

Exploring the repertoire of cross-reactive allergens among *Aspergillus fumigatus* and mites: an in-silico approach.

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**Background:** *Aspergillus fumigatus* is an important allergenic source to sensitization to fungus, it has been involved in autoreactivity on dermatitis atopic. Several allergens have been characterized in this source, however, cross reactivity with others important allergenic source different to fungi has not been explored. Here, we advanced in identification of potential cross-reactive allergens with mite specie, *Dermatophagoides pteronyssinus*. **Methods:** Allergen aminoacid sequences from *A. fumigatus* reported in Allergome database, were used as input to search homologous on *D. pteronyssinus* proteome. Later, B cell epitope prediction was performed using Ellipro server, with 3D models of allergens reported in *A. fumigatus* modeled based on homology. Epitope conserved between *A. fumigatus* and *D. pteronyssinus* were visualized on 3D models using PyMOL. **Results:** In total, thirteen allergens from *A. fumigatus* showed some identity level with *D. pteronyssinus*. Some relevant allergens from *A. fumigatus* such as Superoxide dismutase Mn and Thioredoxin share moderate identity level (52 and 43%, correspondly) with proteins in *D. pteronyssinus*. All models exhibited good quality to be used as input in epitope prediction. Ellipro predicted several B cell epitopes highly conserved between *A. fumigatus* and mites. Evolutionary analysis suggests that these epitopes could be involved in cross reactivity of *A. fumigatus* with other allergenic sources. **Conclusion:** These findings revealed that *A. fumigatus* and *D. pteronyssinus* shared cross reactivity allergens, that could exacerbate symptoms in sensitized subjects to *Aspergillus* or mites. Inhibition assays are needed to determine cross reactivity level share between these important allergenic sources.