

Identification and characterization of a novel triyne and cinnamate 4-hydroxylase in *Helichrysum* aureonitens Sch. Bip.

by SAYED MAHDI ZIARATNIA

A thesis submitted in partial fulfillment of the requirements for the degree of

PHILOSOPHIAE DOCTOR

Forestry and Agricultural Biotechnology Institute (FABI)

Department of Plant Science

In the

Faculty of Natural and Agricultural Sciences University of Pretoria

Promoter: Prof. J.J.M. Meyer

Co- promoter: Prof. K.J. Kunert

2009



DECLARATION

I, Sayed Mahdi Ziaratnia, declare that the thesis submitted herewith, for the degree Philosophiae Doctor, to the University of Pretoria, contains my own independent work and has not previously been submitted by me for a degree to this or any other tertiary institution.

S.M. Ziaratnia

May 2009



CONTENTS

Abstract	VII
Thesis composition	XI
Acknowledgements	
List of Figures	
List of Schemes.	
List of Tables	
List of Abbreviations	XXI
Chapter 1: Introduction	
1.1 Medicinal plants past, present	2
1.1.1 Medicinal plants and human health care	2
1.1.2 Medicinal plants in trade	4
1.1.3 Medicinal plants: opportunities	7
1.1.4 Medicinal plants: limitations	9
1.1.5 Production of medicinal compounds	9
1.1.5.1 Traditional cultivation	9
1.1.5.2 Tissue and cell suspension cultures	10
1.1.5.3 Genetic manipulation of medicinal plants	12
1.1.5.4 Pathway engineering in medicinal plants	13
1.2 Medicinal plants in South Africa.	15
1.3 The genus Helichrysum	16
1.3.1 Compounds isolated and identified from the genus <i>Helichrysum</i>	16
1.3.2 Helichrysum aureonitens	17
1.3.3 Medicinal properties of <i>H. aureonitens</i> .	19
1.4 Aim of the study	21
1.5 Objectives of this study	22



Chapter 2: Production of galangin in the cell suspension cultures of *Helichrysum aureonitens*

2.1 A	Abstract	24
2.2 I	ntroduction	25
2.3 N	Material and methods	27
2.3.1	Induction of plant callus and establishment of cell suspension cultures	27
2.3.2	Extraction and thin layer chromatography (TLC)	27
	GC-MS analysis	
2.4 F	Results	29
2.5 I	Discussion	35
2.6 C	Conclusions	36
Chapte	r 3: Isolation, identification and bioactivity of a novel chlorophenol derivative from <i>Helichrysum aureonitens</i> cell suspension cultures	
3.1 A	Abstract	39
3.2 I	ntroduction	40
3.3 N	Materials and methods	42
3.3.1	Induction of plant callus and establishment of cell suspension cultures	42
3.3.2	Extraction	42
3.3.3	Thin layer chromatography (TLC)	42
3.3.4	Isolation and purification of the compound from the ethanol extract of the cell	
	suspension cultures	43
	Identification of the isolated compound from the cell suspension cultures	
	Bioassays	
3.3.6.	1 Antituberculosis activity	4 4
3.3.6.	2 Cytotoxicity assay	45
3.4 F	Results	46
3.4.1	Isolation and purification of compound 1	46
3.4.2	Identification of compound 1	46
	GC-MS analysis of detection of the triyne in the cells and leaves sample	
3.4.4	Instability of the triyne	56
	Bioassays	
	1 Antituberculosis activity	
3.4.5.	2 Toxicity and anticancer activity	57



3.6 Conclusions	63
Chapter 4: Biosynthetic pathway for flavonoids in cell suspension cultures of <i>Helichrysum aureonitens</i>	
4.1 Abstract	65
4.2 Introduction	66
4.3 Materials and methods	71
4.3.1 Plant materials	71
4.3.2 GC-MS analysis	71
4.4 Results	72
4.5 Discussion	81
4.6 Conclusions	87
5.1 Abstract	89
5.1 Abstract	89
5.2 Introduction	90
5.3 Materials and methods	92
5.3.1 Plant materials	92
5.3.2 Genomic DNA extraction	92
5.3.3 PCR amplification of an internal fragment of C4H using degenerated primers	92
5.3.4 Gel recovery and TA cloning	94
5.3.5 Sequencing and alignment	94
5.3.6 Genome walking	96
5.3.6.1 Genomic DNA restriction digestion	96
5.3.6.2 Ligation	96
5.3.6.3 PCR amplification	
•	97

5.3.8 Secondary structure of C4H from <i>H. aureonitens</i>	98
5.4 Results	99
5.4.1 Amplification of an internal fragment of C4H using degenerated primers	99
5.4.2 Genome walking	102
5.4.2.1 Genomic DNA restriction digestion	102
5.4.3 Amplification of the full length cDNA and genomic C4H from <i>H. aureon</i>	itens105
5.4.4 Molecular characterization of the nucleotide sequence of C4	H from
H. aureonitens	106
5.4.5 Phylogenetic tree	112
5.4.6 Secondary and tertiary structures of C4H from <i>H. aureonitens</i>	114
5.5 Discussion	118
5.6 Conclusions	121
napter 6: C4H expression in <i>Pichia pastoris</i>	
napter 6: C4H expression in <i>Pichia pastoris</i> 6.1 Abstract	123
6.1 Abstract	124
6.1 Abstract	124
6.1 Abstract	124
6.1 Abstract	124 131 131
 6.1 Abstract 6.2 Introduction 6.3 Materials and methods 6.3.1 Plant materials 6.3.2 Total RNA isolation and cDNA synthesis 	124 131 131 131
 6.1 Abstract 6.2 Introduction 6.3 Materials and methods 6.3.1 Plant materials 6.3.2 Total RNA isolation and cDNA synthesis 6.3.3 C4H full gene amplification and digestion 	124 131 131 131 132
 6.1 Abstract 6.2 Introduction 6.3 Materials and methods 6.3.1 Plant materials 6.3.2 Total RNA isolation and cDNA synthesis 6.3.3 C4H full gene amplification and digestion 6.3.4 Preparation of the pPICZαC expression plasmids 	124 131 131 131 132 133
 6.1 Abstract 6.2 Introduction 6.3 Materials and methods 6.3.1 Plant materials 6.3.2 Total RNA isolation and cDNA synthesis 6.3.3 C4H full gene amplification and digestion 6.3.4 Preparation of the pPICZαC expression plasmids 6.3.5 Directional cloning of C4H ORF into pPICZαC 	124 131 131 132 133
 6.1 Abstract 6.2 Introduction 6.3 Materials and methods 6.3.1 Plant materials 6.3.2 Total RNA isolation and cDNA synthesis 6.3.3 C4H full gene amplification and digestion 6.3.4 Preparation of the pPICZαC expression plasmids 6.3.5 Directional cloning of C4H ORF into pPICZαC 6.3.6 pPICZαC plasmid and C4H insert ligation 	
 6.1 Abstract 6.2 Introduction 6.3 Materials and methods 6.3.1 Plant materials 6.3.2 Total RNA isolation and cDNA synthesis 6.3.3 C4H full gene amplification and digestion 6.3.4 Preparation of the pPICZαC expression plasmids 6.3.5 Directional cloning of C4H ORF into pPICZαC 6.3.6 pPICZαC plasmid and C4H insert ligation 6.3.7 Preparation of competent TOP 10F' E. coli 	

	6.3.11 Transformation of <i>Pichia pastoris</i> with linearized plasmids	137
	6.3.12 PCR screening of recombinant GS115 clones	138
	6.3.12.1 Genomic DNA isolation	138
	6.3.12.2 PCR screening of recombinant GS115 cells from the isolated genomic DN.	A. 139
	6.3.13 Optimization of the conditions for the expression of C4H in the GS115 cells	140
	6.3.14 Sodium dodecyl sulphate-polyacrylamide (SDS-PAGE) analysis	140
	6.3.15 Silver staining	141
	6.3.16 Western blot analysis of the expressed C4H in <i>Pichia pastoris</i>	141
	6.3.17 Ammonium sulphate precipitation	143
	6.3.18 Purification of the polyhistidineine-tagged protein	144
	6.3.19 Protein determination	144
	6.4 Results	145
	6.4.1 Total RNA isolation and cDNA synthesis	145
	6.4.2 Cloning of C4H with restriction sites (XhoI and Sac II) in a pGEM clo	ning
	vector	146
	6.4.3 Transformation of the pPICZαC containing the C4H ORF into E.	coli
	TOP 10F'	148
	6.4.4 C4H expression in the GS115	153
	6.4.5 Precipitation of C4H expressed in the GS115	153
	6.4.6 Histidine-tagged C4H purification and quantification	156
	6.5 Discussion	158
	6.6 Conclusions	159
Cl	hapter 7: General discussion and perspectives	
	7.1 Introduction	161
	7.2 Cell suspension cultures of <i>Helichrysum aureonitens</i>	162
	7.3 Characterization of flavonoid biosynthesis in Helichrysum aureonitens	163

7.4 Characterization of cinnamate 4-hydroxylase in Helichrysum aureonitens	164
7.5 Further work	165
References	167



Identification and characterization of a novel triyne and cinnamte 4-hydroxylase in *Helichrysum* aureonitens Sch. Bip

by

Sayed Mahdi Ziaratnia

Forestry and Agricultural Biotechnology Institute, Department of Plant Science, University of Pretoria, Pretoria, 0002, South Africa.

Supervisor: Prof. J.J.M. Meyer Department of Plant Science, University of Pretoria, Pretoria, 0002, South Africa.

Co-supervisor: Prof. K.J. Kunert
Forestry and Agricultural Biotechnology Institute, Department of Plant Science, University
of Pretoria, Pretoria, 0002, South Africa.

ABSTRACT

For centuries people have used plants as medicine or food additives with varying success to cure and prevent diseases. Written records about medicinal plants date back at least 5 000 years to the Sumerians. According to World Health Organization (WHO) around 80 % of the population in developing countries is dependent on herbal medicine for basic healthcare needs. Even at the dawn of the twenty-first century, 11 % of the 252 drugs considered as basic and essential by WHO were exclusively of flowering plant origin.



The genus Helichrysum, belongs to the family Asteraceae and is represented by approximately 600 species in Africa, of which 244 species are indigenous in South Africa. In Helichrysum aureonitens, galangin is one of the flavonol compounds with good medicinal properties. H. aureonitens was targeted to be enhanced via cell suspension culture to potentially produce valuable natural products. In ethanol extracts of cell suspension cultures, galangin was not detected even though it was present in the leaves of the intact plants. Some other compounds were induced in higher amounts in the cells of H. aureonitens suspension cultures when compared to that produced in the intact plants. To find out the reasons for the absence of galangin in the cells of *H. aureonitens* suspension cultures, some of the intermediates of the 4'-OH biosynthetic pathway for production of flavonols were analyzed by GC-MS, including cinnamic acid, p-coumaric acid, naringenin and kaempferol. None of these were detected in the *H. aureonitens* cell suspension cultures. The major compound from H. aureonitens cell suspension cultures was isolated and identified as a new chlorophenol compound named 4-chloro-2-(hepta-1,3,5-triyne-1-yl)phenol (a triyne). This triyne has previously been proposed as being an intermediate in the acetylene biosynthetic pathway in *Helichrysum spp.*, however only the methyl ether form had previously been isolated from the roots of H. coriaceum. The trivine isolated from the H. aureonitens cell suspension cultures in the present study was detected in intact plant extracts, but at very low concentrations. Results of the anti-tuberculosis assay of the cell suspension culture extracts and the trivne showed that the minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) of the ethanol extract of cell suspension cultures against Mycobacterium tuberculosis H37Rv were found to be



1.0 mg/ml and 2.0 mg/ml respectively and the triyne was not active at 200 μ g/ml. The ethanol extract of the cell suspension cultures and the triyne were also evaluated for their cytotoxicity against monkey kidney Vero cells and human prostate epithelial carcinoma (DU145) cell lines. The inhibitory concentrations (IC₅₀) of the crude extract and the triyne was found to be 12.11 and 1.51 μ g/ml against the Vero cells respectively. The crude extract and the triyne showed similar activity in the prostate cancer cell lines by exhibiting IC₅₀ values of 3.52 and 2.14 μ g/ml respectively. The triyne therefore warrants further investigation for its potential as an anticancer drug.

Flavonoids represent the major phenolic compounds which are responsible for the medicinal properties in the *Helichrysum* genus. Some of flavonols, including kaempferol, quercetin, and galangin are also present in *H. aureonitens*. In this study both galangin and kaempferol (containing a 4'-OH group) were detected in leaf samples of *H. aureonitens*. But GC-MS analysis of the leaf samples of *H. aureonitens* did not show the existence of biosynthetic intermediates such as *p*-coumaric acid and naringenin (compounds having a 4'-OH) while cinnamic acid and some other compounds with no OH at the 4' position on the B ring, were detected. The chemical structure analysis of the isolated compounds showed that they are pinocembrin chalcone, pinocembrin, pinobanksin and galangin, all containing no OH group at the 4' position. This indicates that some part of the 4'-OH biosynthetic pathway for 4'-OH flavonoids is not functional in *H. aureonitens*. Since the only (yet identified) enzyme responsible for hydroxylation at the 4' position on the B ring is cinnamate 4-hydroxylase (C4H), it can be postulated that C4H might be able to hydroxylate other substrates in *H. aureonitens* plants.



One copy of C4H was isolated and cloned from *H. aureonitens*. It has 1518-base pairs (including stop codon, TAA) and an open reading frame encoding a 506-amino-acid polypeptide. It showed the highest homologies to *Echinacea angustifolia* (Asteraceae) C4H with 83.6 % identity on the nucleotide level but 93 % identity on the amino acid level. The genomic DNA sequence of the isolated C4H from *H. aureonitens* indicates the presence of three introns with a longer size compared to the *Arabidopsis thaliana* C4H gene structure. The presence of the first intron has not been reported before in the C4H gene from other plants and it is therefore a new finding from the isolated C4H in *H. aureonitens*.

To check the putative isolated C4H, the full length cDNA of C4H was isolated from *H. aureonitens* and for the first time integrated in a secreted expression vector, pPICZαC, and transformed into *Pichia pastoris*. After the 48 hrs induction protein was collected, precipitated by ammonium sulphate and finally column purified. The results of SDS-PAGE electrophoresis and Western blot showed the expression of a protein with a size of 50-60 kDa. The calculated mass of C4H with regarding to a polyhistidine tag is about 60.5 kDa. The secreted expression was found as an effective system for the production of a soluble C4H protein with easy purification.



THESIS COMPOSITION

Chapter 1: Introduces briefly the history of medicinal plants in the world and discusses its benefits for human health. It also reviews the current situation of the medicinal plant product trade in the world focusing on the international trade of these plants. This chapter discusses the opportunities and limitations of the production of products from medicinal plants and also reports on the application of modern techniques for natural products production. In the last part of the chapter, there is an introduction to the genus of *Helichrysum* as well as a description of the medicinal properties of the isolated compounds from *H. aureonitens*.

Chapter 2: Reports on the establishment of *H. aureonitens* cell suspension cultures. This chapter focuses on the chemical analysis of the galangin intermediates based on the 4'-OH biosynthetic pathway of flavonols.

Chapter 3: Deals with the isolation and identification of the major compound from the *H*. *aureonitens* cell suspension cultures. The chapter also reports on the characteristics of the major compound and crude extracts of the *H. aureonitens* cell suspension cultures including, their toxicity, anti-TB (*Mycobacterium tuberculosis*) as well as anticancer activity.

Chapter 4: Investigates the 4'-OH biosynthetic pathway for flavonol production in *H*. *aureonitens* by the detection of flavonol intermediates in the leaf samples. It also reports on



the detection of some other intermediates of the non 4'-OH biosynthetic pathway of flavonols which can be involved in the galangin production of *H. aureonitens* plants. Finally it is postulated that the difference between these two biosynthetic pathways is the functionality of cinnamate-4-hydroxylase (C4H).

Chapter 5: Focuses on the full length isolation and characterization of C4H in *H. aureonitens*. It includs the neucleotide, amino acid sequence, gene structure and the phylogenetic relationships between the isolated C4H from *H. aureonitens* and those in other plants.

Chapter 6: Presents the expression of C4H in the yeast, *Pichia pastoris* with the secreted system of expressed protein into the medium. The precipitation and purification of C4H will also be discussed in this chapter.

Chapter 7: Summarizes the results of this study regarding the novel phenolic compound isolated from *H. aureonitens*, and as well as the characterization of the isolated and expressed C4H. Finally this chapter outlines possible further research which includes the functional expression of the isolated C4H from *H. aureonitens* in yeast and also determine the function of this gene in the *H. aureonitens* cells as well as the characterization of C4H from other *Helichrysum* species.



ACKNOWLEDGMENTS

Thanks to the almighty **God** for giving me the opportunity and ability to complete my research. I should also thank him for his best gift to us, the holy, Quran that has taught us to think about everything that is around us. My sincere thanks to his messenger, Mohammad, who said that "an hour thinking is better than 60 years of worship without thinking", and has also recommended us to learn from the cradle to the grave.

I am highly thankful for my parents' encouragement to pursue science as a career. Although they are no longer with me, I'm sure they are happy that this is the product of their efforts and support many years ago.

Based on the advice from the Quran that says your teachers are highly respected and Ali, Mohammad's substitute, who said that "I would be a slave of a person who teaches me a letter", the author wishes to express sincere appreciation to Prof. J.J. Marion Meyer as supervisor and Prof. Karl J. Kunert as co-supervisor for all their patience, support and guidance throughout this study. I thank them for the very good mentoring discussions and useful advice that has led to the completion of this scientific accomplishment.

It gives me a big pleasure to thank Dr. Ahmed Hussein whose scientific support and guidance in the chemical isolation and purification part of this project is really unforgettable.

My sincere thanks go to Dr. Christine Maritz-Oliver whose scientific advice and guidance helped me to undertake the protein expression part of this study. Her help is really appreciated.

I'm indebted to the Khorasan Science and Food Industry Institute-Mashhad, Iran for the financial support that allowed me to accomplish this study.



I'm very grateful to the Plant Science Department for all the support and for giving me the opportunity to visit and study at the Riken Institute in Japan. National Research Foundation for financial support. Forestry and Agricultural Biotechnology Institute (FABI) for providing such a wonderful and high standard environment for me to complete my project.

I'm also pleased to thank Prof. Toshiya Muranaka and his research team, especially Dr. Hikaru Seki, and Ohyama Kiyoshib at the RIKEN Plant Science Centre, Yokohama, Japan for their assistance in the molecular biology and chemical analysis.

In addition, special thanks to Prof. Namrita Lall, Dr. Getu Beyene, Dr. Urte Schluter, Dr. Quenton Kritzinger and his wife, Angelique whose advice and support were helpful throughout this undertaking. Thanks also to the members of the Lategan lab, as well as the Plant Science Department, especially René Swart whose support made my stay at the Plant Science Department as comfortable as possible.

Last, but not least, I would like to express my sincere thanks to all my friends and relatives, Mr and Mrs Hassan Zadeh for their kindly support of my family particularly while I was not with them. A special word of thanks and appreciation to my wife, Fereshteh, my daughters, Negar and Nafiseh for their patience, support, encouragement and for creating a very peaceful environment for me to undertake this project.



LIST OF FIGURES

Chapter 1	Page
Figure 1.1.	Traded medicinal plants, cultivated or of wild origin
Figure 1.2.	Isolated compounds from different parts of Helichrysum species
Figure 1.3.	Aerial parts of Helichrysum aureonitens
Chapter 2	
Figure 2.1.	Comparison of the galangin production in the leaf and in cell suspension cultures of
	Helichrysum aureonitens with different solvents
Figure 2.2.	GC-MS analysis of the cell suspension culture extracts for the detection of cinnamic acid
Figure 2.3	GC-MS analysis comparison of the galangin production in the leaf and in cell suspension
riguic 2.5.	cultures of <i>H. aureonitens</i>
Eigura 2.4	
rigure 2.4.	GC-MS analysis of the cell suspension culture extracts for the detection of p-coumaric acid
Figure 2.5.	GC-MS analysis of the cell suspension culture extracts for the detection of naringenin 33
C	GC-MS analysis of the cell suspension culture extracts for the detection of
S	kaempferol
Chapter 3	
Figure 3.1.	Results of developed collected fractions from the Sephadex column on TLC plates 47
Figure 3.2.	Chemical structure of the major compound based on the results of NMR (carbon
	number) (4-chloro-2-(hepta-1,3,5-triyne-1-yl)-phenol)
Figure 3.3.	Chemical structure of the major compound based on the results of NMR (HBMC
	correlation)
Figure 3.4.	MS spectrum of the triyne using ESI
Figure 3.5.	¹ H-NMR of the trivne

Figure 3.6.	¹³ C-NMR of the triyne	52
Figure 3.7.	HMQC of the triyne	53
Figure 3.8.	HMBC of the triyne and the other major compound	54
Figure3.9.	Detection of the triyne in different ethanolic extracts of Helichrysum aureonitens	55
Figure 3.10	. Two dimension thin layer chromatography (TLC) of the triyne	56
Figure 3.11	l. Effect of the ethanol crude extracts and the isolated the triyne (µg/ml) on the growth	1
	of Vero and DU145 cell lines	58
Figure 3.1	2. Proposed biosynthetic pathway for the chlorophenol compounds in Helichrysum	7
	coriaceum	62
Chapter 4		
Figure 4.1.	Molecular structure of the flavone backbone	69
Figure 4.2.	Chemical structures of some members of flavonols	70
Figure 4.3	GC-MS analysis of the presence of cinnamic acid in leaf extracts of Helichrysum	y
	aureonitens	75
Figure4.4.	GC-MS analysis of the absence of p-coumaric acid in leaf extracts of Helichrysum	y
	aureonitens	76
Figure 4.5.	GC-MS analysis of the absence of naringenin in leaf extracts of Helichrysum aureonitens'	77
Figure 4.6.	GC-MS analysis of the presence of kaempferol in leaf extracts of Helichrysum aureonitens.	78
Figure 4.7.	GC-MS analysis of the presence of galangin in leaf extracts of Helichrysum aureonitens	79
Figure 4.8	. MS spectra of intermediates of the non 4'-OH biosynthetic pathway of flavonols	s
	production in Helichrysum aureonitens	80
Figure 4.9.	A metabolic channel model for independent pathways to G and S monolignols	86
Chapter 5		
Figure 5.1.	C4H gene map in Arabidopsis thaliana (NC_003071.3)	00
Figure 5.2	. Amplification of the internal partial fragment of C4H from the genomic DNA or	f
	Helichrysum aureonitens by degenerated primers	00

Figure 5.3	6. Multi-alignment of the sequences of the internal fragment of C4H in Helichry.	um
	aureonitens from eight colonies with C4H homologies of other plants	101
Figure 5.4	. Complete digestion of the genomic DNA using blunt-end restriction enzymes, Pro-	иII
	and StuI	103
Figure 5.5	. PCR amplification for the first genome walking with $E \omega RV$ and $S \omega I$ DNA digestion	1 03
Figure 5.6	. PCR amplification for the first genome walking with PvuII and StuI digested DNA	for
	the second genome walking	105
Figure 5.7	. C4H genomic DNA sequence from Helichrysum aureonitens	108
Figure 5.8	. C4H gene structure in Helichrysum aureonitens	109
Figure 5.9	cDNA full length sequence of the C4H in Helichrysum aureonitens (1518 bp including st	юр
	codon, TAA)	110
Figure 5.1	0. Multi-alignment of C4H amino acid from Helichrysum aureonitens with C4H homolog	ģes
	from other plants.	111
Figure 5.1	1. Phylogenetic tree of the C4H in Helichrysum aureonitens.	113
Figure 5.12	2. Secondary structure of C4H from Helichrysum aureonitens was predicted in Psi-pred	1.115
Figure 5.1.	3. Protein alignments between C4H amino acid sequences from Helichrysum aureonit	ens
	and a cytochrome P450.	116
Figure 5.14	4. RASMOL secondary structure model for C4H from Helichrysum aureonitens	117
Chapter 6		
Figure 6.1.	Insertion of the homologous genes into the AOX1 locus of Pichia pastoris	127
Figure 6.2	• Insertion of the multiple heterologous genes into the expression pPICZ plasmids	128
Figure 6.3	6. Structures of pPICZ vectors used for the expression of the heterologous gene in	an
	EasySelect TM Pichia expression system	129
Figure 6.4	. Total RNA and synthesized cDNA from plants of Helichrysum aureonitens	145
Figure 6.5	. Double digestion of the pGEM cloning vector with and without the insert (C4H) w	rith
	XhoI and Sac II	146
Figure 6.6	Drectional cloning strategy of C4H into pPICZαC for expression in <i>Pichia pastoris</i>	147

Figure 6.7.	Colony screening of the E. colia strain TOP 10 after transformation by electroporatio	n
	with AOX1 primers1	l 48
Figure 6.8.	Double digestion with XhoI and SacII of the selected plasmids containing C4H1	l 49
Figure 6.9.	Transformation of pPICZαC into <i>Pichia pastoris</i> GS115 cells by electroporation1	l 50
Figure 6.10	Linearalization of pPICZα C with <i>PmeI</i> .	151
Figure 6.11	. Genomic DNA isolated from selected colonies of Pichia pastoris after transformatio	n
	with pPICZαC which contains the C4H insert ed by electroporation1	152
Figure 6.12	. PCR amplification of the α -factor plus C4H from the genomic DNA of GS1151	152
Figure 6.13	3. Expression of albumine and of C4H integrated in a secretion pPICZαC plasmids is	n
	Pichia pastoris GS1151	l 5 4
Figure 6.14	4. Ammonum phosphate precipitation of the expressed C4H in Pichia pastoris GS11	5
	cells	l55
Figure 6.15	. Silver stained SDS-PAGE analysis of the purified tagged-C4H through the column1	157



LIST OF SCHEMES

Chapter 4	Page
Scheme 4.1. Biosynthetic pathway of flavonoids	68
Scheme 4.2. 4'-OH biosynthetic pathway for flavonols originating from p-coumaric acid	73
Scheme 4.3. The proposed alternative biosynthetic pathway for galangin production	in
Helichrysum aureonitens originating from cinnamic acid	74
Scheme 4.4. Proposed biosynthetic pathway of flavonols in the leaves of Helichrys	sum
aureonitens.	83
Scheme 4.5. The lignin biosynthetic pathway	84



LIST OF TABLES

	Pa	ge
Table	1.1. Some of the most economically important pharmaceuticals (or their precursors)	
	derived from plants	3
Table	1.2. List of the important countries for trading of medicinal plants	4
Table	1.3. List of some cell suspension cultures with higher production of secondary	
	metabolites as compared to what is present in intact plants12	2
Table	3.1. NMR data of the isolated compound (CDCl ₃ , 300 MHz/75 MHz)4	3
Table	5.1. List of plants for designing the degenerated primers to amplify the internal	
	fragment in C4H9	3
Table	5.2. List of primers for the identification and amplification of the C4H gene in	
	Helichrysum aureonitens99	5
Table	6.1. Primers for the amplification of the C4H for expression in <i>Pichia pastoris</i>	2
Table	6.2. Primers used in colony PCR to detect positive clones harboring the C4H insert	5

LIST OF ABBREVIATIONS

¹³C-NMR: Carbon-nuclear magnetic resonance

¹H-NMR: Proton-nuclear magnetic resonance

2D-TLC: Two-dimensional TLC

4CL: 4-Coumarate:CoA ligase

AgNO₃: Silver nitrate

AOX: Alcohol oxidase

ATG: Methionine (start codon)

ATP: Adenosine-5'-triphosphate

BA: 6-benzylaminopurine

BMGY: Buffered Glycerol-complex medium

BMMY: Buffered Methanol-complex medium

bp: Base pair

BSA: Bovine serum albumin

C4H: Cinnamate-4-hydroxylase

CaCl₂: Calcium Chloride

CAD: Cinnamyl alcohol dehydrogenase

CCoA-3H: Coumaroyl-coenzyme A 3-hydroxylase

CCR: Cinnamoyl-CoA reductase

CDCl₃: Deuterated chloroform

cDNA: Complimentary DNA

CHI: Chalcone isomerase

CHS: Chalcone synthase



CODEHOP: Consensus-degenerate hybrid oligonucleotide primers

COMT: Caffeic acid 3-O-methyltransferase

COSY: Correlated spectroscopy

CPR: Cytochrome P450 oxidoreductase

CTAB: Cetyltrimethylammonium bromide

dATP: Deoxyadenosine triphosphate (A)

dCT: Deoxycytidine triphosphate (C)

DDT: Dichlorodiphenyltrichloroethane

dGTP: Deoxyguanosine triphosphate (G)

DMF: Dimethylformamide

DMSO: Dimethylsulfoxide

DNA: Deoxyribonucleic acid

DNase: Deoxyribonuclease

dNTP: Deoxynucleoside triphosphate

dTTP: Thymidine triphosphate (T)

E. coli: Escherichia coli

EDTA: Ethylenediamine tetra acetic acid

EtOH: Ethanol

F3H: Flavonone 3-hydroxylase

F5H: Flavonone 5-hydroxylase

FLS: Flavonol synthase

g: Gram

GC: Gas chromatography

GC-MS: Gas chromatography-mass spectrometry

gDNA: Genomic DNA



h: hours

His-tag: Polyhistidine (6xHis) tag

HIV: Human immunodeficiency virus

HMBC: Heteronuclear multiple bond correlation

HMQC: Heteronuclear multiple quantum correlation

IC₅₀: The half maximal inhibitory concentration

IR: Infrared spectra

KAc: Potassium acetate

KCl: Potassium chloride

KEX2: The preliminary cleavage of the signal sequence by the KEX2 gene product

L: Litre

LB: Luria broth

LC-MS: Liquid chromatography-mass spectrometry

M: Molar

MBC: Minimum bactericidal concentration

MeOH: Methanol

MgCl₂: Magnesium chloride

MHz: Megahertz

MIC: Minimum inhibitory concentration

min: Minutes

mL: Millilitres

mM: Millimolar

MnCl₂: Manganese chloride

mRNA: Messenger ribonucleic acid

MS medium: Murashige and Skoog medium



MS: Mass spectrometry

Myc-tag: Myc epitope tag

Na₂CO₃: Sodium carbonate

Na₂S₂O₃: Sodium thiosulfate

NAA: α-Naphthalene acetic acid

NaAc: Sodium acetate

NaCl: Sodium chloride

NADPH: Nicotinamide adenine dinucleotide phosphate

NaH₂PO₄: Sodium dihydrogen phophate

NaOAc: Sodium acetate

NaOH: Sodium hydroxide

ng: Nanogram

NMR: Nuclear magnetic resonance

OD: Optical density

ORF: Open reading frame

P. pastoris: Pichia pastoris

PAL: Phenylalanine ammonia lyase

PCR: Polymerase chain reaction

Pmol: Pico mole

PMSF: Phenyl methyl sulphonyl fluoride

PVDF: Polyvinylidene fluoride

RAPD: Random amplification of polymorphic DNA

RNA: Ribonucleic acid

rpm: Revolutions per minutes

S. cerevisiae: Saccharomyces cerevisiae



sd H₂O: Sterile distilled water

SDS: Sodium dodecyl sulphate

SDS-PAGE: Sodium dodecyl sulphate-polyacrylamide gel electrophoresis

TAE: Tris-acetate EDTA

TAL: Tyrosine ammonia-lyase

Taq: Thermus aquaticus

TB: Tuberculosis

TEMED: N,N,N',N'-tetramethyl-ethylenediamine

TLC: Thin layer chromatography

Tris: 2-Amino-2-(hydromethyl)propane-1.3 diol

tRNA: Transfer RNA

U: Unit

UV: Ultraviolet

WHO: World Health Organization

YNB: Yeast nitrogen base with ammonium sulphate without amino acids

YPDS: Yeast extract peptone dextrose medium