Human pathogen Fusarium oxysporum α-mating pheromone: ten amino acids code for structure and function

P01-13

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The ascomycete fungui *Fusarium oxysporum* is a highly destructive plant pathogen and an emerging human pathogen. During sexual development, ascomycete fungi produce two types of peptide pheromones: a and α. The function of a-pheromones seem to be highly conserved among ascomycetes; however, until very recently (1) no structural information have been described at atomic detail.

To perform their function as sexual chemoattractants, α-pheromones should be sensed by membrane receptors Ste2 and Ste3. In order to understand the mechanisms of interaction and activation of its receptors, structural information regarding these pheromones is essential.

Solution NMR was employed to characterize the structures of the α-pheromone peptide in different environments. In all conditions, α-pheromone adopts a defined secondary structure. The central residues are crucial to define the structure in solution, the β-turn centered in Gly 6 and Gln 7 is a hallmark of the α-pheromone structure.

Atomic interactions with membrane mimetics have ALSO been identified by NOE data. DPC and Gemini surfactants were employed as suitable membrane mimetic, as they form appropriate micelles for NMR studies.

The large proportion of Trp (3/10 residues) play an important role in the interaction with micelles, thus their position in sequence is critical for their specificity. By NMR we have quantified the intermolecular interaction at atomic level. Based on the NMR results, a 3D model of the interaction between pheromones and micelles is proposed.

Finally, the presence of two Cys residues adds the possibility of being reduced or oxidized. We studied changes in the interaction with membranes associated to this redox process that can be important for the recognition of its receptors.

1) S. Vitale, A. Partida-Hanon, S. Serrano, A. Martínez del Pozo, A. Di Pietro, D. Turrà, and M. Bruix. J. Biol. Chem. 292, 3591-3602 (2017).