LIST OF SYMBOLS AND ABBREVIATIONS

Symbols	Name
A_{600nm}	Absorbance at 600 nm
N_i	The number of trials for experiment
I	i designed at their assigned level
U	The experiment number
Y	Trial number
L_8, L_{27}	Number of trial experiment in Taguchi DOE
$Y_{p/x}$	Biochemical yield coefficient, product formed per unit mass of cell biomass
$Y_{x/s}$	Biochemical yield coefficient, cell biomass formed per unit mass of substrate consumed
$Y_{p/s}$	Biochemical yield coefficient, product formed per unit mass of substrate consumed
K	Mycelial branching level parameter
N_t	Number of hyphal tips
N_s	Number of hyphal segments
L_t , L_{av}	Total hyphal length, average hyphal length
G	Hyphal growth unit
X_c	Critical biomass concentration
E	Mean hyphal extension rate
μ_x , μ	specific growth rate of the mycelium, microscopic and macroscopic,
X	Cell biomass
S	Substrate concentration
K_s	Substrate saturation constant

K_i	Inhibition constant
μ_m	Maximum specific growth rate
X_m	Maximum cell biomass concentration
Q_P	Specific rate of product formation

Abbreviations	**Name**
kDa	Kilo-Dalton
AFP	Antifungal protein
Glc-NAc	α-1,4-linked *N*-acetyl glucosamine
ICU	Intensive care unit
AIDS	Acquired immune-deficiency syndrome
OFAT	One factor at a time
C/N	Carbon to nitrogen ratio
CSL	Corn steep liquor
PP	Proteose peptone
MTCC	Microbial type culture collection
NCIM	National collection of industrial microorganism
DOE	Design of experiment
OA	Orthogonal array
MIC	Minimum inhibitory concentration
SEM	scanning electron microscopy
AFM	atomic force microscopy
SDS-PAGE	Sodium dodecyl-sulfate-polyacryl amide gel electrophoresis
ESI-MS	Electron spray ionization-Mass spectrometry
FTIR	Fourier transform infrared spectroscopy
MALDI-MS	Matrix assisted laser desorption/ionization-Mass spectrometry

TOF	Time of flight
Rpm	Revolution per minute
S/N	Signal to noise ratio
ANOVA	Analysis of variance
SI	Severity index
INTER COLS	Interaction columns in Taguchi DOE
RMSE	Root mean square error
AICc	Akaike information criteria, corrected
EDTA	Ethylene-diamine-teraacetic acid
TCEP	Tris(2-carboxyethyl)phosphine
PBS	phosphate buffered saline
CMC	Carboxy-methyl cellulose
BLAST	Basic local alignment search tool
GTP	Guanidine tri-phosphate

PREFACE

Candida albicans is resistant to several individual antifungal antibiotics; there is a requirement to identify other antimicrobial proteins or peptides like inhibitory substances. In this thesis, we attempted to develop a selection criterion – based on combinatorial approach of one factor at a time (OFAT) and Taguchi DOE orthogonal array methods – for potential antifungal compound as well as antitumor compounds production from *Aspergillus giganteus* MTCC 8408.

In chapter 1, we demonstrated the variations of antifungal protein (afp) in cells induced by a treatment, correlated to the mechanism of action and characterization. Fungal infections with emerging threats of candidiasis were well described. Antifungal synthetic drugs belong to 3 distinct classes. Each class is characterized by a unique mode of action. Drugs known to induce various types of metabolic disturbances as well as cytotoxicity were well described.

Chapter 2 generalized the classification and sources of antifungal protein with *in silico* study, MICs observation, Molecular characterization, functional mechanism and range of organism impact.

Chapter 3 indicated the materials and methods of antifungal protein biosynthesis, isolation and purification of protein, molecular characterization, peptide mass finger printing associated with MASCOT analysis and in silico investigation.

Chapter 4 generalized the results on afp biosynthesis which showed OFAT variations induced by preliminary screening of most influential factors (culture pH, temperature, slant age, inoculum volume, agitation and C/N, K^+/Ca^{2+}, Mg^{2+}/Na^+ ratio) could be related to the submerged fermentation of *Aspergillus giganteus* MTCC 8408.