



Genomic Studies of the Polyketide Synthase Genes :

Generation of a BAC-Based Physical Map of the Red Raspberry Genome



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ATPER2013-June 1-2, 2013 Stockholm, Sweden.



OUTLINES : Red Raspberry & Polyketide synthase (PKS)

- Red raspberry
- Anthocyanins / health benefits
- Polyketide Synthase (PKS)/Biosynthetic pathway
- Molecular Plant Breeding and Applications









- I. Why Red Raspberry ?
- Small fruit / 37 countries world wild
- Powerful flavour and colour
- Commercially important fruit
- Food industrial manufacturing / fresh fruit market
- Source of Anthocyanins
- Red raspberry cultivars and improvement
 - disease resistances
 - trait qualities















How important is anthocyanins ?

- Responsible for fruit colour and aroma
- Having significant antioxidant properties :
 - promoting health
 - improving vision
 - preventing cancer
 - controlling diabetes
 - retarding the effects of aging
 - preventing the loss of memory and mortor skills





Anthocyanins in Red raspberry !!

ANTHOCYANINS CONTENT OF FRUIT



Tab. 1 Concentrations of total anthocyanins (TA) (mg CGE/l)^a, total polyphenols (TP) (mg GAE/l)^a, antioxidant activity of red fruit juices (µmol TE/ml)^b, and TA/TP ratio

	Total anthocyanins [mg/l]	Total polyphenols [mg/l]	Antioxidant activity [µmol TE/ml]	TA/TP
Black currant	1543.89 ± 5.5	2770.94 ± 63.9	30.15	0.56
Red raspberry	217.39 ± 5.2	1234.27 ± 54.8	8.20	0.18
Blackberry	739.93 ± 37.5	1831.21 ± 111.6	8.75	0.40
Sour cherry	369.36 ± 2.4	2054.43 ± 140.2	12.52	0.18
Sweet cherry	256.60 ± 2.5	1566.84 ± 130.2	4.07	0.16
Strawberry	205.98 ± 2.2	1271.85 ± 106.9	4.39	0.16
Chokeberry	3042.20 ± 196.3	9154.47 ± 595.4	72.44	0.33
Elderberry	4188.63 ± 257.0	6361.89 ± 298.9	62.14	0.66

a values are means ± SD (n=3); antioxidant activity determined after 15 min

Ba R⁷ R^6

Selected anthocyanidins and their substitutions

sic structure	Anthocyanidin	R ₃ ′	R_4'	R ₅ ′	R ₃	R ₅	R ₆	R ₇
	Aurantinidin	-H	-OH	-H	-OH	–OH	-OH	–OH
	Cyanidin	-OH	-OH	–H	-OH	-OH	-H	-OH
R ^{3'}	Delphinidin	-OH	-OH	-OH	-OH	-OH	-H	-OH
2' 3' 4' R4'	Europinidin	-OCH ₃	-OH	-OH	-OH	-OCH ₃	-H	-OH
	Luteolinidin	-OH	-OH	–H	-H	-OH	-H	-OH
2 6' ^{5'} R ^{5'}	Pelargonidin	–H	-OH	–H	-OH	–OH	-H	-OH
R^3	Malvidin	-OCH ₃	-OH	-OCH ₃	-OH	-OH	-H	-OH
-	Peonidin	-OCH ₃	-OH	-H	-OH	-OH	-H	-OH
	Petunidin	–OH	-OH	-OCH ₃	-OH	-OH	-H	-OH
	Rosinidin	-OCH ₃	-OH	-H	-OH	-OH	-H	-OCH ₃





What is Polyketide synthase (PKS) ?

- A large family of enzymes



- Produce aromatic polyketides / flavour, colour
- Have been found in microbial, plants and animals
- Are precursor for the next steps
- There are three types of PKS ; I, II and III Type III : higher plants







Polyketide biosynthesis pathway







Molecular plant breeding and applications ** Crossing 2 characteristically different cultivars

1. Markers / quality trait loci (QTL) / which chromosome / where on chromosome / linkage mapping



North America X European

- 2. Genome sequence studies / 1 2 3 4 5 6 7 sequence of DNA / DNA variation / gene structure / Physical mapping / comparative mapping or integrated mapping / compare with the other related plants
- 3. Expression / Genetic engineering





II. Material & Methodology



 Construction : A BAC library a BAC library from genomic DNA isolated from red raspberry cv. Glen Moy screen positive BAC clones with CHS11 probe 	 2. Analysis BAC clones : positive BAC clones restriction digestion, southern blotting, PCR using primers derived gene sequences for red raspberry cv. Royalty carry out 454 sequencing for each BAC 	 3. Construction : fosmid library by partially mechanical shearing digestion - screen by - colony hybridization, - PCR, - restriction digestion, - paired-end fosmid sequencing to help assemble 454 data for <u>BACs</u> 	 4. Generation : physical map detailed annotation gene order agarose fingerprinting by rare cutter enzyme digestion MTP ** comparison to cut map of 454 assembly 	 5. Bioinformatics : Information of genes on the chromosomal region annotation genetic variation comparison to red raspberry cv. Latham and related fruits
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III. Results

i Analysis : positive BAC clones



BAC clones contain ~ 130-200 kb of DNA









ii Construction of Fosmid library



A sub-library contains more manageable sizes ~ 36-40 kb of DNA





iii Assembly of BAC sequences

SIPBS

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) 😔				24P12-raw	data assembly
+	Assembly Parameters AbN	Assemble Automatic	ally Assemble Inter	actively Assen	hale to Reference	
Para	ameters: (Dirty Data, With	ReAligner, 3' go	ap placement): Mir	n Overlap = 20	, Min Match =	85%
	Name	Size	Quality	Kind	Label	Modified
42	718000000489	266 BPs	97.7%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:06
- - ₽	718000000490	202 BPs	98.0%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:06
- 12	718000000494	274 BPs	69.7%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:06
- 12	718000000495	437 BPs	84.0%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:06
- 12 - SA	718000000496	253 BPs	99.2%	DNA Fragment	_	Wed, Aug 25, 2010 17:23:06
- 121 - 121	718000000497	386 BPS 339 BPs	97.6%	DNA Fragment	-	Wed, Aug 25, 2010 17:28:06
10	7180000000499	444 BPs	94.1%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:06
12	718000000500	331 BPs	60.4%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:06
42	718000000501	163 BPs	98.2%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:06
- 1 2	718000000502	154 BPs	77.9%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:06
12	718000000503	210 BPs	97.1%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:06
- 12	718000000506	157 BPs	93.0%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:06
- 20	7180000000508	228 BPs 429 BP≤	97.4% 76.9%	DNA Fragment	-	Wed, Aug 25, 2010 17:28:06
12	7180000000510	222 BPs	81.5%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:06
12	71800000000513	357 BPs	97.5%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:06
1	7180000000514	347 BPs	93.7%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:06
(🕨 🔤	Contig[0001]	117033 BPs		Contig of 252	-	Tue, Jun 14, 2011 18:29:58
	Contig[0066]	312 BPs		Contig of 2	-	Tue, Jun 14, 2011 18:28:58
			20	M05-1-row	data assemb	du la
			23	SINIOS-1-Taw	uata assemb	"Y
+	Assembly Parameters AbN	Assemble Automatic	ally Assemble Inte	ractively Asser	mble to Reference	
Band	motong: (Dintu Data Uith	Pollignon 2' g	an nigoarant): Mi	n Ouenlan = 20	Min Match -	
Fare	Name	Filter, 3 g	ap placement): III	N Overtap = 26	, nin naten -	Modified
-Eat	Name	5120	Quality	KING	Label	Modified
-8	718000000661	235 BPs	97.9%	DNA Fragment	-	wed, Aug 25, 2010 17:23:08
12	/18000000663	429 BPs	74.1%	DNA Fragment	-	wed, Aug 25, 2010 17:23:08
- 18 20	718000000664	258 BPs	55.8%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:08
18 18	718000000665	443 BPs	72.9%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:08
- 42	718000000666	418 BPs	80.9%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:08
- 18	718000000667	402 BPs	85.8%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:08
- 1 ⊠	718000000669	227 BPs	87.7%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:08
- 1 ⊠	718000000670	372 BPs	84.7%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:08
- 4⊠	718000000671	350 BPs	83.4%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:08
- 4 ≧	718000000672	295 BPs	96.6%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:08
- 12	718000000673	481 BPs	87.3%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:08
- 1 2	718000000674	338 BPs	70.4%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:08
- 18	718000000675	245 BPs	86.9%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:08
12	71800000676	417 BPs	77.5%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:08
	Contig[0001]	24672 BPs		Contig of 59	-	Tue, Jun 14, 2011 17:58:22
۵ 🖌	Contig[0002]	46085 BPs		Contig of 65	-	Tue, Jun 14, 2011 17:58:29
۵	Contig[0003]	95469 BPs)	Contig of 171	-	Tue, Jun 14, 2011 17:58:32
۵ 🌾	Contig[0006]	7298 BPs		Contig of 19	-	Tue, Jun 14, 2011 17:58:24
	Contig[0085]	357 BP#		Contig of 2	-	Tue, Jun 14, 2011 17:56:46
			21012	1 raw data	accombly C	DE
00			51012	-1-raw uata	assembly .5	
	Assembly Parameters AbN	Assemble Automati	cally Assemble int	eractively Ass	emble te Referenc	ce 🖀
			-			
Para	ameters: (Dirty Data, With	ReAligner, 3' ç	pap placement): M	in Overlap = 2	20, Min Match	= 85%
	Name	Size	Quality	Kind	Label	Modified
12	718000000992	407 BPs	71.5%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:10
42	718000000994	311 BPs	99.7%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:10
42	718000000995	350 BPs	85.4%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:10
42	7180000000997	347 BPs	93.4%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:10
١Ū,	718000000998	227 BPs	86.3%	DNA Fragment	-	Wed, Aug 25, 2010 17:23:10
	Contig[0001]	33478 BPs		Contig of 140	-	Sat. Mar 9, 2013 20:42:56
	Contia[0003]	4456 BP<		Contig of 14	-	Sat. Mar 9, 2013 20:42:34
	Contig[0004]	4795 BP=		Contig of 15	-	Sat Mar 9 2013 20:42:34
	Contig[0007]	1284Z DD-		Contig of 47	_	Sat Mar 9 2017 20:42:54
	Contig[0007]	11700 00-		Contig of 47	_	Cat. Mar. 9, 2017 20:42:35
	Contig[0008]	11760 BPS		Contig of 29	-	Sat, mar 9, 2015 20:42:44
	Contig[UU13]	22146 BPs		Contig of 62	-	sat, Mar 9, 2013 20:42:53
	Contig[0016]	9420 BPs		Contig of 16	-	5at, Mar 9, 2013 20:42:44





B) 29M05

454 sequencing and assembly : - 24P12 ~ 117 kb / 12 FES - 29M05 ~ 98 – 120 kb / 18 FES





iv. Genetic organization and sequence variation



Each BAC carries 2 regions of PKS genes





Amino acid sequence

- PKS1

- PKS5

		20		40		60
PKS1 R Royalty PKS1–GM29–48 PKS5–GM24–72	MVTVDEVRKA MVTVDEVRKA MVTV <mark>E</mark> EVRKA	QRAEGPATIL QRAEGPATIL QRAEGPATUL 80	AIGTATPP AIGTATPP GHRNGNSSOP	NCVDQSTYPD NCVDQSTYPD VWTRARTPTT 100	YYFRITKSEH YYFRITKSEH TFVSPTASTR	KTELKEKFOR 58 KTELKEKFOR 58 LSSKRNSSAC 60
PKS1 R Royalty PKS1–GM29–48 PKS5–GM24–72	MCDKSMIKKR MCDKSMIKKR <mark>VS</mark> DKSMIKKR	YMYLTEEILK YMYLTEEILK YMYLTEEILK	EN P SMC EYMA EN P SMC EYMA D N P SMC EYMA	PSLDARQDMV PSLDARQDMV PSLDARQDMV	VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE	AATKAIKEWG 118 AATKAIKEWG 118 AATKAIKEWG 120
PKS1 R Royalty PKS1–GM29–48 PKS5–GM24–72	QPKSKITHLV QPKSKITHLV QPKSKITHLV	FCTTSGVDMP FCTTSGVDMP FCTTSGVDMP 200	GADYQLTKLL GADYQLTKLL GADYQLTKLL	GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM 220	MYQQGCFAGG MYQQGCFAGG MYQQGCFAGG	TVLRLAKDLA 178 TVLRLAKDLA 178 TVLRLAKDLA 180 240
PKS1 R Royalty PKS1-GM29-48 PKS5-GM24-72	ENNKGARVLV ENNKGARVLV ENN <mark>R</mark> GARVLV	VCSEITAVTF VCSEITAVTF VCSEITAVTF 260	RGPSDTHLDS RGPSDTHLDS RGPSDTHLDS	LVGQALFGDG LVGQALFGDG LVGQALFGDG 280	AAAIIVGSDP AAAIIVGSDP AAAIIVGADP	LPDIERPLFE 238 LPDIERPLFE 238 LPEIERPLFE 240 300
PKS1 R Royalty PKS1–GM29–48 PKS5–GM24–72	LV SAAQT I LP LV SAAQT I LP LV SAAQT I LP	D SDGA I DGH L D SDGA I DGH L D SDGA I DGH L 320	REVGLTFHLL REVGLTFHLL REVGLTFHLL	KDVPGLISKN KDVPGLISKN KDVPGLISKN 340	I EKSLNEAFK I EKSLNEAFK I EKSLNEAFK	PLDITDWNSL 298 PLDITDWNSL 298 PLDITDWNSL 300 360
PKS1 R Royalty PKS1–GM29–48 PKS5–GM24–72	FWI AH PGGPA FWI AH PGGPA FWI AH PGGPA	ILDQVEAKLG ILDQVEAKLG ILDQVETKLG 380	LKPEKLEATR LKPEKLEATR LKPEKLEATR	NILSEYGNMS NILSEYGNMS HILSEYGNMS	SACVLFILDE SACVLFILDE SACVLFILDE	VRRKSVANGH 358 VRRKSVANGH 358 VRKKSAANGL 360
PKS1 R Royalty PKS1-GM29-48 PKS5-GM24-72	KTTGEGLEWG KTTGEGLEWG KTTGEGLEWG	VLFGFGPGLT VLFGFGPGLT VLFGFGPGLT	VETVVLHSVA VETVVLHSVA VETVVLHSVG	AST 391 AST 391 VTA 393		
A		20 1		40	_	60 I
PKS1-GM29-48 PKS5 R Royalty PKS5-GM24-72	MVTVDEVRKA MVTVDEVRKA MVTV <mark>E</mark> EVRKA	QRAEGPATIL QRAEGPATVL QRAEGPATVL	AIGTATPP AIGTATPP <mark>GHRN</mark> G <mark>NSSQ</mark> P	NCVDQSTYPD NCIDQSTYPD VWTRARTPTT	YYFRITKSEH YYFRITNSEH TEVSPTASTR	KTELKEKFOR 58 KTELKEKFOR 58 LSSKRNSSAC 60
PKS1–GM29–48 PKS5 R Royalty PKS5–GM24–72	MCDKSMIKKR MCDKSMIKKR <mark>VS</mark> DKSMIKKR	YMYLTEEILK YMYLTEEILK YMYLTEEILK 144	ENPSMCEYMA ENPSMCEYMA DNPSMCEYMA	PSLDARQDMV PSLDARQDMV PSLDARQDMV 16	VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE	AATKAIKEWG 118 AATKAIKEWG 118 AATKAIKEWG 120 180
PKS1–GM29–48 PKS5 R Royalty PKS5–GM24–72	QPKSKITHLV QPKSKITHLV QPKSKITHLV	FCTTSGVDMP FCTTSGVDMP FCTTSGVDMP	GADYQLTKLL GADYQLTKLL GADYQLTKLL	GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM 220	MYQQGCFAGG MYQQGCFAGG MYQQGCFAGG	TVLRLAKDLA 178 TVLRLAKDLA 178 TVLRLAKDLA 180 240
PKS1–GM29–48 PKS5 R Royalty PKS5–GM24–72	ENN <mark>K</mark> GARVLV ENNRGARVLV ENNRGARVLV	VCSEITAVTF VCSEIXAVTF VCSEITAVTF	RGPSDTHLDS RGPSDTHLDS RGPSDTHLDS	LVGQALFGDG LVGQALFGDG LVGQALFGDG	AAAIIVG <mark>S</mark> DP AAAIIVGADP AAAIIVGADP	LPDIERPLFE 238 LPKIERPLFE 238 LPEIERPLFE 240
PKS1-GM29-48 PKS5 R Royalty PKS5-GM24-72	LVSAAQTILP LVSAAQTILP LVSAAQTILP	D SDGA I DGHL D SDGA I DGHL D SDGA I DGHL	REVGLTFHLL REVGLTFHLL REVGLTFHLL	KDVPGLISKN KDVPGLISKN KDVPGLISKN	I EKSLNEAFK I EKSLNEAFK I EKSLNEAFK	PLDITDWNSL 298 PLDITDWNSL 298 PLDITDWNSL 300
PKS1–GM29–48 PKS5 R Royalty PKS5–GM24–72	FWI AHPGGPA FWI AHPGGPA FWI AHPGGPA	I LDQVEAKLG I LDQVETKLG I LDQVETKLG	LKPEKLEATR LKPEKLEATR LKPEKLEATR	NILSEYGNMS HILSEYGNMS HILSEYGNMS	SACVLFILDE SACVLFILDE SACVLFILDE	VRRKSVANGH 358 VRRKSATNGL 358 VRKSAANGL 360
PKS1–GM29–48 PKS5 R Royalty PKS5–GM24–72	KTTGEGLEWG KTTGEGLEWG KTTGEGLEWG	VLFGFGPGLT VLFGFGPGLT VLFGFGPGLT	VETVVLHSV <mark>A</mark> VETVVLHSVG VETVVLHSVG	AST 391 VTA 391 VTA 393		
В		20		40		60
PKS1-GM29-48 CHS5 R Meeker PKS5-GM24-72	MVTVDEVRKA MVTVDEVRKA MVTV <mark>E</mark> EVRKA	QRAEGPATIL QRAEGPATIL QRAEGPATUL 80	AIGTATPP AIGTATPP GHRNGNSSOP	NCVDQSTYPD NCVDQSTYPD VWTRARTPTT 100	YYFRITKSEH YYFRITKSEH TFVSPTASTR	KTELKEKFOR 58 KTELKEKFOR 58 LSSKRNSSAC 60 120
PKS1-GM29-48 CH55 R Meeker PKS5-GM24-72	MCDKSMIKKR MCDKSMIKKR <mark>VS</mark> DKSMIKKR	YMYLTEEILK YMYLTEEILK YMYLTEEILK 140	EN P SMC EYMA EN P SMC EYMA D N P SMC EYMA	PSLDARQDMV PSLDARQDMV PSLDARQDMV 160	VVEI PKLGKE VVEI PKLGKE VVEI PKLGKE	AATKAIKEWG 118 AATKAIKEWG 118 AATKAIKEWG 120 180
PKS1-GM29-48 CHS5 R Meeker PKS5-GM24-72	QPKSKITHLV QPKSKITHLV QPKSKITHLV	FCTTSGVDMP FCTTSGVDMP FCTTSGVDMP 200	GADYQLTKLL GADYQLTKLL GADYQLTKLL	GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM 220	MYQQGCFAGG MYQQGCFAGG MYQQGCFAGG	TVLRLAKDLA 178 TVLRLAKDLA 178 TVLRLAKDLA 180 240
PKS1–GM29–48 CHS5 R Meeker PKS5–GM24–72	ENN <mark>K</mark> GARVLV ENNRGARVLV ENNRGARVLV	VCSEITAVTF VCSEITAVTF VCSEITAVTF 260	RGPSDTHLDS RGPSDTHLD <mark>I</mark> RGPSDTHLDS	LVGQALFGDG LVGQALFGDG LVGQALFGDG 280	AAAIIVG <mark>S</mark> DP AAAIIVGADP AAAIIVGADP	LPDIERPLFE 238 LPKIERPLFE 238 LPEIERPLFE 240 300
PKS1-GM29-48 CHS5 R Meeker PKS5-GM24-72	LV SAAQT I LP LV SAAQT I LP LV SAAQT I LP	DSDGAIDGHL DSDGAIDGHL DSDGAIDGHL 320	REVGLTFHLL REVGLTFHLL REVGLTFHLL	KDVPGLISKN KDVPGLISKN KDVPGLISKN XDVPGLISKN	I EKSLNEAFK I EKSLNEAFK I EKSLNEAFK	PLDITDWNSL 298 PLDITDWNSL 298 PLDITDWNSL 300 360
PKS1-GM29-48 CHS5 R Meeker PKS5-GM24-72	FWI AH PGGPA FWI AH PGGPA FWI AH PGGPA	I LDQVEAKLG I LDQVETKLG I LDQVETKLG 380	LKPEKLEATR LKPEKLEATR LKPEKLEATR	NILSEYGNMS HILSEYGNMS HILSEYGNMS	SACVLFILDE SACVLFILDE SACVLFILDE	VRRKSVANGH 358 VRRKSATNGL 358 VRKKSAANGL 360
PKS1-GM29-48 CHS5 R Meeker PKS5-GM24-72	KTTGEGLEWG KTTGEGLEWG KTTGEGLEWG	VLFGFGPGLT VLFGFGPGLT VLFGFGPGLT	VETVVLHSVA VETVVLHSVG VETVVLHSVG	AST 391 VTA 391 VTA 393		
С						

- CHS5



Amino acid sequence

CHS5 of strawberry (*Fragaria vesca* subsp *Vesca*).

CHS of prune (Prunus persical)

There are more	differences
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		20		40		60	
PKS1-GM29-48	MVTVDEVRKA		AL GTATPP		VVERITKSEH	KTELKEKEOR	58
CHS-P. persical	MVTVEEVRKA	QRAEGPATVL	AIGTATPP	NCVDQATYPD	YYFRITNSEH	KTELKEKFQR	58
PKS5-GM24-72	MVTVEEVRKA	QRAEGPATVL	GHRNGNSSQP	VWTRARTPTT	TFVSPTASTR	LSSKRNSSAC	60
Consensus	MVTVEEVRKA	QRAEGPATVL	AIGTATPP	NCVDQ * TYPD	YYFRIT*SEH	KTELKEKFQR	
		80		100		120	
PKS1-GM29-48	MCDKSMIKKR	YMYLTEEILK	ENPSMCEYMA	PSLDARQDMV	VVEIPKLGKE	AATKAIKEWG	118
CHS-P. persical	MCDKSMIKKR	YMYLTEEILK	ENPSMCEYMA	PSLDARQDMV	VVEIPKLGKE	AATKAIKEWG	118
PKS5-GM24-72	VSDKSMIKKR	YMYLTEEILK	D NPSMCEYMA	PSLDARQDMV	VVEIPKLGKE	AATKAIKEWG	120
Consensus	MCDKSMIKKR	YMYLTEEILK	ENPSMCEYMA	PSLDARQDMV	VVEIPKLGKE	AATKAIKEWG	
		140		160		180	
PKS1-GM29-48	QPKSKITHLV	FCTTSGVDMP	GADYQLTKLL	GLRPSVKRLM	MYQQGCFAGG	TVLRLAKDLA	178
CHS-P. persical	QPKSKITHLV	FCTTSGVDMP	GADYQLTKLL	GLRSSVKRLM	MYQQGCFAGG	TVLRLAKDLA	178
PK35-GWI24-72	OPKSKITHLV	FCTTSGVDMP	GADTQLIKLL	CLERSVKRLM	MYOOCCEACC		180
Consensus	QFK3KTTHLV	200	GADIQLIKLL	220	MIQQUEFAGU		
		<u>i</u>		1			
PKS1-GM29-48		VCSELTAVTE	RGPSDTHLDS		AAAIIVGSDP		238
PKS5-GM24-72	ENNRGARVLV	VCSEITAVTE	RGPSDTHLDS	LVGQALFGDG	AAAIIVGADP		240
Consensus	ENNRGARVLV	VCSEITAVTF	RGPSDTHLDS	LVGQALFGDG	AAAIIVGSDP	LPEIERPLFE	
		260		280		300	
PKS1_CM29_48		DSDGALDGHI	REVGLITENT	KDVPGLISKN	IEKSINEAEK		298
CHS-P. persical	VVSAAQTILP	DSDGAIDGHL	REVGLTFHLL	KDVPGLISKN	IEKSLNEAFQ	PLGISDWNSL	298
PKS5-GM24-72	LVSAAQTILP	DSDGAIDGHL	REVGLTFHLL	KDVPGLISKN	IEKSLNEAFK	PLDITDWNSL	300
Consensus	LVSAAQTILP	DSDGAIDGHL	REVGLTFHLL	KDVPGLISKN	IEKSLNEAFK	PLDITDWNSL	
		320		340		360	
PKS1-GM29-48	FWIAHPGGPA	ILDQVEAKLG	LKPEKLEATR	NILSEYGNMS	SACVLFILDE	VRRKSVANGH	358
CHS-P. persical	FWIAHPGGPA	ILDQVE <mark>S</mark> KLA	LKPEKLEATR	HILSEYGNMS	SACVLFILDE	VRKRATKKGL	358
PKS5-GM24-72	FWIAHPGGPA	ILDQVETKLG	LKPEKLEATR	HILSEYGNMS	SACVLFILDE	VRKKSAANGL	360
Consensus	FWIAHPGGPA	I LDQVE * KLG	LKPEKLEATR	HILSEYGNMS	SACVLFILDE	VRKKS*ANGL	
		380 I					
PKS1-GM29-48	KTTGEGLEWG	VLFGFGPGLT	VETVVLHSVA	AST 391			
CHS-P. persical	KTTGDGLDWG	VLFGFGPGLT	VETVVLHSVG	LNA 391			
PK35-GM24-72	KTTGEGLEWG	VLEGEGPGLT	VETVVLHSVG	VIA 393			
Consensus	KIIGEGLEWG	VEFGFGFGET	VETVVLH3VG	A			
		30		40		60	
	_	20 I		40 I	_	60 I)
PKS1-GM29-48	MVTVDEVRKA	QRAEGPATIL	AIGTATPP	40 NCVDQSTYPD	YYFRITKSEH		58
PKS1-GM29-48 CHS5-Fr	MVTVDEVRKA MVTVEEVRKA	QRAEGPATIL QRAEGPATVL	AI GTATPP AI GTATPP	40 I NCVDQSTYPD NCIDQSTYPD	YYFRITKSEH YYFRITNSEH	60 I KTELKEKFQR KAELKEKFQR	58
PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus	MVTVDEVRKA MVTVEEVRKA MVTVEEVRKA	QRAEGPATIL QRAEGPATVL QRAEGPATVL QRAEGPATVL	AIGTATPP AIGTATPP GHRNGNSSQP AI-GTATPP	40 I NCVDQSTYPD NCIDQSTYPD VWTRARTPTT	YYFRITKSEH YYFRITNSEH TFVSPTASTR YYERIT*SEH	60 I KTELKEKFOR KAELKEKFOR LSSKRNSSAC	58 58 60
PKS1–GM29–48 CHS5–Fr PKS5–GM24–72 Consensus	MVTVDEVRKA MVTVEEVRKA MVTVEEVRKA MVTVEEVRKA	QRAEGPATIL QRAEGPATVL QRAEGPATVL QRAEGPATVL 80	AIGTATPP AIGTATPP GHRNGNSSOP AIGTATPP	40 I NCVDQSTYPD NCIDQSTYPD VWTRARTPTT NC*DQSTYPD	YYFRITKSEH YYFRITNSEH TFVSPTASTR YYFRIT*SEH	GC I KTELKEKFQR KAELKEKFQR LSSKRNSSAC K * ELKEKFQR 120	58 58 60
PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus	MVTVDEVRKA MVTVEEVRKA MVTVEEVRKA MVTVEEVRKA	QRAEGPATIL QRAEGPATVL QRAEGPATVL QRAEGPATVL 80	AIGTATPP AIGTATPP GHRNGNSSOP AIGTATPP	40 NCVDQSTYPD NCIDQSTYPD VWTRARTPTT NC*DQSTYPD 100	YYFRITKSEH YYFRITNSEH TFVSPTASTR YYFRIT*SEH	KTELKEKFOR KAELKEKFOR LSSKRNSSAC K*ELKEKFOR 120	58 58 60
PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48	MVTVDEVRKA MVTVEEVRKA MVTVEEVRKA MVTVEEVRKA MCDKSMIKKR	QRAEGPATIL QRAEGPATVL QRAEGPATVL QRAEGPATVL QRAEGPATVL 81 WYLTEEILK	AIGTATPP AIGTATPP GHRNGNSSO AIGTATPP ENPSMCEYMA	40 1 NCVDQSTYPD NCIDQSTYPD VWTRARTPTT NC*DQSTYPD 10 PSLDARQDMV PSLDARQDMV	YYFRITKSEH YYFRITNSEH TFVSPTASTR YYFRIT*SEH VVEIPKLGKE	KTELKEKFOR KAELKEKFOR SSKRNSSAC K*ELKEKFOR 120 AATKAIKEWG	58 58 60 118
PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72	MVTVDEVRKA MVTVEEVRKA MVTVEEVRKA MVTVEEVRKA MCDKSMIKKR MCDKSMIKKR VSDKSMIKKR	20 1 QRAEGPATVL QRAEGPATVL QRAEGPATVL 80 1 YMYLTEEILK YMYLTEEILK YMYLTEEILK	AI GTATPP AI GTATPP GHENGNSSOP AI GTATPP ENPSMCEYMA ENPSMCEYMA DNPSMCEYMA	40 NCVDQSTYPD NCIDQSTYPD VWTRARTPTT NC*DQSTYPD 100 100 100 100 100 100 100 10	YYFRITKSEH YYFRITNSEH TFYSPTASTR YYFRIT*SEH VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE	KTELKEKFOR KAELKEKFOR LSSKRNSSAC K*ELKEKFOR 12 AATKAIKEWG AATKAIKEWG AATKAIKEWG	58 58 60 118 118
PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus	MVTVDEVRKA MVTVEEVRKA MVTVEEVRKA MVTVEEVRKA MCDKSMIKKR MCDKSMIKKR VSDKSMIKKR	QRAEGPATIL QRAEGPATVL QRAEGPATVL QRAEGPATVL QRAEGPATVL MYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK	AI GTATPP AI GTATPP GHRNGNSSOP AI GTATPP ENPSMCEYMA ENPSMCEYMA ENPSMCEYMA ENPSMCEYMA	40 NCVDQSTYPD NCIDQSTYPD VWTRATPTT NC*DQSTYPD PSLDARQDMV PSLDARQDMV PSLDARQDMV PSLDARQDMV	YYFRITKSEH YYFRITNSEH TEVSPTASTR YYFRIT*SEH VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE	KTELKEKFOR KAELKEKFOR LSSKRNSSAC K*ELKEKFOR AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG	58 58 60 118 118 120
PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus	MVTVDEVRKA MVTVEEVRKA MVTVEEVRKA MVTVEEVRKA MCDKSMIKKR MCDKSMIKKR MCDKSMIKKR	20 GRAEGPATVL GRAEGPATVL QRAEGPATVL QRAEGPATVL 9 MYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK 1100	AI GTATPP AI GTATPP GHRNGNSSOP AI GTATPP ENPSMCEYMA ENPSMCEYMA ENPSMCEYMA	40 NCVDQSTYPD NCIDQSTYPD VWTRATTPTT NC*DQSTYPD 10 PSLDARQDMV PSLDARQDMV PSLDARQDMV PSLDARQDMV 16(YYFRITKSEH YYFRITNSEH TFVSPTASTR YYFRIT*SEH VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE	KTELKEKFOR KAELKEKFOR LSSKRNSSAC K*ELKEKFOR 12 AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG	58 58 60 118 118 120
PKS1-GM29-48 CHS5-Fr PKS5-CM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus	MVTVDEVRKA MVTVEEVRKA MVTVEEVRKA MVTVEEVRKA MCDKSMIKKR VSDKSMIKKR MCDKSMIKKR	QRAEGPATIL QRAEGPATVL QRAEGPATVL QRAEGPATVL QRAEGPATVL QRAEGPATVL VMVLTEEILK YMVLTEEILK YMVLTEEILK 110	AIGTATPP AI-GTATPP GHRNGNSSP AIGTATPP ENPSMCEYMA ENPSMCEYMA ENPSMCEYMA	40 NCVDQSTYPD NCIDQSTYPD YWTRATPTT NC*DQSTYPD 10 PSLDARQDMV PSLDARQDMV PSLDARQDMV PSLDARQDMV PSLDARQDMV	YYFRITKSEH YYFRITNSEH TFYSPTASTR YYFRIT*SEH VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE	KTELKEKFOR KAELKEKFOR LSSKENSSAC K*ELKEKFOR AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG	58 58 60 118 118 120
PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48 CHS2-Fr	MVTVDEVRKA MVTVEEVRKA MVTVEEVRKA MCDKSMIKKR MCDKSMIKKR VSDKSMIKKR MCDKSMIKKR QRKSKITHLV ORKSKITHLV	QRAEGPATIL QRAEGPATVL QRAEGPATVL QRAEGPATVL QRAEGPATVL MYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK 140 	AI GTATPP AI GTATPP GHRNGNSSO AI GTATPP ENPSMCEYMA ENPSMCEYMA ENPSMCEYMA ENPSMCEYMA GADYQLTKLL GADYQLTKLL	40 NCVDQSTYPD NCIDQSTYPD VWTRATPTT NC*DQSTYPD 100 PSLDARQDMV PSLDARQDMV PSLDARQDMV PSLDARQDMV 160 160 160 160 160 160 160 160	YYFRITKSEH YYFRITNSEH YYFRITSEH YYFRITSEH VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE	KTELKEKFOR KAELKEKFOR LSSKRNSSAC ATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG I I I TVURLAKDLA	58 58 60 118 118 120 120
PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72	MVTVDEVRKA MVTVEEVRKA MVTVEEVRKA MVTVEEVRKA MCDKSMIKKR MCDKSMIKKR MCDKSMIKKR QPKSKITHLV QPKSKITHLV QPKSKITHLV	QRAEGPATIL QRAEGPATVL QRAEGPATVL QRAEGPATVL QRAEGPATVL MYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK FCTTSGVDMP FCTTSGVDMP	AIGTATPP AIGTATPP GHRNGNSSOP AIGTATPP ENPSMCEYMA ENPSMCEYMA ENPSMCEYMA GADYQLTKLL GADYQLTKLL GADYQLTKLL	40 NCVDQSTYPD NCIDQSTYPD VWTRATPTT NC*DQSTYPD 11 PSLDARQDMV PSLDARQDMV PSLDARQDMV PSLDARQDMV GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM	YYFRITKSEH YYFRITKSEH TFYSPTASTR YYFRIT*SEH VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE MYQQQCFAGG MYQQQCFAGG	KTELKEKFOR KAELKEKFOR LSSKARSSAC K*ELKEKFOR 12 AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG	58 58 60 118 118 120 120 178 178 178
PKS1-GM29-48 CHS5-Fr PKS5-CM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus	MVTVDEVRKA MVTVEEVRKA MVTVEEVRKA MCDKSMIKKR MCDKSMIKKR VSDKSMIKKR QPKSKITHLV QPKSKITHLV QPKSKITHLV	QRAEGPATIL QRAEGPATVL QRAEGPATVL QRAEGPATVL QRAEGPATVL QRAEGPATVL MYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK	AIGTATPP AI-GTATPP GHENGNSSOP AIGTATPP ENPSMCEYMA ENPSMCEYMA ENPSMCEYMA GADYQLTKLL GADYQLTKLL GADYQLTKLL GADYQLTKLL	40 NCVDQSTYPD NCIDQSTYPD VWTRATPTT NC*DQSTYPD PSLDARQDMV PSLDARQDMV PSLDARQDMV PSLDARQDMV 16 GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM	YYFRITKSEH YYFRITNSEH TFYSPTASTR YYFRIT*SEH VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE MYQOGCFAGG MYQOGCFAGG MYQOGCFAGG	KT ELKEKFOR KAELKEKFOR LSSKNSSAC K * ELKEKFOR AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG TVLRLAKDLA TVLRLAKDLA TVLRLAKDLA	58 58 60 118 118 120 178 178 178 180
PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus	MVTVDEVRKA MVTVEEVRKA MVTVEEVRKA MVTVEEVRKA MCDKSMIKKR MCDKSMIKKR MCDKSMIKKR QPKSKITHLV QPKSKITHLV QPKSKITHLV	20 GRAEGPATIL QRAEGPATVL QRAEGPATVL QRAEGPATVL 01 01 01 01 01 01 01 01 01 01	AIGTATPP AIGTATPP GHRNGNSSOP AIGTATPP ENPSMCEYMA ENPSMCEYMA ENPSMCEYMA GADYQLTKLL GADYQLTKLL GADYQLTKLL	40 NCVDQSTYPD NCIDQSTYPD VWTRATPTT NC*DQSTYPD 101 PSLDARQDMV PSLDARQDMV PSLDARQDMV PSLDARQDMV 161 GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM 3220	YYFRITKSEH YYFRITKSEH YYFRITSEH VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE WYQQCFAGG MYQQGCFAGG MYQQCCFAGG	KT ELK EK FOR KA ELK EK FOR LSSK RNSSAC K* ELK EK FOR ATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG ATKAIKEWG ATKAIKEWG ATKAIKEWG ATKAIKEWG ATKAIKEWG AATKAIKEWG	58 58 60 118 118 120 178 178 178
PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus	MVTVDEVRKA MVTVEEVRKA MVTVEEVRKA MCDKSMIKKR MCDKSMIKKR MCDKSMIKKR MCDKSMIKKR QPKSKITHLV QPKSKITHLV QPKSKITHLV	20 GRAEGPATVL GRAEGPATVL QRAEGPATVL QRAEGPATVL QRAEGPATVL MYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK YMYLTEEILK 20 FCTTSGVDMP FCTTSGVDMP FCTTSGVDMP FCTTSGVDMP	AIGTATPP AIGTATPP GHRNGSSOP AIGTATPP ENPSMCEYMA ENPSMCEYMA ENPSMCEYMA GADYQLTKLL GADYQLTKLL GADYQLTKLL GADYQLTKLL	40 NCVDQSTYPD NCIDQSTYPD VWTRATPTT NC*DQSTYPD 10 PSLDARQDMV PSLDARQDMV PSLDARQDMV PSLDARQDMV PSLDARQDMV CLRPSVKRLM GLRPSVKRLM GLRPSVKRLM 227 227 227 227 227 227 227 22	YYFRITKSEH YYFRITKSEH TFYSPTASTR YYFRIT*SEH VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE MYQQGCFAGG MYQQGCFAGG MYQQGCFAGG	KT ELK EK FOR KA ELK EK FOR LSSKARSSAC K * ELK EK FOR 12 AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKELG TVLRLAKDLA TVLRLAKDLA TVLRLAKDLA TVLRLAKDLA	58 58 60 118 120 178 178 178 178
PKS1-GM29-48 CHS5-Fr PKS5-CM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-CM24-72 Consensus PKS1-GM29-48	MVTVDEVRKA MVTVEEVRKA MVTVEEVRKA MCDKSMIKKR MCDKSMIKKR VSDKSMIKKR QPKSKITHLV QPKSKITHLV QPKSKITHLV QPKSKITHLV PKSKITHLV	QRAEGPATIL QRAEGPATVL QRAEGPATVL QRAEGPATVL QRAEGPATVL QRAEGPATVL MYLTEEILK YMYLTEEILK	AIGTATPP AIGTATPP GHRNGNSSOP AIGTATPP ENPSMCEYMA ENPSMCEYMA GADYQLTKLL GADYQLTKLL GADYQLTKLL GADYQLTKLL GADYQLTKLL GADYQLTKLL BRGPSDTHLDS	40 NCVDQSTYPD NCIDQSTYPD VWTRATPTT NC*DQSTYPD 10 PSLDARQDMV PSLDARQDMV PSLDARQDMV PSLDARQDMV 16 GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM	YYFRITKSEH YYFRITKSEH YYFRITSEH VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE MYQQGCFAGG MYQQGCFAGG MYQQGCFAGG MYQQGCFAGG	KTELKEKFOR KAELKEKFOR LSEKENSSAC K*ELKEKFOR AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG TVLRLAKDLA TVLRLAKDLA TVLRLAKDLA TVLRLAKDLA TVLRLAKDLA TVLRLAKDLA TVLRLAKDLA	58 58 60 118 120 178 178 178 178 178 178 238
PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72	MVTVDEVRKA MVTVEEVRKA MVTVEEVRKA MCDKSMIKKR MCDKSMIKKR MCDKSMIKKR MCDKSMIKKR QPKSKITHLV QPKSKITHLV QPKSKITHLV QPKSKITHLV ENNRGARVLV ENNRGARVLV	20 GRAEGPATVL GRAEGPATVL QRAEGPATVL QRAEGPATVL QRAEGPATVL MYLTEEILK YMY	AIGTATPP AIGTATPP GHRNGNSSOP AIGTATPP ENPSMCEYMA ENPSMCEYMA GADYQLTKLL GADYQLTKLL GADYQLTKLL GADYQLTKLL GADYQLTKLL RGPSDTHLDS RGPSDTHLDS	40 NCVDQSTYPD NCIDQSTYPD VWTRATPTT NC*DQSTYPD PSLDARQDMV PSLDARQDMV PSLDARQDMV PSLDARQDMV PSLDARQDMV GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM GLRPSVKRLM	YYFRITKSEH YYFRITKSEH TFVSPTÄSTR YYFRIT*SEH VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE MYQQGCFAGG MYQQGCFAGG MYQQGCFAGG AAAIIVGSDP AAAIIVGSDP	KTELKEKFOR KAELKENSSAC K*ELKENSSAC K*ELKENSSAC AATKAIKEWG	58 58 60 118 118 120 178 178 178 180 238 238 248
PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus PKS1-GM29-48 CHS5-Fr PKS5-GM24-72 Consensus	MVTVDEVRKA MVTVEEVRKA MVTVEEVRKA MCDKSMIKKR MCDKSMIKKR MCDKSMIKKR MCDKSMIKKR QPKSKITHLV QPKSKITHLV QPKSKITHLV QPKSKITHLV QPKSKITHLV QPKSKITHLV QPKSKITHLV QPKSKITHLV QPKSKITHLV QPKSKITHLV QPKSKITHLV QPKSKITHLV QPKSKITHLV	QRAEGPATVL QRAEGPATVL QRAEGPATVL QRAEGPATVL QRAEGPATVL QRAEGPATVL QRAEGPATVL QRAEGPATVL QRAEGPATVL MYLTEEILK YMYLTEEILK	AIGTATPP AIGTATPP GHRNGNSGP AIGTATPP ENPSMCEYMA ENPSMCEYMA ENPSMCEYMA GADYQLTKLL GADYQLTKLL GADYQLTKLL GADYQLTKLL RGPSDTHLDS RGPSDTHLDS RGPSDTHLDS	AD NCVDQSTYPD NCIDQSTYPD VWTRATPTT NC*DQSTYPD PSLDARQDMV PSLDARQDMV PSLDARQDMV PSLDARQDMV PSLDARQDMV SLDARQDV SLDARDV SLDARDV SLDAVS SLDARQDV SLDARDV SLDARDV SLDARDV SLDAVS SLDARDV SLDARDV SLDARDV SLDARDV SLDAVS SLDARDV SLDARDV SLDARDV SLDAVS SLDARDV S	YYFRITKSEH YYFRITKSEH TFYSPKIGKE YYFRIT*SEH VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE VVEIPKLGKE MYQQGCFAGG MYQQGCFAGG MYQQGCFAGG AAAIIVGSDP AAAIIVGSDP AAAIIVGSDP	KT ELKEKFOR KA ELKEKFOR LSKRNSSAC K * ELKEKFOR AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG AATKAIKEWG LURLAKDLA TVLRLAKDLA TVLRLAKDLA TVLRLAKDLA LPDIERPLFE LPEVERPLFE LPEVERPLFE LPEIERPLFE	58 58 60 118 120 178 178 180 178 180 238 238 238 240
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RiPKS1 of BAC24p12

Comparison at Amino acid sequence level with red raspberry PKS cv.

- Royalty
- Meeker

RiPKS1 : PKS5/CHS5/CHS11













V Construction of Physical Map









The MTP and mini physical maps for 117 kb of BAC24P12 and 98 kb of BAC29M05.







Construction of the mini physical map of the two BACs derived from red raspberry cv. Glen Moy genome



IV. Conclusion

- Genetic information of PKS genes in red raspberry
- Fosmid library
- Mini Physical Maps
- The additional information of PKS genes of red raspberry cv. Glen Moy are extensively powerful tool for further studies and applications with the same family and other related fruits as well as other several genes
- Advanced techniques / Molecular or genetic approach use shorter time / provide higher qualities for plants







VI. Acknowledgments :

Dr. Paterson A., Dr Ellis E. M. Special for Dr. Lutz E. M. NSRU, Thailand ATPER



