Itching for Success - Finding New Ways to Tackle House Dust Mite Allergy

Researchers from airmid healthgroup and Maynooth University Department of Biology have published the successful genome sequencing and investigation of the proteome and allergenome of the European house dust mite (Dermatophagoides pteronyssinus).

DUBLIN (PRWEB) June 03, 2019 -- House dust mites are a significant source of indoor allergens worldwide and contribute to the exacerbation of asthma, allergic rhinitis and atopic dermatitis. They are known to contain allergens, proteins that can elicit allergic illnesses in susceptible individuals. Previous studies have shown that approximately 50% of all European homes contain dust mites with approximately 10% of the total population experiencing an allergic response in their presence. Now researchers from Maynooth University Department of Biology and airmid healthgroup have published the successful genome sequencing and investigation of the proteome and allergenome of the European house dust mite (Dermatophagoides pteronyssinus). Supervised by Professor Sean Doyle, the lead Scientist on the project, Rose Waldron, is a PhD student funded by the Irish Research Council Enterprise Partnership Scheme, and airmid healthgroup.

In collaboration with the Genome Evolution laboratory in Maynooth University led by Dr. David Fitzpatrick the team assembled and annotated the genome of the dust mite, and found that it contains 12,530 protein coding genes. Furthermore, using powerful computational approaches they predict that almost 3% of the encoded proteins could potentially cause allergic responses in humans. Specifically, the authors confirmed the presence of 37 previously characterised mite allergens known to cause severe allergic responses. Interestingly, the authors also found the dust mite contains over 1,000 so-called “orphan” genes

Dr. Fitzpatrick explains, “Orphan genes are those that are specific to a particular species and not located in the genomes of other closely related species. Therefore, as well as containing the genes that encode for known allergens, the European dust mite also contains an arsenal of over 1,000 genes whose definite function is currently unknown. Some of these orphan genes may be important allergens themselves.”

The research team also developed a novel protein mass spectrometry method to detect proteins located in house dust samples and found that orphan proteins are highly abundant, including enzymes that may be involved in dust mite growth and survival.

Dr. Natasha Gordon from airmid healthgroup predicts that, “These data may have clinical applications in the development of new allergen-specific tests and immunotherapy that mimics natural exposure, and airmid is really excited by these findings.”

Using machine learning and Artificial Intelligence, the authors also identified genes in the dust mite genome that aid desiccation survival and allow organisms to persist in the environment. The research team thinks that interference with these may represent a way to tackle dust mite infestations, finding seven desiccation resistance proteins.

Ms. Rose Waldron explains, “The computational prediction that the European house dust mite contains desiccation resistance genes was interesting for us as it explains how the mite survives in dust which is an anhydrobiotic (limited water) environment. The real strength of our study was the fact we could experimentally prove that these genes were translated into resistance proteins, thus validating our gene predictions.”
The availability of the European dust mite genome also allowed the authors to undertake an evolutionary analysis of the origin and relationships amongst dust mites from different geographical regions. The study has shown that the European dust mite is more closely related to its African counterpart (Euroglyphus maynei), than to its American counterpart (Dermatophagoides farinae). Their paper is titled ‘Proteome and allergenome of the European house dust mite Dermatophagoides pteronyssinus’ and is freely available online in the peer-reviewed journal PLOS ONE. Mass spectrometry facilities were funded by Science Foundation Ireland and computational facilities were provided by the DJEI/DES/SFI/HEA Irish Centre for High-End Computing (ICHEC).

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