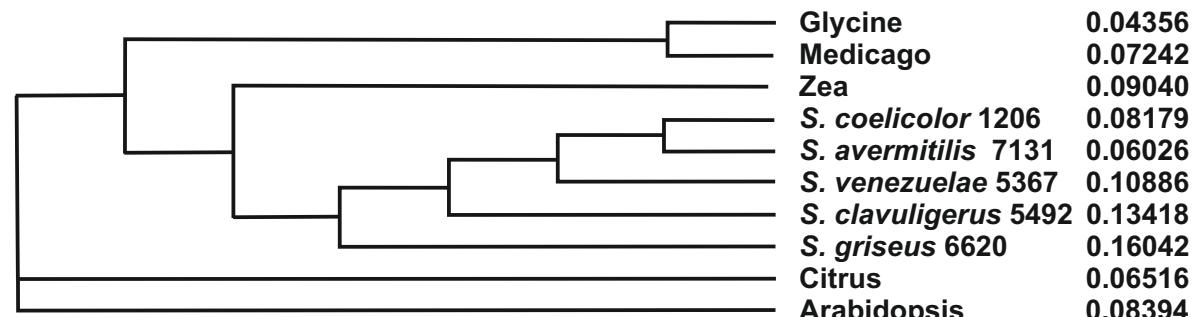


A

	132	to	146	181	to	197	266	to	278	295	to	307
<i>S. clavuligerus</i> 5492	PIAQLG	CAAGGAAVN		SLLSNGL	FGDGIAAAVV		FYIIH	HAGGPRLID	RATLT	EYGN	IASA	
<i>S. coelicolor</i> 1206	PIAQLG	CAAGGAAIN		SLLCNGL	FGDGIAAAVV		FYIVH	HAGGPRLID	RATLT	EYGN	IASA	
<i>S. avermitilis</i> 7131	PIAQLG	CAAGGSAIN		SLLSNGL	FGDGIAAAAR		FYIIH	HAGGPRLID	RATLT	EYGN	IASA	
<i>S. ven</i> 5367	PIAQLG	CAAGGAAIN		SLLSNGL	FGDAVAAA	VV	FYIIH	HAGGPRLID	RATLT	EYGN	IASA	
<i>S. griseus</i> 6620	PIAQLG	CAAGGAAIN		SLLSNGL	FGDALSAAVV		FFIVH	HAGGPRLID	RATLT	TERGN	IASS	
	*	***	***	**	****	*	*	* ***	***	*	* *	*** *
Glycine	MMYQQG	C	FAGGT	TVLR	SLVGQAL	FGDGA	AAVIV	FWIAH	P	GGPAI	L	RHV
Medicago	MMYQQG	C	FAGGT	TVLR	SLVGQAL	FGDGA	AAALIV	FWIAH	P	GGPAI	L	RVL
Citrus	MMYQQG	C	FAGGT	TVLR	SLVGQAL	FGDGA	AAVIV	FWIAH	P	GGPAI	L	RQVL
Arabidopsis	MMYQQG	C	FAGGT	TVLR	SLVGQAL	FGDGA	AAALIV	FWIAH	P	GGPAI	L	RHV
Zea Mays	MMYQQG	C	FAGGT	TVLR	SLVGQAL	FGDGA	AAAVVV	FWVAH	P	GGPAI	L	RHV
	138			188			270			303		

B

Supplementary Material

- Figure S1. A) Conserved sequences around the key amino acids located in chalcone synthases active center. The numbers given in the sequence correspond to *S. clavuligerus* Ncs, where the key amino acids are Cys¹³⁸, Phe¹⁸⁸, His²⁷⁰ and Asn³⁰³.
- B) Phylogenetic tree of plant and *Streptomyces* chalcone synthases. The origin of the sequences used is indicated at the right side. Numbers at the far right side correspond to the genetic distance index.