and machine learning: potential of discriminating and classifying dermatophyte species

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Background

Dermatophytes are responsible for one of the most common human fungal infectious diseases in the world – a leading cause of hair, nail and skin infections in humans known as tinea or ringworm. Conventional laboratory diagnoses comprising microscopy, *in vitro* culture and biochemical tests are time consuming (over three weeks), tedious and require skilled personnel. Molecular diagnostic approaches such as polymerase chain reaction (PCR), PCR-fingerprinting, restriction fragment length polymorphism (RFLP) and restriction enzyme techniques have shown improvements but are neither very cost effective nor feasible for routine clinical testing.

Materials and methods

We have investigated the volatile fingerprints of dermatophyte species using electronic nose based sensor array systems and multivariate statistics. Four *Trichophyton* species (*T. mentagrophytes*, *T. rubrum*, *T. verrucosum* and *T. violaceum*) were grown *in vitro* on agar media as well as in broth culture.

Results

These studies demonstrated that (a) successful differentiation was possible after 96 hours growth using a metal oxide based-sensor system and (b) for a single species the sensitivity of detection was log 3 (10^3 spores ml^{-1}) within 96 hours using the volatile fingerprints[1]. PCA and Cluster analyses techniques were used to extract sensor information for maximising discrimination. This is currently in the process of being utilised for developing the appropriate neural networks for later use with clinical samples as a classifier. Work is also in progress on discrimination between the different sources of the dermatophyte species e.g. human and dog and intra-species variations which would enhance the classification ability of the neural network.

Conclusion

This research is the first to demonstrate that volatile fingerprints can be used for rapid diagnoses of different dermatophytes. This approach could have potential for rapid identification of patient samples reducing significantly the confirmation time. It would then ensure that appropriate treatment is administered for the different fungal species, rather than prolonging it by which time the patient's condition might have considerably altered. Integration of such technologies with bioinformatics approaches will result in a significant enhancement in patient care by faster discovery of diseases and infections.

References

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