

original article

Putative antimicrobial oligopeptides
in grape *Vitis vinifera*Alexander A. Zamyatnin^{1,2}¹ Department of Informatics, Santa Maria Technical University, Valparaiso, Chile² Computer Biochemistry Group, A.N. Bach Institute of Biochemistry, Russian Academy of Sciences, Moscow, Russian Federation**ABSTRACT****Introduction**

Antimicrobial peptides play important role in the innate defense system of plants. Information on more than 200 different plant antimicrobial oligopeptide structures is available today. One only grape antimicrobial oligopeptide has been characterized among thousands grape uncharacterized proteins.

Aim of the study - Methods

This is a structural-functional study of grape *Vitis vinifera* protein sequences as putative precursors of oligopeptides. These structures were compared with oligopeptides of other plants. A special method of computer analysis was developed. The data of Swiss-Prot/TrEMBL database containing primary structures of grape proteins, EROP-Moscow (Endogenous Regulatory OligoPeptides) database containing information on structure and functions of plant oligopeptides, and specially created computer programs were used.

Results

Eleven new structures of putative antimicrobial oligopeptides were predicted as a result. Their similarity with other plant primary structures was from 39.5 to 95.7%. Most of them were antimicrobial agents inhibiting the growth of numerous species of bacteria and fungi. But several structural families showed that some of them have been characterized as toxins or enzyme inhibitors. Also, fifteen grape protein structure sites were found homologues to known regulatory oligopeptides elucidated in other plant species.

Conclusions

It has been shown that grape could contain putative regulatory oligopeptides possessing functions of antibacterial and antifungal agents, toxins, and enzyme inhibitors.

Keywords: *Vitis Vinifera*, Oligopeptides, Sequence Alignment, Oligonucleotide Array, Numerical Analysis (Computer-Assisted), EROP-Moscow oligopeptide database (Endogenous Regulatory OligoPeptides).

INTRODUCTION

It is known that natural oligopeptides may regulate nearly all vital processes.^{1,2} The chemical structure of nearly 7000 oligopeptides from more than 1400 organisms representing all the biological kingdoms³ have been identified today. They possess a wide spectrum of biological activity. More than 600 plant oligopeptides with different types of functional activity have been described for many plants earlier. One only grape oligopeptide with antimicrobial function was extracted and characterized before⁴ whereas information on numerous grape uncharacterized proteins has to be found in public protein databases.

Since antimicrobial peptides play important role in the innate defense system of plants⁵ and represent a relatively unexplored source of antimicrobial peptides of biotechnological potential⁶, it is necessary to obtain more information on their structures and functions. The aim of the current study is the identification of new antimicrobial oligopeptides with the computer structural-functional study of grape *Vitis vinifera* protein sequences.

METHODS

A special method of computer analysis was developed. The data of Swiss-Prot/TrEMBL database containing primary structures of grape proteins, EROP-Moscow (Endogenous Regulatory OligoPeptides) database³ containing information on structure and functions of plant oligopeptides, and specially created computer programs were used. To date, Swiss Prot-TrEMBL database contained more than 7 million entries and EROP-Moscow contained information on structure and functions of 7,393 natural oligopeptides not exceeding 50 amino acid residues.⁷ In total 54,390 SwissProt-TrEMBL grape protein sequences were selected and compared with primary structures of 220 EROP-Moscow antimicrobial agents of 648 plant oligopeptides with criterion of more than 30% identity in the amino acid residue sequences.

RESULTS

This method revealed several new potentially active regulatory oligopeptide sequences (Table 1) after alignment procedure. Fifteen grape protein structure sites were found (I-XV) homologues to known regulatory oligopeptides elucidated in other plant species (from 1 to 17). They belong to 4 structural families. Structures and functions of oligopeptides were

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