

Electronic Supplementary Information

Metabolic engineering with systems biology tools to optimize production of prokaryotic secondary metabolites

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Table S1 Recent studies aimed at optimizing the production of secondary metabolites since 2012.

Secondary metabolite	Application	Production host	Approach	Production improvement	Refs
36-Methyl-FK506	Improving neurite outgrowth activity	<i>Streptomyces</i> sp. KCTC 11604BP $\Delta tcbB$ mutant strain (heterologous host)	Heterologous expression of isobutyrylmalonyl-CoA pathway from <i>Streptomyces</i> sp. CNH189	2-fold increase in titer, compared to the native host	1
5-Oxomilbemycins A3/A4	A precursor of an antiparasitic milbemycin oxime	<i>Streptomyces bingchenggensis</i>	Atmospheric and room temperature plasma (ARTP) mutation system, followed by knocking out a gene responsible for ketonization of 5-oxomilbemycins	Approximately 2-fold increase in titer, compared to the initial strain overproducing milbemycins	2
6-Deoxyerythronolide B	Macrolide core of an antibiotic erythromycin	<i>Bacillus subtilis</i> (heterologous host)	Optimized heterologous expression of 6-deoxyerythronolide B biosynthetic gene cluster from <i>Saccharopolyspora erythraea</i> , followed by removal of native secondary metabolite biosynthetic gene clusters and an operon for propionyl-CoA utilization, and feeding of propionate	43% increase in yield, compared to the initial engineered strain	3
A21978C (daptomycin)	Antibiotic against Gram-positive bacterial pathogens	<i>Streptomyces roseosporus</i>	Reporter-guided <i>rpsL</i> mutation selection method and ribosome engineering using streptomycin	2.2-fold increase in titer, compared to the parent strain	4
Actinorhodin	Antibiotic	<i>Streptomyces coelicolor</i>	Genome-scale metabolic modeling and its use to identify overexpression targets	52-fold increase in titer, compared to the wild-type	5
Actinorhodin	Antibiotic	<i>Streptomyces coelicolor</i>	Overexpression of the gene <i>abrC3</i> encoding a positive response regulator of antibiotic biosynthesis	33% increase in titer, compared to the wild-type	6
Actinorhodin	Antibiotic	<i>Streptomyces coelicolor</i>	Replacement of a promoter of the positive regulator <i>actII orf4</i> with synthetic promoters	Approximately 2.8 times increase in yield on biomass, compared to the wild-type	7
Actinorhodin	Antibiotic	<i>Streptomyces coelicolor</i>	Identification of gene overexpression targets using transcriptome-based metabolic simulation	Up to 2-fold increase in titer, compared to the wild-type	8
Amphotericin B	Antibiotic and antifungal	<i>Streptomyces nodosus</i>	Overexpression of a pathway-specific transcriptional activator (AmphRIV)	4-fold increase in yield on biomass, compared to the untransformed parent strain	9
Ansamitocin	Anticancer	<i>Actinosynnem pretiosum</i>	Increase of the precursor UDP-glucose pool by overexpressing phosphoglucomutase and UDP-	40% greater titer, compared to the control strain	10

Secondary metabolite	Application	Production host	Approach	Production improvement	Refs
			glucose pyrophosphorylase		
Avermectin	Anthelmintic and insecticide	<i>Streptomyces avermitilis</i>	Overexpression of two genes targeted by the TetR family transcriptional regulator SAV151	Approximately 2-3 folds increase in titer, compared to the wild-type	11
Botromycin	Antibiotic	<i>Streptomyces coelicolor</i> (heterologous host)	Heterologous expression of a gene cluster from <i>Streptomyces</i> sp. BC16019 and overexpression of an efflux pump	20-fold increase in titer, compared to the unoptimized transformant of <i>S. coelicolor</i>	12
Bisabolene	Fragrance and food additive	<i>Streptomyces venezuelae</i>	Heterologous expression of a codon optimized bisabolene synthase from <i>Abeis grandis</i> , removal of competing pathways and overexpression of genes encoding farnesyl pyrophosphate synthase	350 times increase in titer, compared to the cumulative terpene titers from the wild-type	13
Chlortetracycline	Antibiotic	<i>Streptomyces aureofaciens</i>	Overexpression of the gene <i>ctcP</i> encoding an FADH ₂ -dependent halogenase responsible for the last step of chlortetracycline biosynthesis	1.73-fold increase in titer, compared to the wild-type	14
Daptomycin	Antibiotic against Gram-positive bacterial pathogens	<i>Streptomyces roseosporus</i>	Ribosome engineering using a diterpenoid antibiotic pleuromutilin	30% increase in titer, compared to the wild-type	15
Daptomycin	Antibiotic against Gram-positive bacterial pathogens	<i>Streptomyces roseosporus</i>	Overexpression of the <i>dptJ</i> gene encoding tryptophan-2,3-dioxygenase	More than 2-fold increase in titer, compared to the wild-type	16
Daptomycin	Antibiotic against Gram-positive bacterial pathogens	<i>Streptomyces roseosporus</i>	Medium optimization using Plackett-Burman design and response surface methodology	2.2-fold increase in titer, compared to the unoptimized medium	17
Daptomycin	Antibiotic against Gram-positive bacterial pathogens	<i>Streptomyces roseosporus</i>	Overexpression of DepR1, a TetR-family transcriptional regulator	41% greater titer, compared to the wild-type, in 50 L bioreactor	18
Deoxyviolacein	Antibacterial, antitumor and antiviral	<i>Escherichia coli</i> (heterologous host)	Division of deoxyviolacein biosynthetic pathway into two modules with L-tryptophan as a key intermediate, and sequential optimization of each module independently using a newly developed biosensor that detects the intracellular pool of L-tryptophan	20% increase in titer, compared to the previously reported recombinant <i>E. coli</i> showing the best production performance	19
Divergolides	Antibacterial and antitumor	<i>Streptomyces</i> sp. W112	Overexpression of a positive regulator of the divergolides biosynthetic pathway	More than 2-fold increase in the titer, compared to the wild-type	20

Secondary metabolite	Application	Production host	Approach	Production improvement	Refs
Doramectin	Anthelmintic	<i>Streptomyces avermitilis</i>	Genome shuffling and ribosome engineering with streptomycin	11.2-fold increase in titer, compared to the parent strain NEAU1069, and production of 930.3 ± 3.8 mg L ⁻¹ from 50 L bioreactor fermentation	21
Erythromycin	Antibiotic	<i>Saccharopolyspora erythraea</i>	Genome-scale metabolic modeling and its use to identify supplementary amino acid to increase the production yield	50% increase in yield on biomass, compared to the unoptimized media	22
Erythromycin	Antibiotic	<i>Escherichia coli</i> (heterologous host)	Enhancing intracellular supply of a precursor propionyl-CoA by removing <i>ygfH</i> gene in addition to heterologous expression of erythromycin biosynthetic gene cluster	7-fold increase in titer, compared to the control strain	23
Erythromycin	Antibiotic	<i>Saccharopolyspora erythraea</i>	Constitutive overexpression of SACE_5599, a positive regulatory protein of erythromycin biosynthesis newly identified using comparative proteome analysis	32% increase in titer, compared to the wild-type	24
Erythromycin	Antibiotic	<i>Escherichia coli</i> (heterologous host)	Reduction in the number of genes and expression plasmids to minimize metabolic burden and plasmid instability	5-fold increase in titer, compared to the control strain	25
Erythromycin	Antibiotic	<i>Saccharopolyspora erythraea</i>	Overexpression of SACE_7301, TetR family regulator	27% greater titer, compared to the industrial strain (WB)	26
Erythromycin	Antibiotic	<i>Saccharopolyspora erythraea</i>	Inactivation of a TetR family transcriptional regulator (SACE_3986) that negatively controls the biosynthesis of erythromycin	54.2% increase in titer, compared to the parent (industrial) strain	27
FK506	Immunosuppressant	<i>Streptomyces tsukubaensis</i>	Enhancing pathway-specific precursor supply via gene amplification and optimization of glucose supply	150% increase in titer, compared to the parent strain	28
FK506	Immunosuppressant	<i>Streptomyces tsukubaensis</i>	Genome-scale metabolic modeling and its use to identify gene knockout and overexpression targets, followed by examination of the effects of combined gene manipulations	1.47-fold increase in titer, compared to the wild-type, from fed-batch fermentation	29
FK506	Immunosuppressant	<i>Streptomyces tsukubaensis</i>	Overexpression of biosynthetic genes associated with FK506 production and external feeding of additional nutrients	146% increase in titer after the combined gene overexpressions, compared to the wild-type, and	30

Secondary metabolite	Application	Production host	Approach	Production improvement	Refs
				additional 70% increase in titer after nutrient feeding	
FK506	Immunosuppressant	<i>Streptomyces</i> sp. RM7011	Random mutagenesis, followed by overexpression of propionyl-CoA carboxylase (PCC) pathway and external feeding of nutrients	11.63-fold increase in titer (RM7011 strain), compared to the wild-type, through random mutagenesis, 1.75-fold increase in titer from overexpression of PCC pathway, compared to the RM7011 strain, and further increase in titer by providing vinyl propionate and Tween 80	31
Gougerotin	Antibiotic	<i>Streptomyces graminearus</i>	Engineering of the biosynthetic gene cluster by removing a pathway-specific regulatory gene and replacing native promoters with constitutive promoters, integration of the engineered gene cluster into the host genome and external feeding of glycine	2.5-fold increase in titer, compared to the wild-type	32
Jadomycin B	Antibiotic	<i>Streptomyces venezuelae</i>	Use of heterologous constitutive promoters locating upstream of jadomycin B biosynthetic gene cluster	2-fold increase in titer, compared to the strain with a widely used constitutive promoter <i>ermE</i> *p	33
Milbemycins A3/A4	Pesticide and veterinary medicine	<i>Streptomyces bingchenggensis</i>	Removal of other byproducts via gene knockouts	74% increase in titer, compared to the milbemycins-overproducing control strain of <i>S. bingchenggensis</i>	34
Mithramycin	Antitumor	<i>Streptomyces argillaceus</i>	Enhancing intracellular supply of two precursors malonyl-CoA and glucose-1-phosphate by preventing their conversions to other metabolites via gene knockouts, and upregulation of their biosynthetic reactions	3.3 and 4.7 times increases in titer, compared to the wild-type strain, in liquid and solid media, respectively	35
Nargenicin A ₁	Antibiotic	<i>Nocardia</i> sp. CS682	Optimization of transformation condition and overexpression of heterologous genes encoding positive regulator of secondary metabolite biosynthesis (<i>S</i> -adenosylmethionine synthetase) or acetyl-CoA carboxylase	2.8- and 3.8-fold increases in titer for overexpression of <i>S</i> -adenosylmethionine synthetase and acetyl-CoA carboxylase, respectively, compared to the wild-type	36

Secondary metabolite	Application	Production host	Approach	Production improvement	Refs
			in order to enhance precursor supply		
Natamycin	Antifungal	<i>Streptomyces chattanoogensis</i>	Overexpression of one of genes encoding phosphopantetheinyl transferases (SchPPT)	40% increase in titer and 24 h faster production, compared to the industrial natamycin producer <i>S. chattanoogensis</i> L10	37
Neomycin	Antibiotic	<i>Streptomyces fradiae</i>	Medium optimization using Plackett-Burman design and response surface methodology	2.7-fold increase in yield from dry coconut oil cake, compared to the unoptimized medium	38
Nosiheptide	Antibiotic	<i>Streptomyces actuosus</i>	Medium optimization using Plackett-Burman design and response surface methodology	1.56-fold increase in titer, compared to the unoptimized medium	39
Phenazine-1-carboxylic acid (Shenqinmycin)	Antibiotic and biopesticide	<i>Pseudomonas aeruginosa</i>	Enhancing fluxes towards phenazine-1-carboxylic acid (PCA) biosynthesis by removing or downregulating competing reactions, and amplifying reactions that increase biosynthesis of PCA and its precursors	53.6-fold increase in titer, compared to the wild-type	40
Pikromycin	Antibiotic	<i>Streptomyces venezuelae</i>	Medium optimization using Plackett-Burman design, method of steepest ascent and response surface methodology	1.5- to 2-fold increase in titer, compared to the unoptimized media	41
Pretubulysin A	Structural core of an anticancer tubulysin	<i>Myxococcus xanthus</i> (heterologous host)	Heterologous expression of a gene cluster from <i>Cystobacter</i> sp. SBCb004 and supplementation of L-pipecolic acid	100-fold increase in titer (0.19 mg L ⁻¹), compared to another heterologous host <i>Pseudomonas putida</i>	42
Pristinamycin II	A component of pristinamycin that is antibiotic	<i>Streptomyces pristinaespiralis</i>	Overexpression of the pristinamycin II biosynthetic gene cluster, knockout of a repressor gene, overexpression of two activator genes, and addition of macroreticular resin	5.26-fold increase in titer, compared to the parental strain, from 5 L bioreactor	43
Spinosad	Antibiotic and pesticide	<i>Saccharopolyspora spinosa</i>	Overexpression of genes associated with biosynthesis of precursors	5-fold increase in titer, compared to the wild-type	44
Spinosad	Antibiotic and pesticide	<i>Saccharopolyspora spinosa</i>	Genome-scale metabolic modeling and its use to examine the effects of supplementary amino acids and transhydrogenase activity on the production yield	86.5% increase in titer, compared to the wild-type	45
Spinosad (spinosyns)	Antibiotic and pesticide	<i>Saccharopolyspora</i>	UV mutagenesis, followed by	7 to 8-fold increase in titer,	46

Secondary metabolite	Application	Production host	Approach	Production improvement	Refs
A and D)		<i>spinosa</i>	heterologous expression of genes from <i>Streptomyces peuceitius</i> , all involved in spinosad biosynthesis	compared the wild-type	
Surfactin	Biosurfactant and plant disease control	<i>Bacillus amyloliquefaciens</i>	Genome shuffling	10.3-fold increase in titer, compared to the wild-type	47
Teicoplanin	Antibiotic	<i>Actinoplanes teichomyceticus</i>	Selection of the <i>hrdB</i> gene encoding principal sigma factor from <i>Actinoplanes missouriensis</i> 431, <i>Micromonospora aurantiaca</i> ATCC 27029 and <i>Salinispora arenicola</i> CNS-205 according to molecular evolutionary analysis, and their expression in <i>A. teichomyceticus</i> L-27 after their random mutagenesis and DNA shuffling	2-fold increase in titer, compared to the industrial producer strain <i>A. teichomyceticus</i> L-27	48
Teicoplanin	Antibiotic	<i>Actinoplanes teichomyceticus</i>	Overexpression of a pathway-specific regulatory gene <i>tei15*</i>	3.5-fold increase in titer, compared to the wild-type, from 3 L bioreactor	49
Thailanstatin A	Anticancer and an analog of spliceostatin	<i>Burkholderia sp.</i> FERM BP-3421	Fermentation media optimization, removal of a reaction converting the target compound into another metabolite, and overexpression of the target compound biosynthetic reaction	More than 40-fold increase in titer (2.5 g L ⁻¹), compared to the wild-type	50
Toyocamycin, tetramycin P, tetrin B and tetramycin A	Antifungal	<i>Streptomyces diastatochromogenes</i>	Ribosome engineering using erythromycin, gentamicin, paromomycin, rifampin and streptomycin	4.1-, 7.8-, 5.1- and 13-fold increases in titer of toyocamycin, tetramycin P, tetrin B and tetramycin A, respectively, using paromomycin, compared to the wild-type	51
Tylactone	A precursor of an antibiotic tylosin	<i>Streptomyces venezuelae</i> (heterologous host)	Enhancing a polyketide precursor ethylmalonyl-CoA by preventing its conversion to other metabolites via a gene knockout, ethylmalonate supplementation in the medium and upregulation of the tylosin biosynthetic pathway	Near 10-fold increase in titer, compared to the parent strain	52
Validamycin A	Antibiotic and antifungal	<i>Streptomyces hygroscopicus</i>	Overexpression of the validamycin biosynthetic gene cluster	34% increase in titer, compared to the wild-type	53

Secondary metabolite	Application	Production host	Approach	Production improvement	Refs
Validamycin	Antibiotic and antifungal	<i>Streptomyces hygroscopicus</i>	Dual knockouts of two γ -butyrolactone receptor genes <i>shbR1</i> and <i>shbR3</i>	55% increase in titer, compared to the wild-type	54
Valinomycin	Antibiotic	<i>Escherichia coli</i> (heterologous host)	Heterologous expression of valinomycin biosynthetic genes from <i>Streptomyces tsusimaensis</i> , followed by production optimization through high cell density cultivation and coexpression of type II thioesterase	13 mg L ⁻¹ , a 43-fold increase in titer, compared to the recombinant <i>E. coli</i> strain before the production optimization	55
Valinomycin	Antibiotic	<i>Escherichia coli</i> (heterologous host)	Optimization of fed-batch cultivation	33-fold increase in titer without external feeding of specific precursors, compared to the batch cultivation	56
WAP-8294A and HSAF (dihydromaltophilin)	WAP-8294A, antibiotic; HSAF, antifungal	<i>Lysobacter enzymogenes</i>	Site-specific integration of ORF8 gene that positively regulates the production of these two compounds	2-fold increase in titer for WAP-8294A and 7-fold increase in titer for HSAF, both compared to the wild-type	57

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§ References in press are indicated with DOI.

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