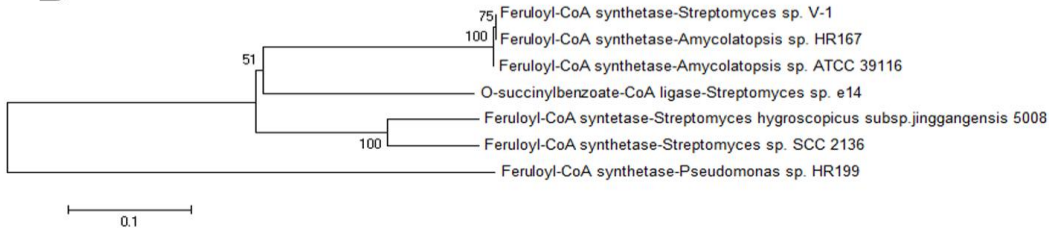


**A**

i	-----MRNEG-----LGSWPARRARKTPHRTALIHDRS-VTYAELYERTTRLAHLR	47
ii	MKDRGDMRNEG-----LGSWPARRARKTPHRTALIHGDTT-VTYAGLYERTTRLAHLR	54
iii	-----VRNQG-----LGSWPVRRARMSPHATAVRHGGA-LTYAELSRVARLANGLR	47
iv	-----VRNQG-----LGSWPVRRARMSPHATAVRHGGA-LTYAELSRVARLANGLR	47
v	-----MRNQG-----LGSWPVRRARMSPHATAVRHGGA-LTYAELSRVARLANGLR	47
vi	-----MRNRG-----IGSWPARRARKTPGRVAVVHGDRV-WTYRQLHERVRLAHLR	47
vii	MRSLEALLPFPGRILELHWAKTREPEQTCVAARAANGEWRRISYAEFMFNVRVIAQSLL	60
	: * : * : * . : . : . : * : * : * : * : * : *	
i	ARGVVRGDRVIAYLGNHPAFLETLFAAGTLGAVFVPLNIRLAEPETAYQLADSGAKALVH	107
ii	DSGVRRGDRVIAYLGNHPASYLETLFAAGTLGAVFVPLNIRLAGPELAYQLTDSGAKALVY	114
iii	AAGVVRGDRVIAYLGNHPAYLETLFACGQAGAVFVPLNIRLGVPELDHALADSGASVLIH	107
iv	AAGVVRGDRVIAYLGNHPAYLETLFACGQAGAVFVPLNIRLGVPELDHALADSGASVLIH	107
v	AAGVVRGDRVIAYLGNHPAYLETLFACGQAGAVFVPLNIRLGVPELDHALADSGASVLIH	107
vi	GLGVGHGDRVIAYLGNHPAFLEALFAAGALGAVFVPLNSRLTAPELAFNLADSGSSVLIH	107
vii	PTGLSAERPLLIVSGNDLEHLQAFGAMTAGIPYCPVSPAYSLLSQDLAKLRHIVGLLQP	120
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i	APSQAPPAAGPPGSTEV-----TYVEVGAAY-----EELLAASDEPID---QPVR	151
ii	GPTFGGLVAGLPGNSDVR-----TYVEVGAAY-----DQLLDMASDEAID---EPVI	158
iii	TPEHAETVAALAAAGRLR-----VPAGE-----LDAADDEPPD---LPVG	144
iv	TPEHAETVAALAAAGRLR-----VPAGE-----LDAADDEPPD---LPVG	144
v	TPEHAETVAALAAAGRLR-----VPAGE-----LDAADDEPPD---LPVG	144
vi	APQAAAAAAGAAATGTGTRRIAVSGPDPVPHEDPG---TLDYETLLAAADTAPLD---EPVA	162
vii	GLVFAADAAPFQRAIETILPDDVPAIFTRGELAGRRTVFSDSLLEQPGGIEADNAFAATG	180
	. . . . . * . . . . . * . . . . .	
i	LDDTCIIMYTSGTTGRPKGAMLTGHNLTWNAFNVLDHDLTADERALVS---APLHHTAGL	209
ii	PDDTCIIMYTSGTTGRPKGAMLTGHNLTWNAFNVLDQDVIIDERALVS---APLHHTAGL	216
iii	LDDVCLLMTYTSSTGRPKGAMLTGHNLTWNCVNVLDLADSERALVA---APLHHAAL	202
iv	LDDVCLLMTYTSSTGRPKGAMLTGHNLTWNCVNVLDLADSERALVA---APLHHAAL	202
v	LDDVCLLMTYTSSTGRPKGAMLTGHNLTWNCVNVLDLADSERALVA---APLHHAAL	202
vi	LDDPCVIMYTSGTTGRPKGAVLSHANITWNSVNVLDLADSERALVA---APLHHTAGL	220
vii	FDITAKFLFTSGSTLPAKAVPTTQMLCANQQMLLQTFPVFGEPPVLDVWLPWNHTFGG	240
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i	NMLTLPVLLKGGTCVLEAFDPA-----TFDLIERHRTIFMFGVPMFDQVARHFR	261
ii	NMLTLPVLLKGGTCVLEAFDPA-----TFDLIERHRTIFMFGVPMFEHVARHFR	268
iii	GMVCLPTLLKGGTVILHSAPDPA-----VLSAVEQERVTLVFGVPTMYQAIAAHFR	254
iv	GMVCLPTLLKGGTVILHSAPDPA-----VLSAVEQERVTLVFGVPTMYQAIAAHFR	254
v	GMVCLPTLLKGGTVILHSAPDPA-----VLSAVEQERVTLVFGVPTMYQAIAAHFR	254
vi	NMTCLPTLLKGGTVILHSAPDPA-----VLELLETLVTLFGVPMYDAMAARFR	272
vii	SHNIGIVLYNGGTYLDDGKPTAQGFATLRNLSEISPTAYLTVPRGWEEELVGLERDST	300
	. * : * * * * * . . . . . * : * * * * * : : : .	
i	WDGADLSSLRILTCGGSPVPT-----PLIARYQERGLTFLQGYGMEAAAPGTLFLDAE	314
ii	WADADLSSLRMLSCGGSPVPT-----PLIAAYQERGLTFLQGYGMEASPGVFLDAE	321
iii	WRSADLSSLRITLLCGGAPVPA-----DLASRYLDRGLAFVQGYGMEAAAPGVFLDRA	307
iv	WRSADLSSLRITLLCGGAPVPA-----DLASRYLDRGLAFVQGYGMEAAAPGVFLDRA	307
v	WRSADLSSLRITLLCGGAPVPA-----DLASRYLDRGLAFVQGYGMEAAAPGVFLDRA	307
vi	WADADLSSLRITLLCGGAPVPE-----RTLAAAYRARGLALQGGYGMEASPGVFLDRE	325
vii	LRERFFARMKLVFFAAAGLSQGIWDRDRVAEQHCGERIRMMAGLGMTETAPSCFTTGG	359
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i	HAVGKAGSAGVPHFFSDVRVVRPDLAPVDVGETGEIVVRGPHVMGSGYWGKPKETAEVFA-	373
ii	HAVTKAGSAGVPHFFSDVRVVRPDLAPADIGETGEVVRGPHVMGSGYWGKLPDETAEVFH-	380
iii	HVAEKIGSAGVPSFFTDVRLAGPSGEPVPPGKGEIVVSGPNVMKGYWGRPEATAEVLR-	366
iv	HVAEKIGSAGVPSFFTDVRLAGPSGEPVPPGKGEIVVSGPNVMKGYWGRPEATAEVLR-	366
v	HVAEKIGSAGVPSFFTDVRLAGPSGEPVPPGKGEIVVSGPNVMKGYWGRPEATAEVLR-	366
vi	RIFAKAGSAGVPHFFTDVRVAGPDRVAPGEPGEILVSGPHVMTGYWGLPRQTADAFTP	385
vii	-PLSMAGYIGLPAAGCEVPLVPVDG-----KLEGRFHGPHVMGSGYWRAPQNAQAFD-	410
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i	-DGWFRSGDAARVDD-----DGYVYIVDRIKDMIISGGENIYPAEIED-QLLAHPDIVEC	426
ii	-DGWFRSGDAARIDE-----DGYVTIIVDRIKDMIISGGENIYPAEIED-QLLAHPDIVEC	433
iii	-DGWFHSGDVATVDG-----DGYFHVVDRLKDMIISGGENIYPAEVEN-ELYGYPGVEAC	419
iv	-DGWFHSGDVATVDG-----DGYFHVVDRLKDMIISGGENIYPAEVEN-ELYGYPGVEAC	419
v	-DGWFHSGDVATVDG-----DGYFHVVDRLKDMIISGGENIYPAEVEN-ELYGYPGVEAC	419
vi	DGGWLRRTGDVARLDE-----DGYAYVVDVVDKMYISGGENIYPAEVED-ALLGHPVAEAC	439
vii	EEGYCSGDAIKLADPADPQKGLMFDGRIAEFDKLSGSGVFSVGLRTRAVLEGGYSVLD	470
	* : * * : * : . . . . . * : * * * * * : * : * : * : *	
i	AVIGVPDD-----TWGEVPRVAVVPREGATLAPDEVIASLGRKAKYKIPKT-	473
ii	AVIGVPDE-----KWGEVPRVAVVPREDVALDPDEVLASLAGRLAKYKIPKS-	480
iii	AVIGVPDP-----RWGEVGRVAVVPADGSRIDGDELLAWLRLTAGYKVPKS-	466
iv	AVIGVPDP-----RWGEVGRVAVVPADGSRIDGDELLAWLRLTAGYKVPKS-	466
v	AVIGVPDP-----RWGEVGRVAVVPADGSRIDGDELLAWLRLTAGYKVPKS-	466
vi	AVVGVDPD-----RWGEVGRVAVVLRPGARADEAGLLAHLHGLRKLAKYKIPKS-	486
vii	VVVAAPDRECLGLLVPRLLDCRALSGLKEASDAEVLASEPVRVAVFADWLKRLNREATG	530
	* . . * * : * : . . . . . * : * : * : * : * : *	
i	-----VVIADALPRTASGKLLKSRVRSRYGTTS-----	501
ii	-----VVLADELPRTASGKLLKSRVRKRYGTNSQSKEDT-----	514
iii	-----VEFTDRLPTTGSGLKGEVRRRFG-----	491
iv	-----VEFTDRLPTTGSGLKGEVRRRFG-----	491
v	-----VEFTDRLPTTGSGLKGEVRRRFG-----	491
vi	-----VVLVETLPRTASGLAKPAIRAAAYAHVADPS-----	518
vii	NASRIWVGLLDTPPSIDKGEVTDKGSINQRAVLQWRSKAVDALYRGEDQSMLRDEATL	589
	* : : * * . * : : . . . . .	

**B**



2

3 **Figure S2. Homologies of feruloyl-CoA synthetase from *Streptomyces* sp. V-1 with**

4 **the CoA ligases from various organisms. A.** The amino acid sequence of

5 feruloyl-CoA synthetase from *Streptomyces* sp. V-1 deduced from *fcs* (*iii*) was aligned

6 to: the amino acid sequence of (*i*) the feruloyl-CoA synthetase from *Streptomyces*

7 *hygroscopicus* subsp. *jinggangensis* 5008 [23], (*ii*) the feruloyl-CoA synthetase from

8 *Streptomyces* sp. SCC 2136 [24], (*iv*) the feruloyl-CoA synthetase from *Amycolatopsis*

9 sp. HR167 [10], (*v*) the acyl-CoA synthetase (AMP-forming) /AMP-acid ligase II

10 from *Amycolatopsis* sp. ATCC 39116 [8], (*vi*) the O-succinylbenzoate-CoA ligase

11 from *Streptomyces* sp. e14 (unpublished data), and (*vii*) the feruloyl-CoA synthetase

12 from *Pseudomonas* sp. HR199 [7]. Amino acids are specified by standard one-letter

13 abbreviations. *Dashes* indicate gaps introduced into the sequences to improve the

14 alignment. **B.** The relationship between the feruloyl-CoA synthetase of *Streptomyces*

15 sp. V-1 and the proteins in panel **A** was displayed as a phylogenetic tree, which was

16 constructed on the basis of the Neighbor-Joining (NJ) method using the ClustalX and

17 MEGA 5.0 softwares. The bar indicates 10% difference in amino acid sequence. The

18 number at the branch point represents the percentage of 1,000 bootstrap repetitions.