

Table S1. Bioactive compounds and feature of lichens isolated from Himalayas.

Sample (Family)	Uses / Activity	Chemical constituent	References*
<i>Usnea</i> sp. (<i>Parmeliaceae</i>)	Endangered medicinal lichen / anti-cancer, anti-proliferative, antioxidant, and anti-inflammatory, etc	Lichenan, Isolichenin, Fatty acids, Depsides, Depsidones, and Benzofurans	[1]
<i>Ramalina</i> sp. (<i>Ramalinaceae</i>)	Alpha-amylase, alpha-glucosidase, antioxidant, and anti-diabetic activities	Salazinic acid, Sekikaic acid, and Usnic acid	[2, 3]

*References

1. Prateeksha, Paliya BS, Bajpai R, Jadaun V, Kumar J, Kumar S, Upreti DK, Singh BR, Nayaka S, Joshi Y, Singh BN. 2016. The genus *Usnea*: a potent phytomedicine with multifarious ethnobotany, phytochemistry and pharmacology. *RSC Adv* 6: 21672-21696.
2. Thadhani VM, Karunaratne V. 2017. Potential of lichen compounds as antidiabetic agents with antioxidative properties: a review. *Oxid. Med. Cell Longev*. 2017: 2079697.
3. Furmanek Ł, Czarnota P, Seaward MRD. 2019. Antifungal activity of lichen compounds against dermatophytes: a review. *J. Appl. Microbiol*. Epub ahead of print.

Table S2. Characteristics of bacteria isolated from lichens, *Usnea* sp. and *Ramalina* sp., from Himalayas.

Strain	Closest relative	Identity (%)	Isolation media	Isolation temperature (°C)
NP007	<i>Methylobacterium tardum</i> strain RB677	99	B's	25
NP008	<i>Methylobacterium radiotolerans</i> strain JCM 2831	98	B's	25
NP010	<i>Methylobacterium radiotolerans</i> strain JCM 2831	98	MY	25
NP011	<i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> strain FZB42	99	MY	25
NP012	<i>Methylobacterium radiotolerans</i> strain JCM 2831	99	B's	25
NP016	<i>Burkholderia sordidicola</i> strain S5-B	99	MY	8
NP020	<i>Methylobacterium radiotolerans</i> strain JCM 2831	99	B's	37
NP021	<i>Staphylococcus epidermidis</i> strain NBRC 100911	99	MY	37
NP030	<i>Bacillus subtilis</i> strain 168	85	B's	25
NP038	<i>Leifsonia lichenia</i> strain 2Sb	99	B's	15
NP043	<i>Pantoea agglomerans</i> strain NBRC 102470	99	MY	8
NP049	<i>Staphylococcus epidermidis</i> strain Fussel	90	MY	25
NP050	<i>Bacillus licheniformis</i> strain DSM 13	99	B's	37
NP054	<i>Streptomyces thinghirensis</i> strain S10	98	B's	25
NP062	<i>Leifsonia poae</i> strain VKM Ac-1401	99	B's	15
NP063	<i>Leifsonia poae</i> strain VKM Ac-1401	99	B's	15
NP069	<i>Leifsonia lichenia</i> strain 2Sb	99	B's	25
NP071	<i>Pseudomonas lutea</i> strain OK2	98	MY	25
NP072	<i>Leifsonia poae</i> strain VKM Ac-1401	99	B's	15
NP073	<i>Leifsonia lichenia</i> strain 2Sb	99	B's	15
NP074	<i>Streptomyces fulvissimus</i> strain DSM 40593	99	ISP4	15
NP077	<i>Leifsonia lichenia</i> strain 2Sb	99	B's	15
NP078	<i>Streptomyces thinghirensis</i> strain S10	99	B's	25
NP086	<i>Methylobacterium tardum</i> strain RB677	99	B's	25
NP088	<i>Bacillus licheniformis</i> strain DSM 13	99	MY	25
NP090	<i>Streptomyces fulvissimus</i> strain DSM 40593	99	ISP4	15
NP091	<i>Bacillus licheniformis</i> strain DSM 13	99	MY	37
NP092	<i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> strain FZB42	99	MY	25
NP093	<i>Paenibacillus taichungensis</i> strain BCRC 17757	98	MY	15
NP094	<i>Bacillus licheniformis</i> strain DSM 13	99	MY	37
NP097	<i>Streptomyces thinghirensis</i> strain S10	99	MY	37
NP108	<i>Rhodococcus jialingiae</i> strain djl-6-2	99	ISP4	25
NP115	<i>Streptomyces thinghirensis</i> strain S10	99	B's	37
NP121	<i>Burkholderia terrestris</i> strain R-23321	97	MY	15

Table S2. Continued.

Strain	Closest relative	Identity (%)	Isolation media	Isolation temperature (°C)
NP125	<i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> strain FZB42	99	MY	37
NP127	<i>Bacillus licheniformis</i> strain DSM 13	99	B's	25
NP131	<i>Burkholderia sordidicola</i> strain S5-B	98	B's	15
NP132	<i>Methylobacterium tardum</i> strain RB677	99	MY	25
NP134	<i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> strain FZB42	99	MY	25
NP139	<i>Caballeronia peredens</i> strain HMF7693	99	B's	25
NP141	<i>Methylobacterium persicinum</i> strain 002-165	98	MY	25
NP142	<i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> strain FZB42	99	MY	25
NP143	<i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> strain FZB42	99	MY	25
NP157*	<i>Bacillus amyloliquefaciens</i> subsp. <i>plantarum</i> strain FZB42	99	MY	25
NP160*	<i>Streptomyces flavofuscus</i> strain NRRL B-2594	98	MY	15
NP161*	<i>Streptomyces pratensis</i> strain ch24	99	ISP4	15
NP167*	<i>Curtobacterium oceanosedimentum</i> strain ATCC 31317	98	R2A	25
NP175*	<i>Bacillus aryabhatai</i> strain B8W22	99	B's	37
NP183*	<i>Bacillus acidicer</i> strain CBD 119	99	B's	37

*isolated from *Ramalina* sp.

Table S3. Presence of PKS and NRPS genes from the lichen-associated bacteria containing antimicrobial activities.

PKS gene name	Closest strain (BLASTX results)			Accession #	Domain	Region
	Description	Query coverage (%)	Percent identity (%)			
NP007-1	Amino acid adenylation domain-containing protein (<i>Bacillus subtilis</i>)	81	41.33	WP_124059874.1	Adenylation	A_NRPS_TubE_like
NP007-2	Amino acid adenylation domain-containing protein (<i>Bacillus subtilis</i>)	85	87.30	WP_122894510.1	Adenylation	A_NRPS_TubE_like
NP007-3	Type I polyketide synthase (<i>Streptomyces</i> sp.)	46	98.23	AWS21951.1	None	Fatty acid PKS
NP007-4	Polyketide synthase of Type I (<i>Bacillus subtilis</i> XF-1)	96	90.00	AGE63558.1	Acyl transferase	PksD
NP011-1	Polyketide synthase (<i>Bacillus</i> sp. WPySW2)	100	98.68	ACG70841.1	Acyl transferase	PksD
NP011-2	Polyketide synthase (<i>Bacillus</i> sp. WPySW2)	100	98.68	ACG70841.1	Acyl transferase	PksD
NP011-3	Glucose 1-dehydrogenase (<i>Microbacterium humi</i>)	73	71.57	WP_091183664.1	Enoyl-[acyl-carrier-protein] reductase (NADH)	FabI
NP011-4	Non-ribosomal peptide synthetase (<i>Bacillus amyloliquefaciens</i>)	99	99.02	WP_049589373.1	Adenylation	Srf_like
NP012-1	Polyketide synthase (<i>Bacillus velezensis</i>)	99	98.25	ASB65451.1	Acyl transferase	PksM
NP020-1	Polyketide synthase (<i>Sphingobacterium</i> sp. A3)	65	59.77	WP_130572051.1	None	PKS
NP021-1	Polyketide synthase (<i>Bacillus amyloliquefaciens</i>)	99	100.00	AWW22989.1	None	Fatty acid PKS
NP021-2	Polyketide synthase (<i>Bacillus velezensis</i>)	98	98.25	ASB65451.1	Acyl transferase	PksM
NP030-1	Non-ribosomal peptide synthetase (<i>Bacillus subtilis</i>)	99	99.13	WP_080121137.1	Acyl transferase	PksD
NP030-2	Polyketide synthase (<i>Bacillus amyloliquefaciens</i>)	99	98.21	AWW22989.1	None	Fatty acid PKS
NP030-3	Polyketide synthase (<i>Bacillus</i> sp. WPySW2)	99	98.67	ACG70841.1	Acyl transferase	PksD

Table S3. Continued.

PKS gene name	Closest strain (BLASTX results)				Domain	Region
	Description	Query coverage (%)	Percent identity (%)	Accession #		
NP030-4	Ketosynthase (<i>Bacillus subtilis</i>)	99	99.14	SAJ35050.1	Acyl transferase	PksD
NP030-5	Non-ribosomal peptide synthetase (<i>Bacillus</i> sp. BA-11)	98	98.15	SSX46824.1	Adenylate forming	AFD_class_I
NP030-6	Non-ribosomal peptide synthetase (<i>Bacillus subtilis</i> subsp. <i>subtilis</i>)	98	89.66	PRS89669.1	None	NRPS
NP043-1	Non-ribosomal peptide synthetase (<i>Erwinia</i> sp. ErVv1)	96	91.82	WP_067707035.1	None	NRPS
NP049-1	Polyketide synthase (<i>Bacillus velezensis</i>)	98	98.25	ASB65451.1	Acyl carrier	Acyltransferase
NP049-2	Type I polyketide synthase (<i>Luteibacter</i> sp. 9133)	99	91.30	WP_052191221.1	Acyl transferase	PKS_AT
NP050-1	Polyketide synthase of Type I (<i>Bacillus subtilis</i> XF-1)	99	97.82	AGE63558.1	Acyl transferase	PksD
NP062-1	Antimicrobial protein (uncultured bacterium)	80	75.25	AQW80360.1	None	Antimicrobial protein
NP062-2	Hybrid non-ribosomal peptide synthetase/Type I polyketide synthase (<i>Streptomyces</i> sp. TverLS-915)	50	55.41	WP_093816860.1	Beta-ketoacyl reductase (KR)	Fatty acid
NP062-3	Hybrid non-ribosomal peptide synthetase/Type I polyketide synthase (<i>Streptomyces</i> sp. H-KF8)	58	60.00	WP_065002037.1	Hybrid NRPS-PKS type I	None
NP071-1	Non-ribosomal peptide synthetase (<i>Pseudomonas</i> sp. FW306-2-2C-D06C)	99	91.18	PMY38939.1	None	NRPS

Table S3. Continued.

PKS gene name	Closest strain (BLASTX results)				Domain	Region
	Description	Query coverage (%)	Percent identity (%)	Accession #		
NP072-1	Putative beta-ketoacyl synthase (<i>Streptomyces</i> sp. MP8E7-PKS1-nr4)	99	95.28	ACI24637.1	Beta-ketoacyl synthase	Fatty acid
NP072-2	Putative beta-ketoacyl synthase (<i>Streptomyces</i> sp. MP8E7-PKS1-nr4)	99	94.81	ACI24637.1	Beta-ketoacyl synthase	Fatty acid
NP073-1	Polyketide synthase (<i>Bacillus</i> sp. WPySW2)	99	97.79	ACG70841.1	Acyl transferase	PksD
NP074-1	Type I polyketide synthase (<i>Streptomyces</i> sp. TP-A0875)	99	98.11	WP_053914804.1	Acyl transferase	PksD
NP088-1	Non-ribosomal peptide synthetase (<i>Bacillus subtilis</i>)	99	98.65	WP_095843472.1	None	EntF
NP090-1	Type I polyketide synthase (<i>Streptomyces</i> sp. TP-A0875)	100	87.16	WP_053914804.1	Acyl transferase	PksD
NP090-2	Type I polyketide synthase (<i>Streptomyces</i> sp. TP-A0875)	99	97.64	WP_053914804.1	Acyl transferase	PksD
NP090-3	Putative beta-ketoacyl synthase (<i>Streptomyces</i> sp. MP8E7-PKS1-nr4)	99	94.81	ACI24637.1	Beta-ketoacyl synthase	Fatty acid
NP090-4	Type I polyketide synthase (<i>Streptomyces</i> sp. TP-A0875)	99	98.11	WP_053914804.1	Acyl transferase	PksD
NP090-5	Antimicrobial protein (uncultured bacterium)	86	48.31	AQW80360.1	None	Antimicrobial protein
NP090-6	Non-ribosomal peptide synthetase (<i>Streptomyces niger</i>)	97	92.51	WP_052863959.1	Adenylation	NRPS

Table S3. Continued.

PKS gene name	Closest strain (BLASTX results)			Accession #	Domain	Region
	Description	Query coverage (%)	Percent identity (%)			
NP091-1	Ketosynthase (<i>Bacillus subtilis</i>)	99	97.41	SAJ35050.1	Acyl transferase	PksD
NP093-1	2,3-Dihydroxybenzoate-AMP ligase (<i>Enterobacter cloacae</i>)	96	68.52	STQ13414.1	None	EntB
NP097-1	Hybrid non-ribosomal peptide synthetase/Type I polyketide synthase (<i>Streptomyces</i> sp. SA3_actG)	98	100.00	WP_010262581.1	Beta-ketoacyl reductase (KR)	Fatty acid
NP108-1	Polyketide synthase (<i>Bacillus velezensis</i>)	98	98.70	ASB65451.1	Acyl transferase	PksM
NP115-1	Polyketide synthase (<i>Bacillus velezensis</i>)	80	88.13	ASB65451.1	Acyl transferase	PksM
NP125-1	Polyketide synthase (<i>Bacillus amyloliquefaciens</i>)	99	99.10	AWW22981.1	None	Fatty acid PKS
NP125-2	Polyketide synthase (<i>Bacillus velezensis</i>)	99	97.83	ASB65451.1	Acyl transferase	PksM
NP127-1	Beta-ketoacyl synthase (<i>Mycobacteroides abscessus</i> subsp. <i>massiliense</i>)	98	97.14	SLB19569.1	None	Beta-ketoacyl synthase
NP132-1	Polyketide synthase (<i>Streptomyces</i> sp.)	84	96.55	QBL56181.1	KS-AT-DH-KR-ACP-KS-AT-DH-KR-ACP-TE	PKS
NP132-2	Hybrid non-ribosomal peptide synthetase/Type I polyketide synthase (<i>Streptomyces</i> sp. SPB78)	98	99.56	WP_009068282.1	Acyl transferase	PksD
NP134-1	Polyketide synthase (<i>Bacillus siamensis</i>)	79	53.70	PIK31931.1	None	PKS

Table S3. Continued.

PKS gene name	Closest strain (BLASTX results)				Domain	Region
	Description	Query coverage (%)	Percent identity (%)	Accession #		
NP139-1	Polyketide synthase (<i>Bacillus amyloliquefaciens</i>)	96	98.64	AWW22987.1	None	Fatty acid PKS
NP139-2	Polyketide synthase (<i>Bacillus velezensis</i>)	93	87.90	QBL98020.1	None	PKS
NP139-3	Type III polyketide synthase (<i>Sphingomonas</i> sp. PAMC 26605)	25	52.81	WP_010184306.1	Predicted naringenin-chalcone synthase	Type III
NP141-1	Polyketide synthase (<i>Bacillus velezensis</i>)	98	98.68	ASB65451.1	Acyl carrier	Acyl transferase
NP142-1	Antimicrobial protein (Uncultured bacterium)	87	55.88	AQW80360.1	None	Antimicrobial protein
NP142-2	Polyketide synthase (<i>Bacillus</i> sp. WPySW2)	99	98.23	ACG70841.1	Acyl transferase	PksD
NP143-1	Non-ribosomal peptide synthetase (<i>Bacillus velezensis</i>)	100	97.39	WP_083059010.1	Adenylation	NRPS_Ta1_like
NP157-1	Type I polyketide synthase (<i>Luteibacter</i> sp. 9133)	98	92.11	WP_052191221.1	Acyl transferase	Fatty acid PKS
NP160-1	Polyketide synthase (<i>Bacillus velezensis</i>)	99	97.83	ASB65451.1	Acyl carrier	Acyl transferase
NP160-2	Polyketide synthase (<i>Bacillus velezensis</i>)	98	97.81	ASB65451.1	Acyl transferase	PksM
NP160-3	Polyketide synthase (<i>Bacillus amyloliquefaciens</i>)	99	99.56	CUB44647.1	None	PksN
NP160-4	Polyketide synthase (<i>Bacillus amyloliquefaciens</i>)	99	98.68	CUB45889.1	None	PksJ
NP160-5	Involved in fengycin synthesis (<i>Bacillus velezensis</i> NAU-B3)	99	98.68	CUH95680.1	Adenylation	FenB

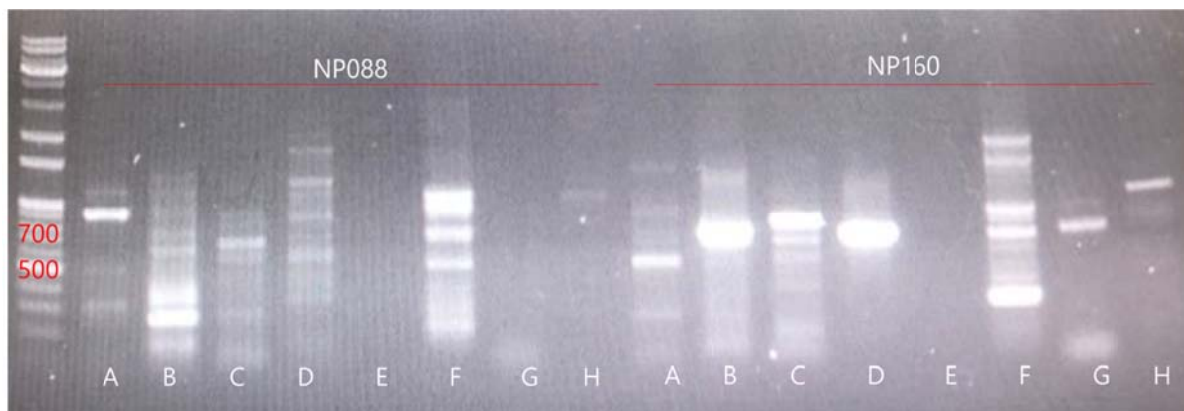
Table S3. Continued.

PKS gene name	Closest strain (BLASTX results)				Domain	Region
	Description	Query coverage (%)	Percent identity (%)	Accession #		
NP160-6	Involved in fengycin synthesis (<i>Bacillus velezensis</i> NAU-B3)	99	97.49	CUH95680.1	Adenylation	FenB
NP161-1	Polyketide synthase (<i>Streptomyces kobenensis</i>)	100	90.75	BAH67414.1	None	Fatty acid PKS
NP167-1	Non-ribosomal peptide synthetase FenB involved in fengycin synthesis (<i>Bacillus velezensis</i> NAU-B3)	99	97.07	CDH95680.1	Adenylation	NRPS
NP175-1	Hybrid non-ribosomal peptide synthetase/Type I polyketide synthase (<i>Streptomyces</i> sp. LcepLS)	93	85.47	WP_093584234.1	None	Hybrid NRPS-PKS type I
NP175-2	Hybrid non-ribosomal peptide synthetase/Type I polyketide synthase (<i>Streptomyces</i> sp. CLI2509)	97	100.00	WP_095682260.1	None	Hybrid NRPS-PKS type I
NP175-3	Hybrid non-ribosomal peptide synthetase/Type I polyketide synthase (<i>Streptomyces</i> sp. SA3_actG)	98	100.00	WP_010262581.1	None	Hybrid NRPS-PKS type I
NP175-4	Non-ribosomal peptide synthetase (<i>Streptomyces</i> sp. SPB78)	38	50.00	WP_078490047.1	None	NRPS
NP183-1	Polyketide synthase (<i>Bacillus amyloliquefaciens</i>)	99	98.21	AWW22989.1	None	Fatty acid PKS

Figure S1. Two lichen species from Himalayas used in this study, *Usnea* sp. (A) and *Ramalina* sp. (B).



Figure S2. PKS fingerprinting results of NP088 and NP160. Results of NP088 PKS fingerprinting and evaluation of PKS and NRPS fingerprinting using *Streptomyces* sp. NP160.



*A, K1F and M6R [10]; B, PKS-I-A and PKS-I-B [21]; C, KSMAF and KSMBR [22]; D, KSI1F and KSI2R [9]; E, 540F and 1100R [23]; F, KS α and KS β [24]; G, A3F and A7R [24]; and H, MTF2 and MTR [24].