

Supplementary Materials

Comparative genomics analysis of keratin-degrading *Chryseobacterium* species reveals their keratinolytic potential for secondary metabolite production

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Figure S1-S5, Table S1-S7.

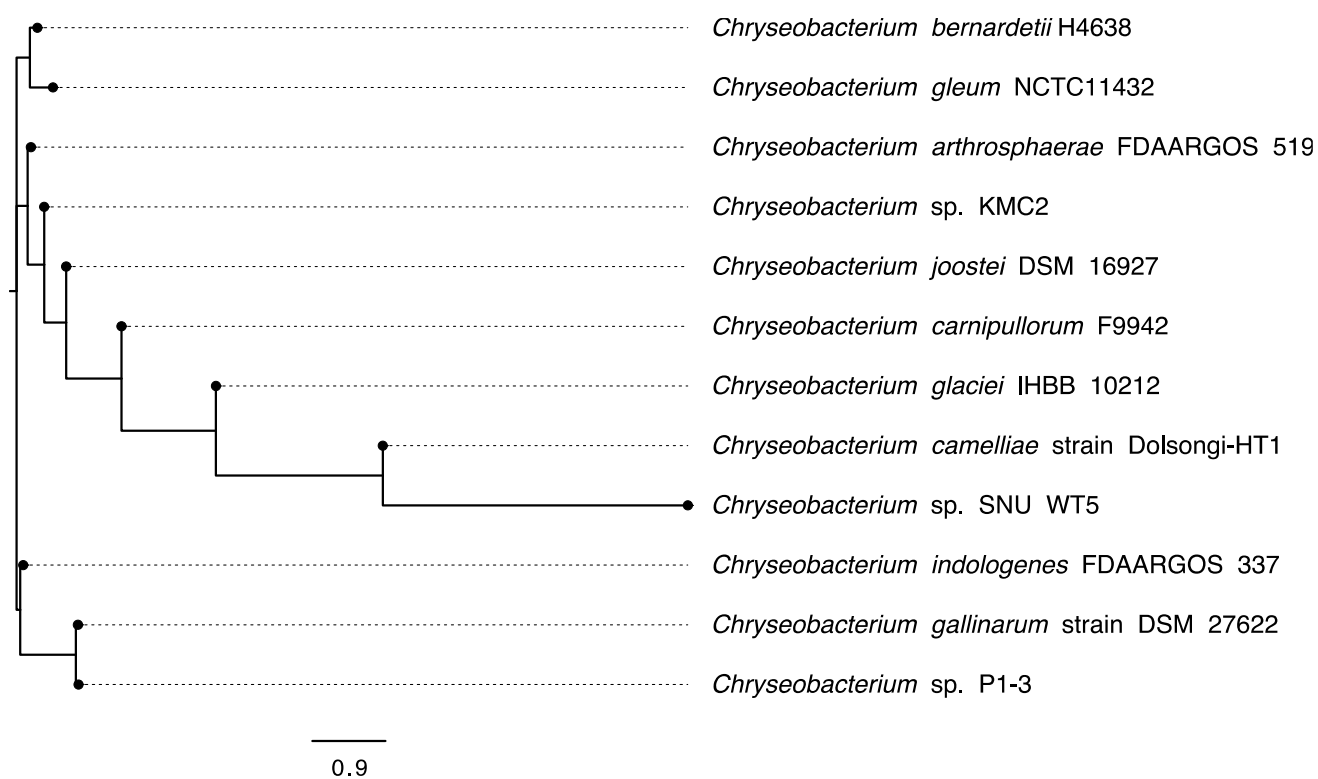


Figure S1. Phylogenetic tree of 12 *Chryseobacterium* genomes based on gene presence-absence patterns. Branch length represents gene gain/lose rates.

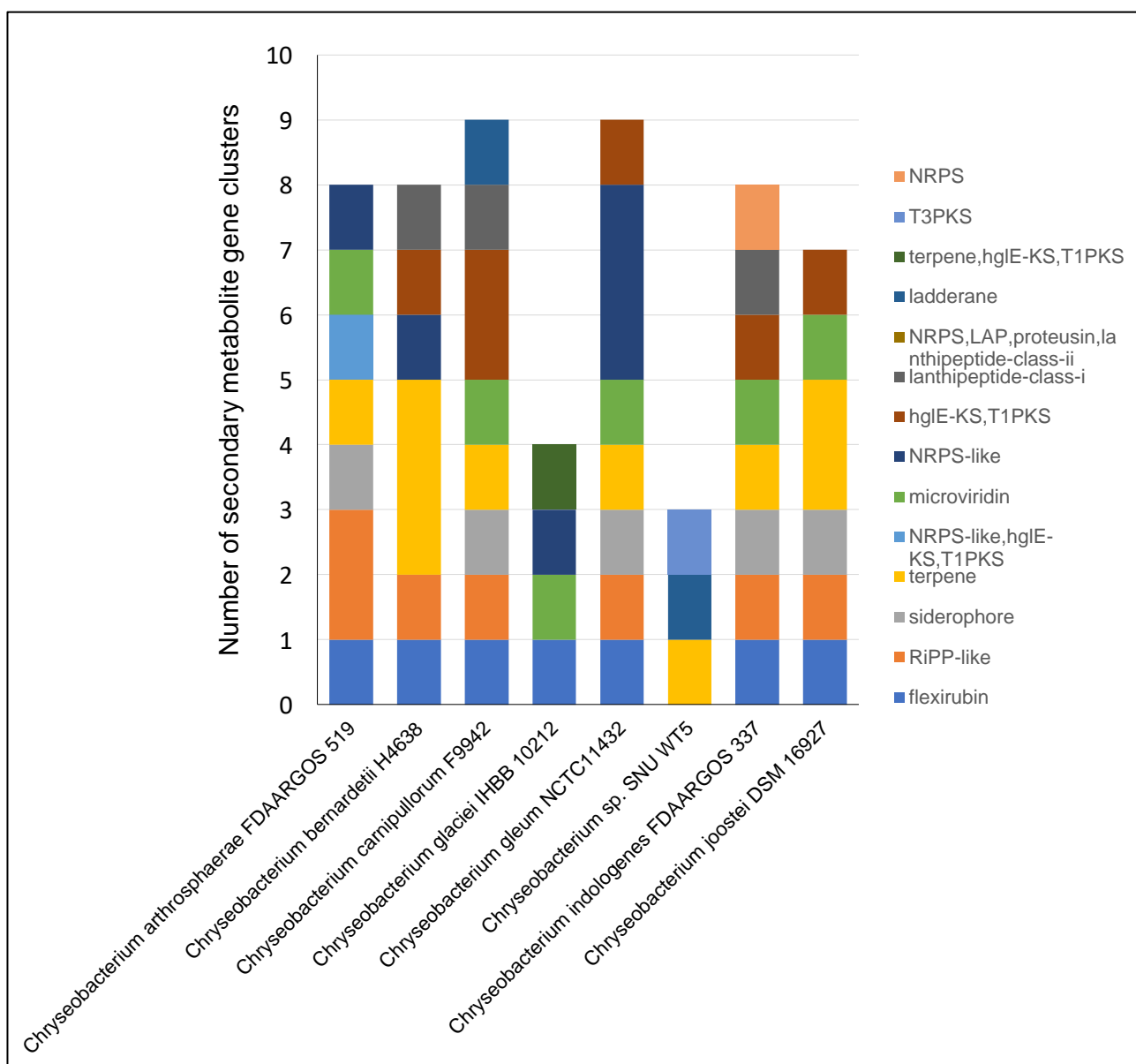


Figure S2. Composition of secondary metabolite gene clusters from eight *Chryseobacterium* genomes.

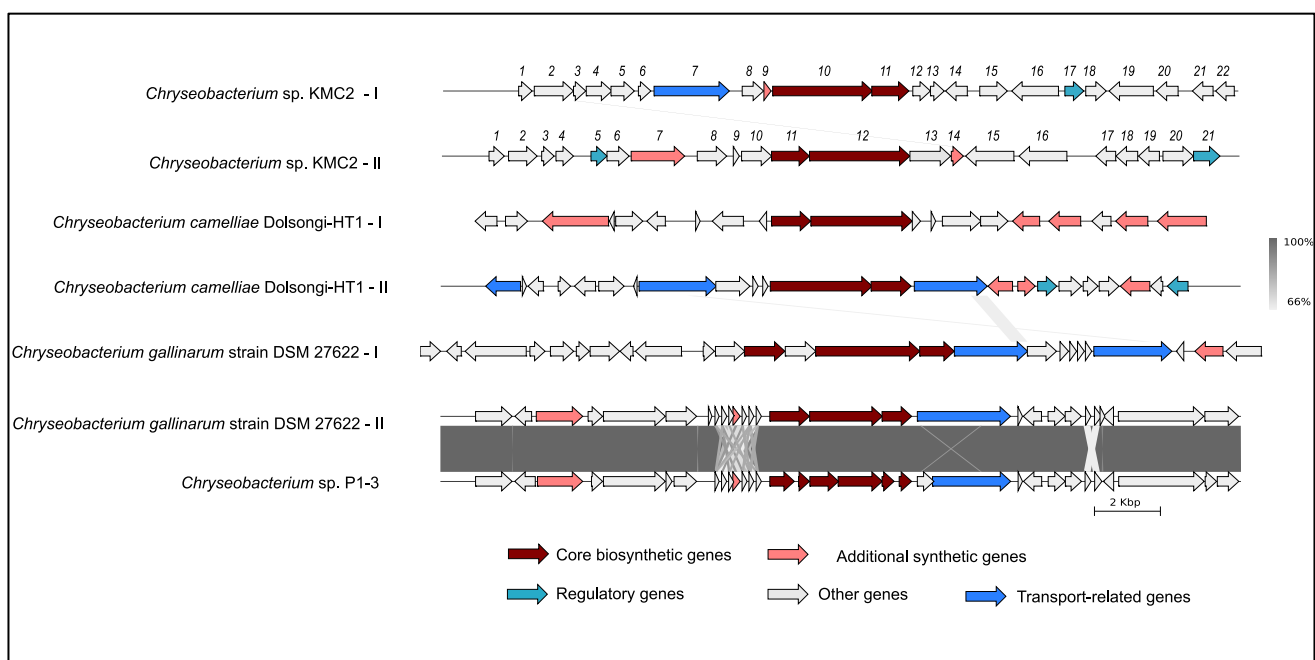


Figure S3. Lanthipeptide gene cluster from four *Chryseobacterium* genomes (Two gene clusters were predicted to synthesize the same secondary metabolite showing as “I” and “II”, respectively). The detailed description of each gene can be found in Table S4&5.

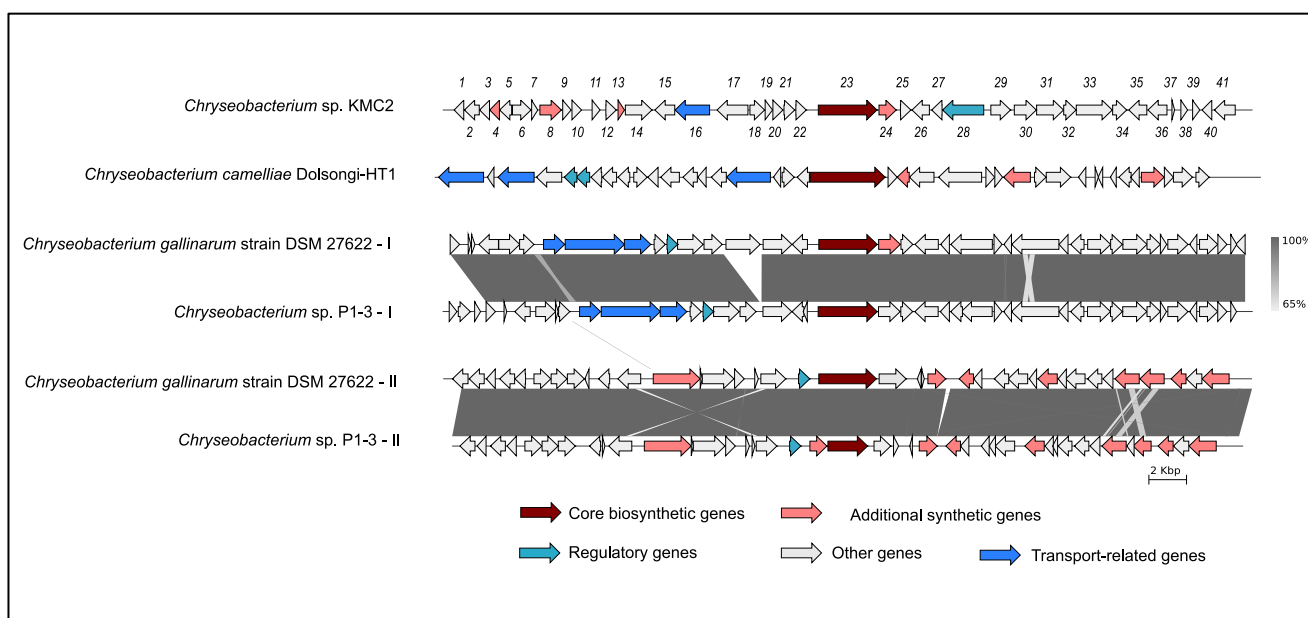


Figure S4. NRPS-like gene cluster from four *Chryseobacterium* genomes (Two gene clusters were predicted to synthesize the same secondary metabolite showing as “I” and “II”, respectively). The detailed description of each gene can be found in Table S6.

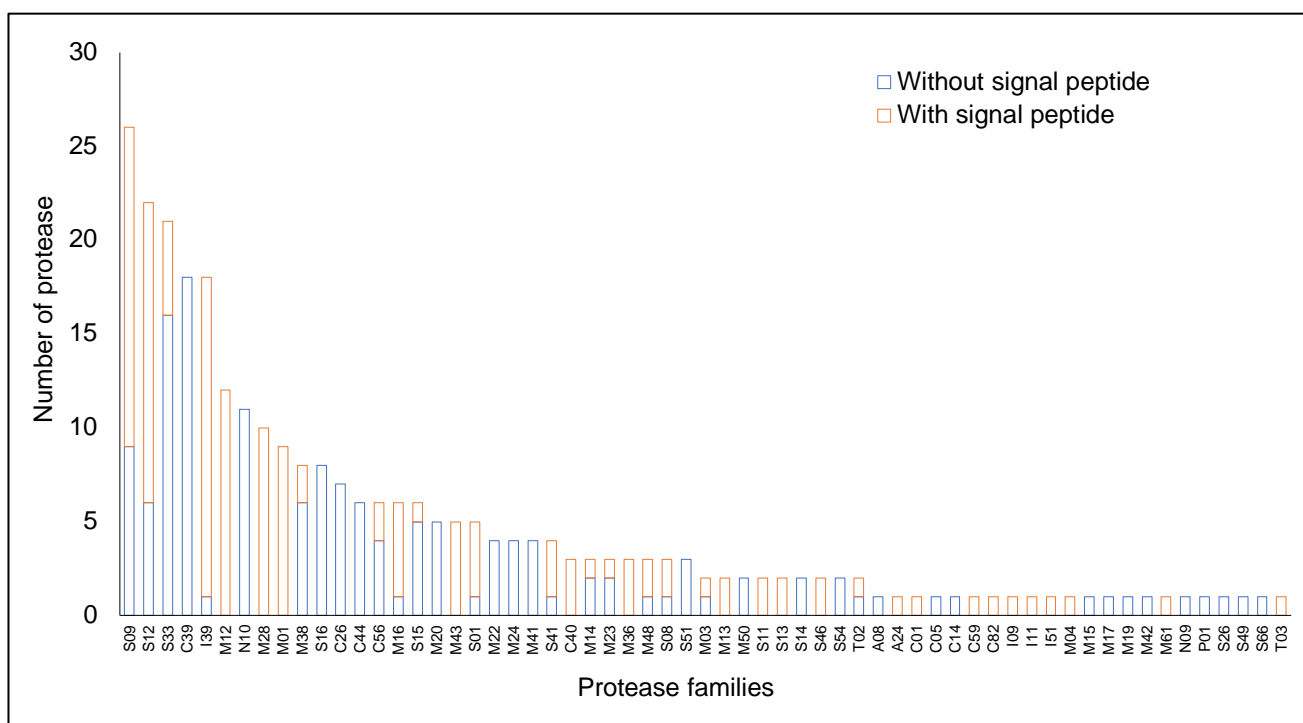


Figure S5. Protease families predicted from *Chryseobacterium* sp. KMC2 genome.

Table S1. The description of flexirubin-type pigment biosynthesis related gene cluster from *Chryseobacterium* sp. KMC2.

Genes	Length (bp)	Functional annotation (Sequence ID from NCBI BLASTP)	Reference in genome
<i>flex1</i>	876	Polysaccharide export protein	KOACACPH_03512
<i>flex2</i>	1119	Decaprenyl-phosphate N-acetylglucosaminophosphotransferase	KOACACPH_03513
<i>flex3</i>	1002	Undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase	KOACACPH_03514
<i>flex4</i>	1071	Formimidoylglutamase	KOACACPH_03515
<i>flex5</i>	2580	DNA topoisomerase I	KOACACPH_03516
<i>flex6</i>	3447	T9SS C-terminal target domain-containing protein (REC74243.1)	KOACACPH_03517
<i>flex7</i>	1140	EpsG family protein (SMC94123.1)	KOACACPH_03518
<i>flex8</i>	1011	hypothetical protein	KOACACPH_03519
<i>flex9</i>	3654	MMPL family transporter (WP_047492502.1)	KOACACPH_03520
<i>flex10</i>	915	Dialkylrecorsinol condensing enzyme DarA (WP_123858105.1)	KOACACPH_03521
<i>flex11</i>	1140	3-oxoacyl-(acyl carrier protein) synthase III	KOACACPH_03522
<i>flex12</i>	432	hypothetical protein	KOACACPH_03523
<i>flex13</i>	444	ABC transporter permease (WP_090026350.1)	KOACACPH_03524
<i>flex14</i>	237	hypothetical protein	KOACACPH_03525
<i>flex15</i>	2913	Insulinase family protein (WP_084087117.1)	KOACACPH_03526
<i>flex16</i>	405	hypothetical protein	KOACACPH_03527
<i>flex17</i>	996	BtrH N-terminal domain-containing protein (WP_047492484.1)	KOACACPH_03528
<i>flex18</i>	759	ABC transporter ATP-binding protein	KOACACPH_03529
<i>flex19</i>	1269	ABC-2 type transporter	KOACACPH_03530
<i>flex20</i>	429	Putative esterase	KOACACPH_03531
<i>flex21</i>	1134	Beta-ketoacyl synthase	KOACACPH_03532
<i>flex22</i>	543	3-oxoacyl-ACP synthase (WP_081989140.1)	KOACACPH_03533
<i>flex23</i>	258	Acyl carrier protein (WP_047492465.1)	KOACACPH_03534
<i>flex24</i>	1236	Beta-ketoacyl synthase	KOACACPH_03535
<i>flex25</i>	1062	Beta-ketoacyl synthase chain length factor (WP_047492459.1)	KOACACPH_03536
<i>flex26</i>	756	Peptidoglycan-N-acetylglucosamine deacetylase	KOACACPH_03537
<i>flex27</i>	627	Outer-membrane lipoprotein carrier protein	KOACACPH_03538
<i>flex28</i>	642	hypothetical protein	KOACACPH_03539
<i>flex29</i>	597	PorT family protein (WP_052188704.1)	KOACACPH_03540
<i>flex30</i>	381	3-hydroxyacyl-ACP dehydratase (WP_081989131.1)	KOACACPH_03541
<i>flex31</i>	477	hypothetical protein	KOACACPH_03542
<i>flex32</i>	1170	Undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase	KOACACPH_03543
<i>flex33</i>	2634	T9SS-dependent M36 family metalloproteinase (WP_123321112.1)	KOACACPH_03544

<i>flex34</i>	2643	T9SS-dependent M36 family metallopeptidase (WP_115919297.1)	KOACACPH_03545
<i>flex35</i>	366	hypothetical protein	KOACACPH_03546
<i>flex36</i>	1686	Acyl-CoA--6-aminopenicillanic acid acyl-transferase (WP_115919299.1)	KOACACPH_03547
<i>flex37</i>	1518	NAD(P)/FAD-dependent oxidoreductase (WP_115919301.1)	KOACACPH_03548
<i>flex38</i>	885	Lipid A biosynthesis acyltransferase (WP_047492440.1)	KOACACPH_03549
<i>flex39</i>	255	Acyl carrier protein	KOACACPH_03550
<i>flex40</i>	1221	Beta-ketoacyl synthase	KOACACPH_03551
<i>flex41</i>	732	3-oxoacyl-[acyl-carrier-protein] reductase FabG	KOACACPH_03552
<i>flex42</i>	1521	Tyrosine 2,3-aminomutase	KOACACPH_03553
<i>flex43</i>	1257	Tryptophan 7-halogenase (WP_084087087.1)	KOACACPH_03554
<i>flex44</i>	609	hypothetical protein	KOACACPH_03555
<i>flex45</i>	1293	Phenylacetate-coenzyme A ligase	KOACACPH_03556
<i>flex46</i>	1689	M23 family metallopeptidase (WP_047492411.1)	KOACACPH_03557
<i>flex47</i>	3396	Isoleucine--tRNA ligase	KOACACPH_03558
<i>flex48</i>	381	RNA polymerase-binding transcription factor DksA	KOACACPH_03559
<i>flex49</i>	246	Rhomboid family protein (WP_076356891.1)	KOACACPH_03560
<i>flex50</i>	195	hypothetical protein	KOACACPH_03561
<i>flex51</i>	639	Lipoprotein signal peptidase	KOACACPH_03562
<i>flex52</i>	645	YdcF family protein (WP_047492396.1)	KOACACPH_03563
<i>flex53</i>	969	Tryptophan--tRNA ligase	KOACACPH_03564
<i>flex54</i>	1284	Sensor histidine kinase	KOACACPH_03565
<i>flex55</i>	672	Phosphate regulon transcriptional regulatory protein PhoB	KOACACPH_03566
<i>flex56</i>	249	hypothetical protein	KOACACPH_03567
<i>flex57</i>	450	PepSY-like domain-containing protein (WP_034692507.1)	KOACACPH_03568
<i>flex58</i>	696	Pyrimidine 5'-nucleotidase YjjG	KOACACPH_03569
<i>flex59</i>	135	hypothetical protein	KOACACPH_03570
<i>flex60</i>	591	RNA polymerase sigma-H factor	KOACACPH_03571
<i>flex61</i>	492	hypothetical protein	KOACACPH_03572

Table S2. The description of microviridin biosynthesis related gene cluster from *Chryseobacterium* sp. KMC2.

Genes	Length (bp)	Functional annotation (Sequence ID from NCBI BLASTP)	Reference in genome
<i>mdnC</i>	384	Putative acyl-CoA thioester hydrolase	KOACACPH_03650
<i>mdnD</i>	798	hypothetical protein	KOACACPH_03651
<i>mdnE</i>	2148	Endonuclease MutS2	KOACACPH_03652
<i>mdnF</i>	510	GNAT family N-acetyltransferase (WP_084086267.1)	KOACACPH_03653
<i>mdnG</i>	642	Uracil-DNA glycosylase	KOACACPH_03654
<i>mdnH</i>	504	hypothetical protein	KOACACPH_03655
<i>mdnI</i>	543	DUF456 domain-containing protein (WP_047487323.1)	KOACACPH_03656
<i>mdnJ</i>	1269	Transporter, small conductance mechanosensitive	KOACACPH_03657
<i>mdnK</i>	720	Pyridoxine 5'-phosphate synthase	KOACACPH_03658
<i>mdnL</i>	780	Esterase YbfF	KOACACPH_03659
<i>mdnA</i>	240	Microviridin (WP_084086262.1)	KOACACPH_03660
<i>mdnB</i>	219	Microviridin (WP_047487341.1)	KOACACPH_03661
<i>mdnM</i>	957	MvdC family ATP-grasp ribosomal peptide maturase (WP_084086261.1)	KOACACPH_03662
<i>mdnN</i>	1005	MvdD family ATP-grasp ribosomal peptide maturase (WP_084086260.1)	KOACACPH_03663
<i>mdnO</i>	1014	NAD-dependent epimerase/dehydratase family protein (WP_047487349.1)	KOACACPH_03664
<i>mdnP</i>	1770	Long-chain-fatty-acid--CoA ligase FadD15	KOACACPH_03665
<i>mdnQ</i>	1059	Diphosphomevalonate decarboxylase (WP_084086257.1)	KOACACPH_03666
<i>mdnR</i>	942	Endonuclease (WP_084086256.1)	KOACACPH_03667
<i>mdnS</i>	444	Nuclear transport factor 2 family protein (WP_084086255.1)	KOACACPH_03668
<i>mdnT</i>	384	VOC family protein (WP_047487892.1)	KOACACPH_03669
<i>mdnU</i>	384	DUF1634 domain-containing protein (WP_047487366.1)	KOACACPH_03670
<i>mdnV</i>	831	Sulfite exporter TauE/SafE family protein (WP_047487368.1)	KOACACPH_03671

Table S3. The description of siderophore biosynthesis related gene cluster from *Chryseobacterium* sp. KMC2.

Genes	Length (bp)	Functional annotation (Sequence ID from NCBI BLASTP)	Reference in genome
<i>speC</i>	576	Crp/Fnr family transcriptional regulator (WP_084084255.1)	KOACACPH_01784
<i>speD</i>	810	Esterase family protein (WP_115917879.1)	KOACACPH_01785
<i>speE</i>	1098	L-lysine 4-hydroxylase	KOACACPH_01786
<i>speF</i>	1512	L-2,4-diaminobutyrate decarboxylase	KOACACPH_01787
<i>speA</i>	2409	Putative siderophore biosynthesis protein	KOACACPH_01788
<i>speH</i>	1317	L-lysine N6-monooxygenase	KOACACPH_01789
<i>speB</i>	1809	IucA/IucC family siderophore biosynthesis protein (WP_047496558.1)	KOACACPH_01790
<i>speI</i>	1404	MATE efflux family protein	KOACACPH_01791
<i>speJ</i>	246	Acyl carrier protein (WP_084084248.1)	KOACACPH_01792
<i>speK</i>	1389	2-succinylbenzoate--CoA ligase	KOACACPH_01793

Table S4. The description of lanthipeptide I biosynthesis related gene cluster from *Chryseobacterium* sp. KMC2.

Genes	Length (bp)	Functional annotation (Sequence ID from NCBI BLASTP)	Reference in genome
<i>lan1</i>	408	hypothetical protein	KOACACPH_00404
<i>lan2</i>	1191	Alanine dehydrogenase	KOACACPH_00405
<i>lan3</i>	372	hypothetical protein	KOACACPH_00406
<i>lan4</i>	774	Histidine kinase (WP_084086149.1)	KOACACPH_00407
<i>lan5</i>	711	Transcriptional regulatory protein NatR	KOACACPH_00408
<i>lan6</i>	378	hypothetical protein	KOACACPH_00409
<i>lan7</i>	2289	Sodium/hydrogen exchanger	KOACACPH_00410
<i>lan8</i>	654	hypothetical protein	KOACACPH_00411
<i>lan9</i>	222	Class I lanthipeptide (WP_047487795.1)	KOACACPH_00412
<i>lan10</i>	3036	Lantibiotic dehydratase domain protein	KOACACPH_00413
<i>lan11</i>	1128	Lanthionine synthetase C family protein	KOACACPH_00414
<i>lan12</i>	540	hypothetical protein	KOACACPH_00415
<i>lan13</i>	417	hypothetical protein	KOACACPH_00416
<i>lan14</i>	663	hypothetical protein	KOACACPH_00417
<i>lan15</i>	843	Cyclohexadienyl dehydrogenase	KOACACPH_00418
<i>lan16</i>	1419	L-serine dehydratase 2	KOACACPH_00419
<i>lan17</i>	579	Transcription regulator, crp	KOACACPH_00420
<i>lan18</i>	624	FMN-dependent NADH-azoreductase 1	KOACACPH_00421
<i>lan19</i>	1344	Ammonia channel	KOACACPH_00422
<i>lan20</i>	666	Alpha/beta hydrolase (WP_115918317.1)	KOACACPH_00423
<i>lan21</i>	630	Protein YceI	KOACACPH_00424
<i>lan22</i>	567	Protein YceI	KOACACPH_00425

Table S5. The description of lanthipeptide II biosynthesis related gene cluster from *Chryseobacterium* sp. KMC2.

Genes	Length (bp)	Functional annotation (Sequence ID from NCBI BLASTP)	Reference in
<i>lan1</i>	804	HTH-type transcriptional activator RhaR	KOACACPH_02362
<i>lan2</i>	927	Transcriptional regulator (WP_084085280.1)	KOACACPH_02363
<i>lan3</i>	636	hypothetical protein	KOACACPH_02364
<i>lan4</i>	660	hypothetical protein	KOACACPH_02365
<i>lan5</i>	600	CDP-alcohol phosphatidyltransferase family protein (WP_115917644.1)	KOACACPH_02366
<i>lan6</i>	1449	Asparagine--tRNA ligase	KOACACPH_02367
<i>lan7</i>	1464	RNA polymerase sigma-54 factor	KOACACPH_02368
<i>lan8</i>	369	hypothetical protein	KOACACPH_02369
<i>lan9</i>	1236	hypothetical protein	KOACACPH_02370
<i>lan10</i>	3051	Lantibiotic dehydratase domain protein	KOACACPH_02371
<i>lan11</i>	1158	Lanthionine synthetase C family protein	KOACACPH_02372
<i>lan12</i>	918	LLM class flavin-dependent oxidoreductase (WP_084085264.1)	KOACACPH_02373
<i>lan13</i>	186	Class I lanthipeptide (WP_047488251.1)	KOACACPH_02374
<i>lan14</i>	891	Carboxypeptidase-like regulatory domain-containing protein (WP_084085262.1)	KOACACPH_02375
<i>lan15</i>	1626	3-[(3aS,4S,7aS)-7a-methyl-1,5-dioxo-octahydro-1H-inden-4-yl]propanoyl:CoA	KOACACPH_02376
<i>lan16</i>	675	Beta-carotene 15,15'-monooxygenase (WP_123942665.1)	KOACACPH_02377
<i>lan17</i>	492	Sigma-70 family RNA polymerase sigma factor (WP_027374652.1)	KOACACPH_02378
<i>lan18</i>	531	hypothetical protein	KOACACPH_02379
<i>lan19</i>	378	hypothetical protein	KOACACPH_02380
<i>lan20</i>	870	Polyphosphate:ADP phosphotransferase	KOACACPH_02381
<i>lan21</i>	465	DUF1573 domain-containing protein (WP_047488266.1)	KOACACPH_02382

Table S6. The description of NRPS-like biosynthesis related gene cluster from *Chryseobacterium* sp. KMC2.

Genes	Length (bp)	Functional annotation (Sequence ID from NCBI BLASTP)	Reference in
<i>nrpsl1</i>	1110	DUF1624 domain-containing protein (WP_052188696.1)	KOACACPH_01527
<i>nrpsl2</i>	519	Thioredoxin family protein (WP_047492101.1)	KOACACPH_01528
<i>nrpsl3</i>	396	hypothetical protein	KOACACPH_01529
<i>nrpsl4</i>	357	hypothetical protein	KOACACPH_01530
<i>nrpsl5</i>	144	hypothetical protein	KOACACPH_01532
<i>nrpsl6</i>	1014	Nucleoid-associated protein (WP_047492108.1)	KOACACPH_01533
<i>nrpsl7</i>	960	hypothetical protein	KOACACPH_01534
<i>nrpsl8</i>	750	Fumarate reductase iron-sulfur subunit	KOACACPH_01535
<i>nrpsl9</i>	1917	Fumarate reductase flavoprotein subunit	KOACACPH_01536
<i>nrpsl10</i>	657	Succinate dehydrogenase cytochrome b subunit (WP_047492118.1)	KOACACPH_01537
<i>nrpsl11</i>	1431	Putative malate transporter YflS	KOACACPH_01538
<i>nrpsl12</i>	1164	Porin (WP_084085123.1)	KOACACPH_01539
<i>nrpsl13</i>	1050	Linear amide C-N hydrolase (WP_047492125.1)	KOACACPH_01540
<i>nrpsl14</i>	2193	Sensor histidine kinase	KOACACPH_01541
<i>nrpsl15</i>	552	Biliverdin-producing heme oxygenase (WP_047492131.1)	KOACACPH_01542
<i>nrpsl16</i>	927	Malate dehydrogenase	KOACACPH_01543
<i>nrpsl17</i>	555	hypothetical protein	KOACACPH_01544
<i>nrpsl18</i>	918	Proline iminopeptidase	KOACACPH_01545
<i>nrpsl19</i>	3117	Linear gramicidin synthase subunit D	KOACACPH_01546
<i>nrpsl20</i>	555	Putative glycolipid-binding domain-containing protein (WP_157969889.1)	KOACACPH_01548
<i>nrpsl21</i>	573	Crp/Fnr family transcriptional regulator (WP_047492147.1)	KOACACPH_01549
<i>nrpsl22</i>	537	GNAT family N-acetyltransferase (WP_047492150.1)	KOACACPH_01550
<i>nrpsl23</i>	393	AMP-dependent synthetase and ligase	KOACACPH_01551
<i>nrpsl24</i>	786	hypothetical protein	KOACACPH_01552
<i>nrpsl25</i>	1647	Alkaline phosphatase PafA	KOACACPH_01553
<i>nrpsl26</i>	1842	Vitamin B12 transporter BtuB	KOACACPH_01554
<i>nrpsl27</i>	1059	hypothetical protein	KOACACPH_01555
<i>nrpsl28</i>	1419	CCA-adding enzyme	KOACACPH_01556
<i>nrpsl29</i>	348	Nuclear transport factor 2 family protein (WP_047492172.1)	KOACACPH_01557
<i>nrpsl30</i>	549	Threonylcarbamoyl-AMP synthase	KOACACPH_01558
<i>nrpsl31</i>	483	IS200/IS605 family transposase (WP_115918710.1)	KOACACPH_01559
<i>nrpsl32</i>	513	DinB family protein (WP_047492181.1)	KOACACPH_01560

<i>nrpsl33</i>	447	GNAT family N-acetyltransferase (WP_047492184.1)	KOACACPH_01561
<i>nrpsl34</i>	1140	Cystathionine beta-lyase	KOACACPH_01562
<i>nrpsl35</i>	324	Gliding motility protein GldC (WP_047492191.1)	KOACACPH_01563
<i>nrpsl36</i>	984	Gliding motility protein GldB (WP_081989115.1)	KOACACPH_01564
<i>nrpsl37</i>	639	Internalin J	KOACACPH_01565
<i>nrpsl38</i>	522	Acetyltransferase	KOACACPH_01566
<i>nrpsl39</i>	531	N-acetyltransferase (WP_115918805.1)	KOACACPH_01567
<i>nrpsl40</i>	792	NH(3)-dependent NAD(+) synthetase	KOACACPH_01568
<i>nrpsl41</i>	516	Ribonuclease	KOACACPH_01569

Table S7. The description of genes and metabolic pathways related to keratin utilization in *Chryseobacterium* sp. KMC2 genome.

Gene order	EC number	KO number	Functional annotation	Metabolic pathway	Reference in genome
1	2.6.1.42	K00826	Branched-chain-amino-acid aminotransferase	Metabolism of Leucine and Isoleucine	KOACACPH_00391/KOACACPH_04122
2	1.2.4.4	K11381	3-methyl-2-oxobutanoate dehydrogenase	Metabolism of Leucine and Isoleucine	KOACACPH_00351
3	2.3.1.168	K09699	Dihydrolipoyllysine-residue (2-methylpropanoyl)transferase	Metabolism of Leucine and Isoleucine	KOACACPH_03134
4	1.3.8.7	K00248, K00249	Acyl-CoA dehydrogenase	Metabolism of Leucine and Isoleucine	KOACACPH_01887
5	4.2.1.18	K13766	Methylglutaconyl-CoA hydratase	Metabolism of Leucine and Isoleucine	KOACACPH_03720
6	4.1.3.4	K01640	Hydroxymethylglutaryl-CoA lyase	Metabolism of Leucine and Isoleucine	KOACACPH_03960
7	1.3.8.1	K00248	Acyl-CoA dehydrogenase	Metabolism of Leucine and Isoleucine	KOACACPH_00342/KOACACPH_03381
8	4.2.1.17	K01715, K01692	Enoyl-CoA hydratase	Metabolism of Leucine and Isoleucine	KOACACPH_03576/KOACACPH_01888/KOACACPH_01890
9	1.1.1.35	K01782, K07516	3-hydroxyacyl-CoA dehydrogenase	Metabolism of Leucine and Isoleucine	KOACACPH_03378
10	2.3.1.16	K00623	Acetyl-CoA acyltransferase	Metabolism of Leucine and Isoleucine	KOACACPH_03380
11	2.3.3.1	K01647	Citrate synthase	TCA cycle	KOACACPH_01094/KOACACPH_01792
12	4.2.1.3	K01681	Aconitase	TCA cycle	KOACACPH_03590
13	1.1.1.42	K00031	Isocitrate dehydrogenase	TCA cycle	KOACACPH_00544
14	1.2.4.2	K00164, K01616	Oxoglutarate dehydrogenase	TCA cycle	KOACACPH_00825
15	2.3.1.61	K00658	Dihydrolipoyl succinyltransferase	TCA cycle	KOACACPH_00826
16	1.8.1.4	K00382	Dihydrolipoyl dehydrogenase	TCA cycle	KOACACPH_00132/KOACACPH_00765
17	6.2.1.5	K01902, K01903, K02381	Succinate-CoA ligase	TCA cycle	KOACACPH_01458/KOACACPH_03423
18	2.8.3.18	K01067, K18118	Succinyl-CoA:acetate CoA-transferase	TCA cycle	KOACACPH_02425
19	1.3.5.1	K00240	Succinate dehydrogenase	TCA cycle	KOACACPH_01535/KOACACPH_01536/KOACACPH_02931/KOACACPH_02932

20	4.2.1.2	K01676, K01677, K01678, K01679	Fumarate hydratase	TCA cycle	KOACACPH_02695/KOACACPH_02696
21	1.1.5.4	K00116	Malate dehydrogenase (quinone)	TCA cycle	KOACACPH_02576
22	1.1.1.37	K00024	Malate dehydrogenase	TCA cycle	KOACACPH_01543
23	4.1.1.49	K01610	Phosphoenolpyruvate carboxykinase (ATP)	Glycolysis/Gluconeogenesis	KOACACPH_00978
24	4.2.1.11	K01689	Phosphopyruvate hydratase	Glycolysis/Gluconeogenesis	KOACACPH_01093
25	5.4.2.11	K01834	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	Glycolysis/Gluconeogenesis	KOACACPH_01759
26	5.4.2.12	K15633	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	Glycolysis/Gluconeogenesis	KOACACPH_03235
27	2.7.2.3	K00927	Phosphoglycerate kinase	Glycolysis/Gluconeogenesis	KOACACPH_03849
28	1.2.1.12	K00134	Glyceraldehyde-3-phosphate dehydrogenase	Glycolysis/Gluconeogenesis	KOACACPH_03436
29	1.2.1.9	K00131	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	Glycolysis/Gluconeogenesis	KOACACPH_00524
30	4.1.2.13	K01624	Fructose-bisphosphate aldolase	Glycolysis/Gluconeogenesis	KOACACPH_03902/KOACACPH_04210
31	2.7.1.11	K00850, K21071	6-phosphofructokinase	Glycolysis/Gluconeogenesis	KOACACPH_03435
32	3.1.3.11	K03841	Fructose-bisphosphatase	Glycolysis/Gluconeogenesis	KOACACPH_01662
33	5.4.2.2	K01835	Phosphoglucomutase	Glycolysis/Gluconeogenesis	KOACACPH_03206
34	2.7.1.40	K00873	Pyruvate kinase	Pyruvate metabolism	KOACACPH_02949
35	1.2.4.1	K00161, K00162	pyruvate dehydrogenase	Pyruvate metabolism	KOACACPH_03262/KOACACPH_02307
36	2.3.3.5	K01659	2-methylcitrate synthase	Propanoate metabolism	KOACACPH_01884
37	4.2.1.79	K01720	2-methylcitrate dehydratase	Propanoate metabolism	KOACACPH_01885
38	4.2.1.99	K01682	2-methylaconitate hydratase	Propanoate metabolism	KOACACPH_03589
39	1.2.4.4	K11381	3-methyl-2-oxobutanoate dehydrogenase	Propanoate metabolism	KOACACPH_00351
40	2.3.1.168	K09699	Dihydrolipoyllysine-residue (2-methylpropanoyl)transferase	Propanoate metabolism	KOACACPH_03134
41	4.1.3.30	K03417	2-methylisocitrate lyase	Propanoate metabolism	KOACACPH_01883
42	2.5.1.6	K00789	S-adenosylmethionine synthase	Metabolism of Methionine and Cysteine	KOACACPH_03573

43	2.1.1.37	K00558	DNA (cytosine-5-)-methyltransferase	Metabolism of Methionine and Cysteine	KOACACPH_02976
44	3.3.1.1	K01251	Adenosylhomocysteinase	Metabolism of Methionine and Cysteine	KOACACPH_03683
45	4.2.1.22	K01697	Putative cystathionine beta-synthase	Metabolism of Methionine and Cysteine	KOACACPH_01627
46	4.4.1.1	K01758	L-methionine gamma-lyase	Metabolism of Methionine and Cysteine	KOACACPH_01562
47	2.6.1.1	K00812	Aspartate/prephenate aminotransferase	Metabolism of Phenylalanine, Tyrosine, Glutamate and Aspartate	KOACACPH_02216
48	4.3.1.1	K01744	Aspartate ammonia-lyase	Metabolism of Phenylalanine, Tyrosine, Glutamate and Aspartate	KOACACPH_04295
49	4.1.1.19	K01585	Biosynthetic arginine decarboxylase	Metabolism of Arginine	KOACACPH_01491
50	3.5.3.11	K01480	Agmatinase	Metabolism of Arginine	KOACACPH_01493
51	2.5.1.16	K00797	Polyamine aminopropyltransferase	Metabolism of Arginine	KOACACPH_01104
52	1.5.99.6	K00316	Spermidine dehydrogenase	Metabolism of Arginine	KOACACPH_01105
53	1.2.1.3	K00128	Aldehyde dehydrogenase (NAD+)	Metabolism of Arginine	KOACACPH_01832/KOACACPH_01990
54	2.6.1.19	K07250, K13524	4-aminobutyrate aminotransferase	Metabolism of Arginine	KOACACPH_03346
55	1.2.1.24	K08324	Succinate-semialdehyde dehydrogenase (NAD+)	Metabolism of Arginine	KOACACPH_02948
56	1.2.1.79	K00135	Succinate-semialdehyde dehydrogenase (NADP+)	Metabolism of Arginine	KOACACPH_02948
57	2.7.7.4	K00955	Sulfate adenylyltransferase	Sulfur metabolism	KOACACPH_01861/KOACACPH_01862
58	2.7.1.25	K00955	Adenylyl-sulfate kinase	Sulfur metabolism	KOACACPH_01862
59	1.8.4.8	K00390	Phosphoadenosine phosphosulfate reductase	Sulfur metabolism	KOACACPH_01860
60	1.8.1.2	K00380	Sulfite reductase (NADPH) flavoprotein alpha-component	Sulfur metabolism	KOACACPH_01866
61	1.8.1.2	K00381	Sulfite reductase (NADPH) hemoprotein beta-component	Sulfur metabolism	KOACACPH_01867
62	1.8.7.1	K00392	Assimilatory sulfite reductase	Sulfur metabolism	KOACACPH_01867
