Same action from different scaffolds

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Motivation

Antimicrobial proteins (AMPs) are the main defence weapons adopted by innate immunity against pathogens. In order to ascertain any possible evolutionary relationship we analyzed the functional features of four antimicrobial proteins belonging to both plant and animal kingdoms. Puroindoline A (PINA) and puroindoline B (PINB) are two AMPs isolated from wheat seed. They exert strong antimicrobial activity in vitro against plant and animal pathogens (Capparelli et al., 2006; Capparelli et al., 2005; Dubreil et al., 1998). Puroindolines are able to permeabilize biological membranes in a voltage-dependent manner and the permeabilization mechanism is due to the formation of selective ion channels in target membranes (Charnet et al., 2003). Lysozyme (Lys) is a component of both phagocytic and secretory granules of neutrophils and is also produced by monocytes, macrophages, and epithelial cells. Lysozyme is an enzyme directed against bacterial peptidoglycan. Lysozyme is highly active against many Gram-positive species, but it appears to be ineffective against Gram-negative bacteria (Ellison et al., 1991) unless potentiated by certain cofactors (lactoferrin, antibody-complement complexes, or hydrogen peroxide and ascorbic acid). Lactoferrin (Lf) is an iron-binding protein first recognized in milk and then in other human epithelial secretions and barrier fluids. Lactoferrin inhibits microbial growth by sequestering iron essential for microbial respiration (Arnold et al., 1977). It can also be directly microbicidal (Arnold et al., 1982), an activity that is concentrated in its N- terminal cationic fragment 'lactoferricin'.

We report on a comparative analysis of functionality of puroindolines, lysozyme and lactoferrin and on the related bioinformatic analysis of their structural properties.

Methods

A preliminary multiple sequence alignment was obtained on the four amino acid sequences using ClustalW. Domains, families and functional sites were considered on each protein sequence according to the results obtained using the InterPro database.

Results

The experimental functional analysis of puroindolines, lysozyme and lactoferrin revealed a common behavior based on their similar biological action. A preliminary bioinformatic analysis based on multiple sequence alignment did not highlight clear sequence conservation in the four sequences. Therefore we propose to investigate the structural relationships among the four antimicrobials by a comparative functional analysis of protein domains.

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