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Identification and characterization of biosynthetic gene clusters from halophilic marine fungus *Eurotium rubrum*

Obul Reddy Bandapali¹, Jens Frederik Teilfeldt Hansen², Alisha Parveen³, Pradeep Phule⁴, Emmagouni Sharath Kumar Goud⁵, Suraj Kumar Acharya⁶, Jens Laurids Sørensen⁷ & Abhishek Kumar^{8,*}

¹Division of Pediatric Neurooncology, German Cancer Research Center (DKFZ), German Cancer Consortium (DKTK), Hopp Children's Cancer Center (KiTZ), and Heidelberg University, Medical Faculty, D-69120 Heidelberg, Germany;

o.bandapalli@dkfz-heidelberg.de

²Department of Biochemistry, McGill University, Montréal, QC H3G 0B1, Canada and Department of Chemistry and Bioscience, Aalborg University, Niels Bohrs Vej 8, DK-6700 Esbjerg, Denmark; jens.hansen@mail.mcgill.ca

³Institute of Molecular Medicine and Cell Research, Albert Ludwigs University Freiburg, Stefan Meier Strasse 17, 79104, Freiburg, Germany; alisha.parveen@uniklinik-freiburg.de

⁴Institute of Bioinformatics, International Technology Park, Bangalore, 560066 India; pradeep@ibioinformatics.org

⁵Institute of Bioinformatics, International Technology Park, Bangalore, 560066 India; sharath@ibioinformatics.org

⁶Institute of Bioinformatics, International Technology Park, Bangalore, 560066 India; suraj@ibioinformatics.org

⁷Department of Chemistry and Bioscience, Aalborg University, Niels Bohrs Vej 8, DK-6700 Esbjerg, Denmark; jls@bio.aau.dk

⁸Institute of Bioinformatics, International Technology Park, Bangalore, 560066 and Manipal Academy of Higher Education (MAHE), Manipal 576104, Karnataka, India; abhishek@ibioinformatics.org

* Correspondence: abhishek@ibioinformatics.org; Tel.: +91 80-2841-6140 (A.K.)

Abstract: *Eurotium rubrum* is a halophilic marine ascomycete, which can bear the hypersalinity of the Red Sea and proliferate, while most living entities cannot bear this condition. Recently, a 26.2 Mb assembled genome of this fungus had become available. Marine fungi are fascinating organisms capable of harboring several biosynthetic gene clusters (BGCs), which enables them to produce several natural compounds with antibiotic and anticancerous properties. Understanding the BGCs are critically important for the development of biotechnological applications and the discovery of future drugs. There is no knowledge available on the BGCs of this halophilic marine ascomycete. Herein, we set out to explore and characterize BGCs and the corresponding genes from *E. rubrum* using bioinformatic methods. We deciphered 36 BGCs in the genome of *E. rubrum*. These 36 BGCs can be grouped into four non-ribosomal peptide synthetase (NRPS) clusters, eight NRPS-like (NRPSL) BGCs, eight type I polyketide synthase (T1PKS), 10 terpene BGCs including one β -lactone cluster, four hybrid BGCs, and two siderophore BGCs. This study is an example of marine genomics application into potential future drug-like compound discovery.

Keywords: Biosynthetic gene clusters; *Eurotium rubrum*; halophilic; marine genomics; nonribosomal peptide synthetase; T1pks; Terpene;

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1. Introduction

The Dead Sea is an excellent niche for testing the survival skills of many living organisms because it is the most hypersaline habitats on our planet [1]. The brines of the Dead Sea has a salinity level upto 348 g l⁻¹ [1]. This makes it unbearable for most of the living entities, so the majority of species living here stay in their dormant stages to survive this hypersalinity and they return to the normal stages during reduced salinity either by rare heavy flooding events [2] or by underwater fresh water springs [3]. Only a limited number of organisms survive during the conditions of hypersalinity like halobacteria, *Dunaliella parva* Lerche (a green algae) and some species of fungi. One of these fungi is the ascomycete *Eurotium rubrum*, which survive in the Red sea. Recently the genome of this marine fungus has become available with a genome size of 26.2 Mb [4]. Generally, marine fungi are considered as an excellent source of bioactive compound and their genomes harbors many biosynthetic gene clusters (BGCs) from which these natural compounds are produced [5-8]. One of the best examples of marine fungi producing such beneficial compounds is *Scopulariopsis* producing the anti-cancerous scopularide [5]. Herein, our aim is to unravel the BGCs of the halophilic marine fungus *E. rubrum* using the recently available genome. We also carried out extensive characterization of these BGCs and corresponding genes producing natural compounds. We identified 36 BGCs in the *E. rubrum* genome and we designated them as EruBGC1 to EruBGC36, which are classified into four nonribosomal peptide synthetase (NRPS) clusters, eight each NRPS-like (NRPSL) BGC and T1PKS, 10 terpene BGCs, four hybrid BGCs, and two siderophore BGCs.

2. Results & Discussion

2.1. Overview of BGCs of *E. rubrum* genome

We identified 36 biosynthetic gene clusters (BGCs) in the 26.2 Mb assembled genome of *E. rubrum*. These 36 clusters are designated as EruBGC1 to EruBGC36 (**Tables 1-5**), and this list has four non-ribosomal peptide synthetase (NRPS) clusters (**Table 1**), eight each NRPS-like (NRPSL) BGC (**Table 2**) and T1PKS (**Table 3**), ten terpene BGCs including β -lactone producing BGC (**Table 4**), four hybrid BGCs (**Table 5**) and two siderophore BGCs (**Table 6**). The hybrid BGCs consist of four different clusters, namely, NRPS, indole (EruBGC7), T1PKS, indole (EruBGC17), T1PKS, NRPS-like (EruBGC28) and T1PKS, NRPS (EruBGC30, **Table 5**).

2.2. Summary of BGCs encoding NRPS from *E. rubrum*

There are four BGCs in the genome of *E. rubrum*, which encode NRPS genes and corresponding proteins (**Table 1**). The cluster EruBGC2 is localized on the scaffold00002 (KK088412.1) spanning in about 58 kb region from 40,834-98,875 bp (**Table 1**). This cluster has 18 genes in total with core NRPS gene as EURHEDRAFT_469898 and this BGC is conserved with top hits are in genomes of *Saccharopolyspora flava*, two species of *Gordonia* and *Streptomyces* sp. (**Fig. S1**). The core NRPS protein (nonribosomal siderophore peptide synthase SidC, GenBank ID - EYE98782.1) of this BGC is 4734 amino acid long, sharing sequence identities 93% and 65% each with orthologs from *Aspergillus cristatus*, *A. flavus* (strain NRRL3357) and *A. oryzae* (strain 3.042), respectively (**Fig. 1B**).

The second NRPS cluster (EruBGC14) contains 13 genes with size of 43.1 kb on the scaffold00008 (KK088418.1) ranged from 5,62,619 bp to 6,05,729 bp (**Table 1**). It has no homology with any clusters in sequenced genomes (**Fig. S1**). The core NRPS protein (EYE96553.1) of this BGC is known as acetyl-CoA synthetase-like protein with length of 1037 amino acids long chain and it shares sequence identities 55% and 38% with AMP-dependent synthetase/ligase (CRL27778.1) and NRPS (XP_754251.1) from *Penicillium camemberti* and *Aspergillus fumigatus*, respectively (**Fig. 1B**).

EruBGC25 is the third NRPS cluster that localized on the scaffold00034 (KK088444.1) harboring 14 genes within 46.2 kb (**Table 1**). This BGC shows similarities with clusters of multiple strains of *Pseudomonas*, *Photobacterium temperata* and *Bradyrhizobium yuanmingense* (**Fig. S1**). The core protein of this cluster is NRPS6 (EYE91538.1) with 6 protein domains (**Fig. 1A**) and several annotated hits in different *Aspergillus* genome (**Fig. 1A**). The fourth NRPS cluster (EruBGC32) resides on the scaffold00058 is 33.5 kb long with total of 14 genes (**Table 1**). It shows homologies with NRPS clusters from *Chitinophaga eiseniae*, *Myxococcus xanthus* and *Archangium violaceum* Cb, respectively (**Fig. S1**). It has five core genes (**Table 1**), which encodes for NRPS proteins namely EYE90154.1, EYE90155.1, EYE90156.1, EYE90157.1 and EYE90158.1 (**Fig. 1E**) with at least three domains as adenylation, peptidyl carrier protein and condensation (**Fig 1**).

2.3. There are 8 NRPS-like BGCs in the *E. rubrum* genome

We identified eight NRPS-like BGCs (**Table 2**). The first NRPS-like BGC is EruBGC4, which is mapped to a 41.2kb region on the scaffold00003 (KK088413.1) with total 19 genes (**Table 2**). This cluster has homologs in three bacteria namely *Acetivibrio cellulolyticus*, *Xanthobacter autotrophicus* and *Frankia* species (**Fig. S2A**). The core protein of EruBGC4 is acetyl-CoA synthetase-like protein (EYE98346.1) with NRPS domains (**Fig. 1**) and several annotated hits during homology detection (**Fig.**

S3A). The second NRPS-like BGC (EruBGC10) is located in the ~42kb on the scaffold00005 (KK088415.1) with 17 genes (Table 2). EruBGC10 has hits in several bacterial genomes with top are *Desulfovibrio ferrireducens*, *Salinispora arenicola* and *Nostoc linckia* (Fig. S2B). The core enzyme of this cluster is hypothetical protein (EYE97683.1), however it has NRPS domains (Fig. 1) and we found several annotated hits as NRPS-like proteins from *Aspergillus* strains (Fig. S3B).

Fig 1. Summary of non-ribosomal peptide synthetase (NRPS).

A. Overview of protein domain of NRPS and NRPS-like BGCs of marine *E. rubrum*.

B-E - Re-annotation and phylogenetic analyses of core NRPS proteins

The third NRPS-like BGC (EruBGC18) is mapped to the scaffold00013 (KK088423.1) in a 43.2 kb region (1,25,819bp-1,69,069bp), which harbors 11 genes (Table 2). This BGC has no homologous clusters (Fig. S2C). The core protein of this cluster (EYE95070.1) is known as a putative NRPS-like enzyme and it is 1048 residues long. It shares 78% of sequence identities each with linear gramicidin synthase subunit D (GAO87904.1) from *A. udagawae*, putative NRPS-like enzyme (EDP49425.1) from *A. fumigatus* A1163 and a putative NRPS-like enzyme (XP_001257972.1) from *A. fischeri* NRRL 181 (Fig. S3C). The fourth NRPS-like BGC, EruBGC20 is localized on the scaffold00027 (KK088437.1) with 12 genes in a region of 34.6 kb (Table 2). EruBGC20 has no homologous clusters in the public databases (Fig. S2D). The core protein of this cluster (EYE92311.1) is known as an NRPS-like enzyme and it is 1045 residues long. This protein shares 59% and 56% identities with putative NRPS-like

enzymes of *A. clavatus* NRRL 1 (XP_001268898.1) and *A. bombycis* (OGM48478.1), respectively (**Fig. S3D**).

The fifth NRPS-like BGC, EruBGC22 is ~44 kb long on scaffold00028 from 1,36,752 bp to 1,81,201 bp harboring 18 genes (**Table 2**). EruBGC22 has homologous clusters in strains of *Aspergillus*, *Trichophyton*, *Exophiala dermatitidis*, *Botryotinia fuckeliana*, *Leptosphaeria maculans* and *Colletotrichum higginsianum* (**Fig. S2E**). Top 2 hits of EruBGC22 are AP007155.1_c2 from *Aspergillus oryzae* RIB40 (42% identities) and AM270078.1_c1 from *A. niger* contig (35% identities). This BGC is capable of producing four dehydrogenases like aryl-alcohol dehydrogenase (EYE92212.1), L-aminoadipate-semialdehyde dehydrogenase (EYE92214, **Fig. S3D**), xanthine dehydrogenase (EYE92216.1) and aldehyde dehydrogenase (EYE92219.1). The core protein of this cluster has 1426 residues (EYE92214) with 83%, 80% and 70% sequence identities with L-aminoadipate-semialdehyde dehydrogenases of *A. oryzae* (OOO09926.1) and *A. udagawae* (GAO83448.1) and Male sterility, NAD-binding of *P. griseofulvum* (KXG50863.1). This protein is a key intermediate compound in Δ^1 -piperidine-6-carboxylic acid (P6C) [9]. As per L-lysine degradation pathway, it is catalyzed as a product of saccharopine by *Saccharopine dehydrogenase* (SDH, EC:1.5.1.-). Hence, it is a major component of pathway of swainsonine synthesis and swainsonine has anticancerous and immune regulatory roles [10]. Additionally, this BGC is also carrying a gibberellin 3-beta hydroxylase (EYE92206.1), which shares 87% identities with isopenicillin N synthase (CRL25624.1) from *Penicillium camemberti*.

The sixth NRPS-like BGC (EruBGC29) is mapped to scaffold00040 in a ~36 kb region with 9 genes in this BGC (**Table 2**). This BGC has counterparts in both bacteria (*Mycobacterium marinum*, *Rhodococcus* and *Streptomyces* strains) and ascomycetes (*Aspergillus* strains, **Fig. S2F**). This core protein of EruBGC29 is putative NRPS-like protein (EYE90955.1), which is 1292 amino acid long. This protein shares 82% and 81% of sequence identities with gramicidin synthase subunit D (OKP10752.1) from *P. subrubescens* and AMP-dependent synthetase/ligase (CDM33966.1) from *P. roqueforti* FM164 (**Fig. S3G**). The seventh NRPS-like cluster (EruBGC31) has 12 genes and it is located in the scaffold00054 (KK088464.1) with the fragment size of 41.7kb. This cluster has homologs in several bacteria namely *Chitinophaga eiseniae*, *Myxococcus xanthus* and strains of *Archangium* and *Streptomyces* (**Fig. S2G**). EruBGC31 is encoding for acetyl-CoA synthetase-like protein (EYE90264.1) as core enzyme with two NRPS domains (**Fig 1**) and annotated hits in *Penicillium brasilianum* and *Trichophyton* (**Fig. S3G**). The eighth NRPS-like BGC, EruBGC34 is the fifth BGC found on scaffold00064 (KK088474.1), spanning seven genes in 30.1 kb region (**Table 2**). We do not detect any fungal homologous clusters in public databases for EruBGC34, however there is only one known bacterial BGC in *Streptomyces celluloflavus* strain NRRL B-2493 (**Fig. S2H**). Acetyl-CoA synthetase-like protein (EYE90083.1, 1653 residues) with conserved protein domains (**Fig 1**) is the core protein of EruBGC34 with top 2 known homologs being AMP-dependent synthetase/ligase (OQE47426.1/80% identity) from *P. griseofulvum* and AMP-dependent synthetase/ligase (XP_016602600.1/79%) from *P. expansum* (**Fig. S3H**).

2.4. Summary of T1pks producing BGCs from *E. rubrum*

There are eight BGCs in the genome of *E. rubrum*, which encode T1pks genes (**Table 3**) and corresponding proteins are listed in **Fig 2** with their protein domains. The first T1PKS cluster EruBGC3 is localized on the scaffold00002 (KK088412.1) in a region of 47.8 kb and it harbors 18 genes (**Table 3**). This BGC has homologous BGCs in several strains of *Mycolicibacterium* and *Kitasatospora aureofaciens*, respectively (**Fig. S4A**).

Fig 2. Summary of protein domains in PKS encoding by marine *E. rubrum*.

The core protein is putative polyketide synthase with different PKS domains (EYE99293.1, Fig 2) and upon homology detection, it has several hits with annotation as PKS proteins (Fig. S5A). This BGC is similar to cornexistin BGCs (Fig. S4A) from *Paecilomyces divaricatus* (MIBiG ID - BGC0001436 and BGC0001557). This suggested that this BGC is potent producer of cornexistin (molecular formula - C₁₆H₂₀O₆, Fig 2), which has herbicidal activity. The second T1PKS cluster, EruBGC5 is locate on scaffold00003 (KK088413.1) with a size of 46.7kb and this fragment has 14 genes (Table 3). EruBGC5 has homologs in several bacterial genomes including several *Streptomyces* species (Fig. S4B). The core protein of EruBGC5 is polyketide synthetase PksP (EYE98507.1, Fig 2) and it has annotated hits from several *Aspergillus* strains (Fig. S5B). This BGC is capable of producing naphthopyrone as this cluster has similarities with naphthopyrone cluster (MIBiG ID - BGC0000107) from *Aspergillus nidulans* FGSC A4 (Fig. S4B). The third T1pks BGC (EruBGC8) has a size of 45.4kb on the scaffold00004 (KK088414.1) with 20 genes (Table 3), which is similar to piericidin A1 and aflatoxin BGCs from *Streptomyces piomogenus* and *Aspergillus ochraceoroseus*, respectively (Fig. S4C). The core protein is polyketide synthetase with several PKS-based domains (EYE98259.1, Fig 2) and it has homologs in several *Aspergillus* species (Fig. S5C). This cluster is capable of producing desmethyl TAN-1612 (C₂₁H₁₈O₉, Fig 2), which harbors a tetracyclic naphthacenedione core structure. The fourth T1PKS cluster (EruBGC11) is mapped on the scaffold00005 (KK088415.1) with 18 genes within a 46kb fragment (Table 3). This fragment has homologous BGCs in several bacterial strains like *Kamtonema formosum*,

Streptomyces bingchenggensis and *Nocardia veterana* (Fig. S4C). The core enzyme of EruBGC11 is polyketide synthase (EYE97768.1) with multiple PKS domains (Fig 2) plus annotated hits to multiple *Aspergillus* strains (Fig. S5D). The fifth T1pks-BGC (EruBGC13) is located on the scaffold00007 (KK088417.1) with 15 genes in a region of 46.3kb (Table 3). PKS16 protein (EYE96821.1) is the backbone enzyme of EruBGC13 with multiple PKS domains (Fig 2). It has annotated hits in different ascomycetes (Fig. S5E). The sixth (EruBGC23) and seventh (EruBGC24) T1pks clusters are located on the scaffold00032 (KK088442.1) with sizes 47.5kb (14 genes) and 48kb (21 genes), respectively (Table 3). EruBGC23 has homologs in *Colwellia psychrerythraea*, *Cyanothece* sp. and several strains of *Streptomyces* (Fig. S4F), while EruBGC24 has similar clusters in *Mycobacterium malmoeense*, *Scytonema* sp., *Chitinophaga* sp. and several strains of *Streptomyces* (Fig. S4G), plus it has also matched with asperfuranone in MIBiG database (Fig. S4G). The core proteins of these two clusters are EYE91651.1 and EYE91696.1, which are annotated as hypothetical protein and putative polyketide synthase, respectively. However, upon scanning annotated homologs, we found that these proteins are T1PKS (Figs. S5F-G), which is also supported by their protein domain organization (Fig 2). The eighth T1pks cluster (EruBGC35) is localized on scaffold00077 in a region of 19.3 kb and it possesses total 8 genes (Table 3). This BGC is homologous cluster in *Saccharothrix espanaensis*, *Amycolatopsis keratiniphila* and *Amycolatopsis keratiniphila* (Fig. S4H). The core PKS enzyme of EruBGC35 is thiolase-like protein (EYE89967.1), which is 385 residues with tryptophan dimethylallyltransferase (Trp_DMAT, PF11991) domain and it has 75-77% sequence identities with homologs from other ascomycetes (Fig. S5H).

2.5. Summary of terpene BGCs from *E. rubrum*

We identified ten terpene-based BGCs in *E. rubrum* genome (table 4). The first terpene BGC EruBGC1 is localized on the scaffold00002 (KK088412.1) with 2 genes in a total size of 11.8 kb region (Fig. S5 and table 5) and it has no homologous BGC in any known microbial genome (Fig. S4A). The core protein of EruBGC1 is terpenoid synthase (EYE98762.1), 362 residues with trichodiene synthase (TRI5, PFAM ID - PF06330) domain (Fig. 3). This protein shares sequence identities of 50% to 57% with homologs in related ascomycetes (Fig. S5). The second terpene producing EruBGC6 is of 21.1 kb region on the scaffold00003 (KK088413.1) with 9 genes. It has single homologous BGC matching in the genome of *Lentzea jiangxiensis* (Fig. S4A). There are two terpenoid synthases as EYE98616.1 and EYE98617.1 as core proteins of EruBGC6 with size 337 and 335 residues long with TRI5 (PF06330) and polyprenyl synthetic (PF00348) domain, respectively. EYE98616.1 shares >70%-80% sequence identities with orthologs in other ascomycetes (Fig. S6), whereas EYE98617.1 has >53%-<75% sequence identities with orthologs in other ascomycetes (Fig. S7).

The third terpene BGC, EruBGC16 is localized on the scaffold00008 (KK088420.1) in a region of 22.3 kb from 1,52,089 bp-1,74,460 bp. EruBGC16 shares homologous BGCs from several strains of *Gordonia* (Fig. 4C). respectively. EruBGC16 is 100% identical to clavatic acid (Fig. 4C) producing BGC (MIBiG accession ID - BGC0001248) from *Hypholoma sublateritium*. This indicates that this cluster is capable of producing clavatic acid (molecular formula – C₃₆H₅₈O₈, Fig 3). The core protein of EruBGC16 is a lanosterol synthase (EYE95851.1) and it possesses two squalene-hopene cyclase protein domains (Fig identities 98% each and 88% for lanosterol synthase (Fig. S8) from *A. cristatus* (ODM19928.1), *A. lentulus* (GAQ08994.1) and *A. udagawae* (GAO84757.1), respectively.

Fig 3. Summary of domain architecture of terpene BGCs of the marine *E. rubrum* genome.

The 21.6 kb-long fourth BGC terpene BGC, EruBGC19 is mapped on to scaffold00014 (KK088424.1) with 12 genes in total. It shares homologous BGC from *Lysinibacillus massiliensis* and several *Teredinibacter* strains (Fig S4D). This cluster is producing squalenstatin S1 (Fig 3) with 60% identities with squalenstatin S1 producing BGC from *Aspergillus* sp. Z5 (BGC0001839, Fig S4D). This illustrates that EruBGC19 is a potent producer of squalenstatin S1 (C₃₅H₄₆O₁₃, Fig 3). The core enzyme of this cluster is farnesyl-diphosphate farnesyltransferase (EYE94773.1), which is 476 residues and harbors a SQS-PSY (PF00494) domain (Fig 3E). EYE94773.1 shares >80-<95%, with top homologs (Fig. S9). The fifth terpene BGC, EruBGC21 is mapped to scaffold00027 (KK088437.1) from 1,86,829 bp to 2,07,933 bp with total size of 21.1 kb region, possessing 10 genes. It has no homologous BGCs in other species when scanned in public databases (Fig S4E). The core protein of this cluster is terpenoid synthase (EYE92376.1), 340 amino acids long with polyprenyl synthetic (PF00348) domain (Fig 3F). This protein has 85% sequence identities with orthologs in *Aspergillus* strains (Fig. S10). The sixth terpene cluster, EruBGC26 possesses seven genes in the 24.3 kb region in the scaffold00035 (KK088445.1). EruBGC26 has homologous BGC in *Beijerinckia indica* subsp. *indica* ATCC 9039 and several strains of *Nitrosomonas* and *Methylocapsa* (Fig S4F). The core enzyme of this BGC is 1149 residues long squalene cyclase (EYE91407.1), with two squalene-hopene cyclase protein domains (Fig 3G) as SQHop_cyclase_N (PF13249) and SQHop_cyclase_C (PF13243) and these domains are capable

of producing prenyltransferases. Sequence analysis reveals that squalene cyclase (EYE91407.1) has 55-57% sequence identities with orthologs from different *Aspergillus* species (**Fig. S11**).

The seventh terpene cluster (EruBGC27) is 15kb long with 6 genes, which is harbored on the scaffold00036 (KK088446.1). This cluster is novel as we did not find any similar cluster in public databases (**Fig S4G**). The core backbone of EruBGC27 is terpenoid synthase (EYE91365.1), which is 305 residues long without any protein domain (**Fig 3H**). This protein has 62-65% sequence identities with orthologs from different *Aspergillus* species (**Fig. S11**). The eighth terpene BGC (EruBGC33) is located on the scaffold00060 (KK088470.1) harboring 7 genes in a 19.7kb fragment and this cluster has homologs in *Pseudomonas* sp., *Rhizobium* sp., *Massilia* sp., and *Sandaracinus amylolyticus* (**Fig S4H**). The core protein of EruBGC33 is a phytoene synthase (EYE90127.1) possessing squalene/phytoene synthase (SQS_PSY, PF00494) towards the C-terminal end (**Fig 3H**). EYE90127.1 has homologs in different *Aspergillus* strains with sequence identities of 64-67% (**Fig. S12**). The ninth terpene cluster, EruBGC36 is mapped to scaffold00079 (KK088489.1) with 9 genes in a region 16.5 kb, but it has three homologous BGCs in different bacterial genomes as *Granulicella pectinivorans*, *Streptomyces ochraceiscleroticus* and *Delta proteobacterium* (**Fig S4I**). The core protein of this cluster is a squalene cyclase (EYE89949.1), harboring two squalene-hopene cyclase protein domains (**Fig 3G**) namely SQHop_cyclase_N (PF13249) and SQHop_cyclase_C (PF13243). This protein has sequence identities of 64-67% with homologs from different *Aspergillus* strains (**Fig. S13**). The 10th terpene-based EruBGC15 is β -lactone cluster on the scaffold00008 (KK088420.1) with 10 genes spanning a size of 24.5 kb. This BGC has homologous clusters in *Thauera* sp. K11 (NZ_CP023439_c5), several strains *Mycobacterium* and *Bacillus subtilis* (**Fig S4J**). This cluster produces two core proteins as acetyl-CoA synthetase-like protein (EYE95809.1) and aldolase (EYE95810.1) with harboring protein domains as AMP-binding (PF00501) and AMP-binding_C (PF13193), and Carboxyl_trans (PF01039), respectively (**Fig 4K**). Acetyl-CoA synthetase-like protein (EYE95809.1) depicts 68-79% identities with close homologs from two *Penicillium* species and *A. udagawae* (**Fig S14**), whereas aldolase (EYE95810.1) shows >68-73% sequence identities with selected ascomycetes (**Fig S15**).

2.6. There are four hybrid BGCs in marine *Eurotium* genome

The first hybrid BGC is EruBGC7, which is mapped to scaffold00003 (KK088413.1). This fragment has a size of 44.2 kb with 17 genes (**Table 5**) and it has counterparts in several strains of *Bacillus*, plus *Amycolatopsis keratiniphila*, *Actinoplanes awajinensis* and *Allokutzneria albata* (**Fig S16A**). EruBGC7 is producing a product of hybrid of NRPS and indole with help of three major proteins as aromatic prenyl-transferase (EYE98742.1), acetyl-CoA synthetase-like protein (EYE98744.1) and putative dimethylallyl tryptophan synthase (EYE98746.1, **Fig 1**). The second hybrid BGC is EruBGC17 as a hybrid of T1PKS and indole genes localized on scaffold00012 (KK088422.1) in a 93.3 kb region with 36 genes (**Fig S16A**). EruBGC17 has homologous BGCs in several strains of *Streptomyces* plus *Mycobacterium*, *Kitasatospora*, and *Frankia* (**Fig S16B**). There are three main core proteins of this cluster as ketoacyl-synt-domain-containing protein (EYE95320.1), polyketide synthase (EYE95336.1, **Fig 2**) and aromatic prenyltransferase (EYE95342.1). This cluster is capable of producing epipyriculol (C₁₄H₁₆O₄, **Fig 2F**) with phytotoxic properties. The third hybrid BGC (EruBGC28) is a 50.3kb region (with 19 genes) on the scaffold00036 (KK088447.1). EruBGC28 has orthologous clusters in several strains of *Mycobacterium* and *Methylobacter* (**Fig S16C**). This BGC is encoding a hybrid product based on T1PKS as 6-methylsalicylic acid synthase MsaS (EYE91246.1, **Fig 2**) and NRPS-like as ochratoxin A non-ribosomal peptide synthetase (EYE91247.1, **Fig 1**). The end product of this cluster is

asperlactone (C₉H₁₂O₄, **Fig 2G**) with nematocidal, insecticidal, antibacterial, and antifungal properties. The fourth hybrid cluster (EruBGC30) is mapped on the scaffold00043 (KK088453.1) a ~67kb region with 22 genes. This cluster has homologous BGCs in several bacterial genomes with the top three being *Streptomyces violens*, *Actinosynnema* sp., and *Mycobacterium* sp. (**Fig S16D**). This cluster is a hybrid of T1PKS (EYE90804.1, **Fig 2**) and NRPS (EYE90819.1 - acetyl-CoA synthetase-like protein, **Fig 1**).

2.7. Overview of siderophore BGCs from *E. rubrum*

We have detected two BGCs in *Eurotium* genome, which are capable of producing siderophores namely EruBGC9 and EruBGC12 (**Table 6**). EruBGC9 is the siderophore producing BGC on the scaffold00005 (Genbank ID KK088415.1) from 110,568 bp to 122,685 bp in 11.9 kb region. This cluster has no homologous clusters in public databases. However, the siderophore producing protein (GenBank Id - EYE97444.1) is largely somewhat hypothetical as homology detection using BLASTP resulted in 64% and 62% sequence identities with aerobactin siderophore biosynthesis, IucA/IucC from *Penicillium roqueforti* FM164 (GenBank ID - OOO13908.1) and taurine catabolism dioxygenase TauD/TfdA from *Aspergillus oryzae* (GenBank ID - OOO13908.1), respectively (**Fig. 4A**).

Fig 4. Overview of siderophore producing proteins and their domains encoded by biosynthetic gene clusters EruBGC6 and EruBGC12.

It also shows 65.24%, 65.23% and 64.22% sequence identities with IucC family-domain-containing proteins from *A. tamaritii* (KAE8167994.1), *A. pseudotamaritii* (KAE8143495.1) and *A. caelatus* (XP_031924195.1), respectively (**Fig. 4B**). The second siderophore BGC, EruBGC12 is mapped to scaffold00007 (KK088417.1) from 372,420-384,556 bp with total size of 12.1 kb. It has no similarities with any known BGCs in the known databases. The core protein of this cluster is EYE96808.1 which has similar protein domains as of EYE97444.1 (from EruBGC6). These two proteins have similar size with three domains required for siderophore biosynthesis (**Fig. 4**), namely siderophore synthetase component, RhbC (COG4264), IucA_IucC (Pfam ID - PFAM04183) and ferric iron reductase FhuF (Pfam ID - PFAM06276). This suggests that these two proteins have capabilities for producing siderophore.

Advancement in genomics technologies has helped us in setting up multi-omics mining affords to explore the SM producing capability of marine fungi and understanding their genomic location, regulatory mechanisms and conditions in these SM compounds can be activated [11]. We have utilized multi-omics methods for characterization of marine fungi with focus on deciphering their capabilities of producing SM like *Calcarisporium* sp. KF525 and *Pestalotiopsis* sp. KF079 and *Scopulariopsis* [5, 6]. These studies hinted that marine fungi are the excellent sources of bio-active compounds [5-8] with antibacterial and anti-cancerous properties like scopularide A and B [5]. All in all, this study unravelled 36 BGCs from marine *E. rubrum*. It clearly supports the same idea that marine fungi are rich source of the future drugs [12-16]. Omics approaches have widely open genetics and biotechnological applications focusing the marine species as exemplified by biotechnological applications as textile dyes of two laccase-encoding genes from marine *Pestalotiopsis* sp. KF079 [17]. In similar fashion, this study opens up the opportunities for future explorations of marine *E. rubrum* and BGCs for potential roles as future drugs.

3. Materials and Methods

3.1. Collection of genome and protein sequences from halophilic marine fungus *Erutium rubrum*

We downloaded the genomic and protein sequence data of the halophilic marine fungus *E. rubrum* from GenBank using assembly accession - GCA_000600275.1.

3.2. Identification of putative secondary metabolite producing proteins

Initially, we screened putative secondary metabolites encoding proteins using BLASTP [18] with an E-value < $1e^{-10}$ after setting up the local BLAST database.

3.3. Identification of biosynthetic gene clusters (BGCs)

We analysed *E. rubrum* genome for putative BGC clusters by antiSMASH5 [19], using the standard parameters with options of bacterial and fungal BGC scanning set ups.

3.4. Identification of biosynthetic gene clusters (BGCs)

We identified the functional domains of PKSs and NRPSs as previously described [20], using a combinations of tools namely antiSMASH5 [19], NCBI Conserved Domain Database [21], InterPro [22] and the PKS/NRPS Analysis Web-site [23]. We performed several rounds of specialized BLAST [18] for scanning homologs of genes and /or corresponding proteins at an E-value < $1e^{-10}$. We identified Pfam domains using HMMER [24].

3.5. Re-annotation of core proteins of BGCs

Annotation of proteins of interests using BLAST [18] and scanned annotated BLAST hits with minimum coverage of 70% of query and minimum sequence identity of 50%.

3.6. Protein sequence and phylogenetics analyses

We carried out protein sequence analysis of core proteins using COBALT [25]. We performed phylogenetic analyses of core proteins using annotated proteins using Distance tree method. We visualised the resulted phylogenetic trees using Blast Tree View.

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Appendix A

Appendix A carries all supplementary data.

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Table 1. Overview of NRPS-producing BGCs, their genes and proteins.

BGC ID	Scaffold ID	Scaffold	From	To	Size (bp)	Total genes	JGIDB ID*	Gene ID	Gene start	Gene end	Strand	Protein ID	Protein Description
EruBGC2	KK088412.1	scaffold00002	40,834	98,875	58,042	18	Eurhe1_38298	EURHEDRAFT_38298	42040	42983	+	EYE98773.	hypothetical protein EURHEDRAFT_38298
							7	7				1	7
							Eurhe1_44642	EURHEDRAFT_44642				EYE98774.	MFS multidrug transporter
							6	6				1	
							Eurhe1_40798	EURHEDRAFT_40798				EYE98775.	hypothetical protein EURHEDRAFT_40798
							3	3				1	3
							Eurhe1_44660	EURHEDRAFT_44660				EYE98776.	FRE family ferric- chelate reductase
							9	9				1	
							Eurhe1_40798	EURHEDRAFT_40798				EYE98777.	hypothetical protein EURHEDRAFT_40798
							5	5	50594	51044	+	1	5
							Eurhe1_52001	EURHEDRAFT_52001				EYE98778.	putative oxidoreductase
							3	3	51677	52858	-	1	
							Eurhe1_40798	EURHEDRAFT_40798				EYE98779.	hypothetical protein EURHEDRAFT_40798
							6	6	53292	54684	-	1	6
							Eurhe1_40798	EURHEDRAFT_40798				EYE98780.	MFS general substrate transporter
							7	7	55871	56804	+	1	

							Eurhe1_51211 2	EURHEDRAFT_51211 2	57331	59129	+	EYE98781. 1	sugar transporter
							Eurhe1_46989 8	EURHEDRAFT_4698 98	60833	75085	-	EYE98782. 1	nonribosomal siderophore peptide synthase SidC
							Eurhe1_37387 2	EURHEDRAFT_37387 2	76902	78875	+	EYE98783. 1	acetyl-CoA synthetase-like protein
							Eurhe1_52784 7	EURHEDRAFT_52784 7	79463	80838	-	EYE98784. 1	hypothetical protein EURHEDRAFT_52784 7
							Eurhe1_52784 8	EURHEDRAFT_52784 8	82178	83581	+	EYE98785. 1	putative apoptosis inducing factor
							Eurhe1_44722 3	EURHEDRAFT_44722 3	84385	86581	-	EYE98786. 1	hypothetical protein EURHEDRAFT_44722 3
							Eurhe1_51211 7	EURHEDRAFT_51211 7	87053	88317	-	EYE98787. 1	TfdA family taurine dioxygenase
							Eurhe1_38299 9	EURHEDRAFT_38299 9	88995	90874	+	EYE98788. 1	MFS transporter
							Eurhe1_37387 8	EURHEDRAFT_37387 8	93058	95210	-	EYE98789. 1	hypothetical protein EURHEDRAFT_37387 8
							Eurhe1_37387 9	EURHEDRAFT_37387 9	96126	97332	+	EYE98790. 1	voltage-gated K+ channel beta subunit

EruBGC1	KK088418.	scaffold0000	5,62,61	6,05,72			Eurhe1_41105	EURHEDRAFT_41105				EYE96550.	hypothetical protein EURHEDRAFT_41105
4	1	8	9	9	43,111	13	7	7	568147	569436	+	1	7
							Eurhe1_35549	EURHEDRAFT_35549				EYE96551.	hypothetical protein EURHEDRAFT_35549
							2	2	572151	572439	-	1	2
							Eurhe1_35549	EURHEDRAFT_35549				EYE96552.	hypothetical protein EURHEDRAFT_35549
							5	5	572584	581454	-	1	5
							Eurhe1_44077	EURHEDRAFT_4407				EYE96553.	acetyl-CoA synthetase-like protein, partial
							3	73	582618	585729	-	1	
							Eurhe1_45298	EURHEDRAFT_45298				EYE96554.	putative oxidoreductase
							4	4	586701	587823	-	1	
							Eurhe1_45293	EURHEDRAFT_45293				EYE96555.	MFS general substrate transporter
							7	7	589552	591166	+	1	
							Eurhe1_45298	EURHEDRAFT_45298				EYE96556.	hypothetical protein EURHEDRAFT_45298
							3	3	591955	593518	-	1	3
							Eurhe1_52996	EURHEDRAFT_52996				EYE96557.	Clavaminatase synthase- like protein
							1	1	593762	594735	-	1	
							Eurhe1_40162	EURHEDRAFT_40162				EYE96558.	Zn-dependent exopeptidase
							1	1	595193	597383	+	1	

							Eurhe1_41106 3	EURHEDRAFT_41106 3	597638	598435	-	EYE96559. 1	hypothetical protein EURHEDRAFT_41106 3
							Eurhe1_35557 7	EURHEDRAFT_35557 7	599314	601173	+	EYE96560. 1	translation initiation factor 4B
							Eurhe1_35561 8	EURHEDRAFT_35561 8	602403	602886	-	EYE96561. 1	hypothetical protein EURHEDRAFT_35561 8
							Eurhe1_37649 1	EURHEDRAFT_37649 1	604233	605100	+	EYE96562. 1	hypothetical protein EURHEDRAFT_37649 1
EruBGC2 5	KK088444. 1	scaffold0003 4	2,03,39 7	2,49,60 2	46,206	14	Eurhe1_41641 2	EURHEDRAFT_41641 2	203474	203999	-	EYE91530. 1	hypothetical protein EURHEDRAFT_41641 2
							Eurhe1_24234 9	EURHEDRAFT_24234 9	204801	206200	+	EYE91531. 1	hypothetical protein EURHEDRAFT_24234 9
							Eurhe1_40601 8	EURHEDRAFT_40601 8	206823	207982	+	EYE91532. 1	Aldo/keto reductase
							Eurhe1_24236 0	EURHEDRAFT_24236 0	209840	210420	+	EYE91533. 1	hypothetical protein EURHEDRAFT_24236 0
							Eurhe1_48698 9	EURHEDRAFT_48698 9	213243	214185	-	EYE91534. 1	oxidoreductase

							Eurhe1_53364 7	EURHEDRAFT_53364 7	214621	215888	+	EYE91535. 1	DUF1749-domain- containing protein
							Eurhe1_46468 1	EURHEDRAFT_46468 1	216580	218451	+	EYE91536. 1	MFS general substrate transporter
							Eurhe1_48699 7	EURHEDRAFT_48699 7	219271	223305	+	EYE91537. 1	ABC multidrug transporter SidT
							Eurhe1_52625 1	EURHEDRAFT_5262 51	223396	229602	-	EYE91538. 1	NRPS6, nonribosomal peptide synthase
							Eurhe1_46482 7	EURHEDRAFT_46482 7	230228	231103	-	EYE91539. 1	enoyl-CoA hydratase/isomerase family protein
							Eurhe1_50858 2	EURHEDRAFT_50858 2	231398	232807	+	EYE91540. 1	putative siderophore biosynthesis acetylase AceI
							Eurhe1_46474 9	EURHEDRAFT_46474 9	233983	235121	+	EYE91541. 1	DUF1749-domain- containing protein
							Eurhe1_51839 2	EURHEDRAFT_51839 2	243461	246966	+	EYE91542. 1	hypothetical protein EURHEDRAFT_51839 2
							Eurhe1_24249 0	EURHEDRAFT_24249 0	247891	248425	-	EYE91543. 1	hypothetical protein EURHEDRAFT_24249 0

EruBGC3	KK088468.	scaffold0005					Eurhe1_55089	EURHEDRAFT_5508				EYE90154.	hypothetical protein EURHEDRAFT_5508
2	1	8	1	33,516	33,516	14	8	98	357	756	-	1	98
							Eurhe1_46781	EURHEDRAFT_4678				EYE90155.	acetyl-CoA synthetase-like protein, partial
							8	18	851	2303	-	1	
							Eurhe1_42885	EURHEDRAFT_4288				EYE90156.	acetyl-CoA synthetase-like protein, partial
							1	51	2424	2748	-	1	
							Eurhe1_38221	EURHEDRAFT_3822				EYE90157.	hypothetical protein EURHEDRAFT_3822
							5	15	2895	3421	-	1	15
							Eurhe1_38221	EURHEDRAFT_3822				EYE90158.	amino acid adenylation
							7	17	7470	13516	+	1	
							Eurhe1_38221	EURHEDRAFT_38221				EYE90159.	hypothetical protein EURHEDRAFT_38221
							8	8	13546	13948	+	1	8
							Eurhe1_53451	EURHEDRAFT_53451				EYE90160.	aryl-alcohol dehydrogenase
							8	8	14441	15595	+	1	
							Eurhe1_31716	EURHEDRAFT_31716				EYE90161.	Zn(II)2Cys6 transcription factor
							1	1	16569	18785	-	1	
							Eurhe1_41771	EURHEDRAFT_41771				EYE90162.	MFS general substrate transporter
							5	5	21152	23117	+	1	

							Eurhe1_46782 4	EURHEDRAFT_46782 4	23309	25312	-	EYE90163. 1	hypothetical protein EURHEDRAFT_46782 4
							Eurhe1_40712 8	EURHEDRAFT_40712 8	26070	27975	-	EYE90164. 1	acetamidase
							Eurhe1_41771 7	EURHEDRAFT_41771 7	28663	29027	-	EYE90165. 1	hypothetical protein EURHEDRAFT_41771 7
							Eurhe1_40712 9	EURHEDRAFT_40712 9	30464	32055	+	EYE90166. 1	hypothetical protein EURHEDRAFT_40712 9
							Eurhe1_38222 6	EURHEDRAFT_38222 6	32401	32995	-	EYE90167. 1	hypothetical protein EURHEDRAFT_38222 6

*Core gene is marked by Bold letters

Table 2. Summary of NRPS-like BGCs, their genes and proteins.

BGC ID	Scaffold ID	Scaffold	From	To	Size (bp)	Total	JGIDB ID*	Gene ID	Gene start	Gene end	Strand	Protein ID	Protein Description
EruBG C4	KK0884 13.1	scaffold0 0003	1,32,4 24	1,73,7 00	41,2 77	19	Eurhe1_40 8670	EURHEDRAFT_ 408670	1324 23	1340 73	-	EYE983 37.1	translation initiation factor eIF-2B subunit family protein
							Eurhe1_40 8672	EURHEDRAFT_ 408672	1342 28	1349 57	+	EYE983 38.1	hypothetical protein EURHEDRAFT_408672

							Eurhe1_54 4757	EURHEDRAFT_ 544757	1369 58	1384 94	+	EYE983 39.1	hypothetical protein EURHEDRAFT_544757
							Eurhe1_20 6656	EURHEDRAFT_ 206656	1394 79	1397 04	+	EYE983 40.1	hypothetical protein EURHEDRAFT_206656
							Eurhe1_20 6718	EURHEDRAFT_ 206718	1408 73	1413 29	-	EYE983 41.1	hypothetical protein EURHEDRAFT_206718
							Eurhe1_40 8674	EURHEDRAFT_ 408674	1421 86	1429 13	+	EYE983 42.1	HHE domain protein
							Eurhe1_38 3507	EURHEDRAFT_ 383507	1430 18	1434 54	-	EYE983 43.1	hypothetical protein EURHEDRAFT_383507
							Eurhe1_40 8676	EURHEDRAFT_ 408676	1441 30	1445 69	+	EYE983 44.1	hypothetical protein EURHEDRAFT_408676
							Eurhe1_42 3897	EURHEDRAFT_ 423897	1468 86	1478 67	+	EYE983 45.1	hypothetical protein EURHEDRAFT_423897, partial
							Eurhe1_52 8303	EURHEDRAFT_ 528303	1505 19	1538 66	-	EYE983 46.1	acetyl-CoA synthetase-like protein
							Eurhe1_40 8679	EURHEDRAFT_ 408679	1554 35	1561 29	-	EYE983 47.1	putative nuclear distribution protein RO10
							Eurhe1_52 0495	EURHEDRAFT_ 520495	1564 17	1590 12	-	EYE983 48.1	ubiquitin interaction motif protein
							Eurhe1_40 8681	EURHEDRAFT_ 408681	1601 49	1607 94	+	EYE983 49.1	SET domain-containing protein
							Eurhe1_51 2612	EURHEDRAFT_ 512612	1612 58	1634 60	+	EYE983 50.1	putative AMP-binding enzyme

							Eurhe1_44 8564	EURHEDRAFT_ 448564	1637 50	1650 70	-	EYE983 51.1	Pkinase-domain-containing protein
							Eurhe1_44 7751	EURHEDRAFT_ 447751	1668 30	1675 60	-	EYE983 52.1	hypothetical protein EURHEDRAFT_447751
							Eurhe1_47 1229	EURHEDRAFT_ 471229	1679 69	1697 35	+	EYE983 53.1	putative spermine/spermidine synthase
							Eurhe1_20 6907	EURHEDRAFT_ 206907	1704 00	1722 65	-	EYE983 54.1	hypothetical protein EURHEDRAFT_206907
							Eurhe1_44 8549	EURHEDRAFT_ 448549	1727 81	1737 00	+	EYE983 55.1	hypothetical protein EURHEDRAFT_448549
EruBG C10	KK0884 15.1	scaffold0 0005	7,14,7 45	7,56,6 22	41,8 78	17	Eurhe1_40 9906	EURHEDRAFT_ 409906	7152 01	7170 53	-	EYE976 74.1	putative low affinity glucose transporter MstE
							Eurhe1_40 9911	EURHEDRAFT_ 409911	7212 57	7223 63	-	EYE976 75.1	ketoreductase
							Eurhe1_51 3528	EURHEDRAFT_ 513528	7225 71	7230 51	+	EYE976 76.1	ergosterol biosynthesis protein Erg28
							Eurhe1_40 9912	EURHEDRAFT_ 409912	7231 13	7244 26	-	EYE976 77.1	galactose-1-phosphate uridylyltransferase
							Eurhe1_51 3530	EURHEDRAFT_ 513530	7251 15	7256 17	+	EYE976 78.1	hypothetical protein EURHEDRAFT_513530
							Eurhe1_40 9914	EURHEDRAFT_ 409914	7259 28	7268 72	+	EYE976 79.1	hypothetical protein EURHEDRAFT_409914
							Eurhe1_51 3532	EURHEDRAFT_ 513532	7272 91	7289 71	+	EYE976 80.1	C6 zinc finger domain protein

							Eurhe1_30 2617	EURHEDRAFT_ 302617	7295 95	7310 03	+	EYE976 81.1	S-adenosyl-L-methionine-dependent methyltransferase
							Eurhe1_51 3534	EURHEDRAFT_ 513534	7318 10	7329 33	-	EYE976 82.1	NAD(P)-binding protein
							Eurhe1_40 9919	EURHEDRAFT_ 409919	7347 44	7366 22	+	EYE976 83.1	hypothetical protein EURHEDRAFT_409919
							Eurhe1_40 9920	EURHEDRAFT_ 409920	7372 87	7384 27	+	EYE976 84.1	putative mitochondrial phosphate transporter Pic2
							Eurhe1_38 4497	EURHEDRAFT_ 384497	7395 67	7404 52	+	EYE976 85.1	hypothetical protein EURHEDRAFT_384497
							Eurhe1_47 3822	EURHEDRAFT_ 473822	7409 77	7426 08	-	EYE976 86.1	YagE family protein
							Eurhe1_40 0686	EURHEDRAFT_ 400686	7432 54	7442 98	-	EYE976 87.1	hypothetical protein EURHEDRAFT_400686
							Eurhe1_40 9924	EURHEDRAFT_ 409924	7446 93	7454 60	-	EYE976 88.1	hypothetical protein EURHEDRAFT_409924
							Eurhe1_40 9925	EURHEDRAFT_ 409925	7457 18	7467 09	+	EYE976 89.1	pyrroline-5-carboxylate reductase
							Eurhe1_51 3539	EURHEDRAFT_ 513539	7469 66	7498 27	-	EYE976 90.1	hypothetical protein EURHEDRAFT_513539
EruBG C18	KK0884 23.1	scaffold0 0013	1,25,8 19	1,69,0 69	43,2 51	11	Eurhe1_45 6176	EURHEDRAFT_ 456176	1277 77	1340 48	+	EYE950 66.1	PP2C-domain-containing protein
							Eurhe1_51 5394	EURHEDRAFT_ 515394	1349 07	1412 69	+	EYE950 67.1	hypothetical protein EURHEDRAFT_515394

							Eurhe1_62 120	EURHEDRAFT_ 62120	1415 76	1418 88	+	EYE950 68.1	hypothetical protein EURHEDRAFT_62120
							Eurhe1_41 2373	EURHEDRAFT_ 412373	1427 28	1451 93	+	EYE950 69.1	hypothetical protein EURHEDRAFT_412373
							Eurhe1_47 8800	EURHEDRAFT_ 478800	1458 18	1490 69	+	EYE950 70.1	putative NRPS-like enzyme
							Eurhe1_47 8803	EURHEDRAFT_ 478803	1496 67	1531 91	-	EYE950 71.1	putative DNA damage repair protein Mus42
							Eurhe1_45 6341	EURHEDRAFT_ 456341	1541 05	1565 75	+	EYE950 72.1	hypothetical protein EURHEDRAFT_456341
							Eurhe1_45 6065	EURHEDRAFT_ 456065	1574 17	1591 76	-	EYE950 73.1	WD repeat protein
							Eurhe1_51 5400	EURHEDRAFT_ 515400	1593 88	1608 01	+	EYE950 74.1	sphingomyelinase family protein
							Eurhe1_62 468	THI4	1609 61	1620 15	-	EYE950 75.1	Thi4 family thiamine biosynthetic enzyme
							Eurhe1_40 2732	EURHEDRAFT_ 402732	1626 44	1662 43	-	EYE950 76.1	MFS general substrate transporter
EruBG C20	KK0884 37.1	scaffold0 0027	1	34,99 7	34,9 97	12	Eurhe1_41 5433	EURHEDRAFT_ 415433	162	2061	-	EYE923 08.1	hypothetical protein EURHEDRAFT_415433
							Eurhe1_38 0117	EURHEDRAFT_ 380117	6811	7688	-	EYE923 09.1	hypothetical protein EURHEDRAFT_380117, partial
							Eurhe1_40 5150	EURHEDRAFT_ 405150	9588	1025 8	+	EYE923 10.1	hypothetical protein EURHEDRAFT_405150

							Eurhe1_46 2551	EURHEDRAFT_ 462551	1175 0	1499 7	-	EYE923 11.1	NRPS-like enzyme
							Eurhe1_41 5436	EURHEDRAFT_ 415436	1670 7	1843 8	-	EYE923 12.1	hypothetical protein EURHEDRAFT_415436
							Eurhe1_51 7599	EURHEDRAFT_ 517599	1880 8	1963 1	+	EYE923 13.1	hypothetical protein EURHEDRAFT_517599
							Eurhe1_38 0122	EURHEDRAFT_ 380122	1993 7	2079 9	-	EYE923 14.1	L30e-like protein
							Eurhe1_52 5488	EURHEDRAFT_ 525488	2391 5	2459 0	-	EYE923 15.1	hypothetical protein EURHEDRAFT_525488
							Eurhe1_41 5440	EURHEDRAFT_ 415440	2584 0	2832 1	+	EYE923 16.1	putative oligopeptide transporter, OPT family
							Eurhe1_51 7603	EURHEDRAFT_ 517603	2841 9	2963 7	-	EYE923 17.1	hypothetical protein EURHEDRAFT_517603
							Eurhe1_46 2746	EURHEDRAFT_ 462746	3002 4	3156 5	-	EYE923 18.1	MFS general substrate transporter
							Eurhe1_41 5441	EURHEDRAFT_ 415441	3247 9	3439 3	-	EYE923 19.1	hypothetical protein EURHEDRAFT_415441
EruBG C22	KK0884 38.1	scaffold0 0028	1,36,7 52	1,81,2 01	44,4 50	18	Eurhe1_40 5321	EURHEDRAFT_ 405321	1384 88	1388 76	-	EYE922 04.1	hypothetical protein EURHEDRAFT_405321
							Eurhe1_51 7772	EURHEDRAFT_ 517772	1395 51	1404 85	-	EYE922 05.1	putative 3-ketoacyl-acyl carrier protein reductase
							Eurhe1_38 0296	EURHEDRAFT_ 380296	1411 88	1425 78	-	EYE922 06.1	gibberellin 3-beta hydroxylase

							Eurhe1_46 3259	EURHEDRAFT_ 463259	1432 84	1437 50	+	EYE922 07.1	YjgF-like protein
							Eurhe1_41 5626	EURHEDRAFT_ 415626	1441 69	1449 79	-	EYE922 08.1	Phosphoenolpyruvate/pyruvate domain- containing protein
							Eurhe1_19 7996	EURHEDRAFT_ 197996	1455 56	1470 95	+	EYE922 09.1	putative pantothenate transporter
							Eurhe1_50 6915	EURHEDRAFT_ 506915	1471 87	1492 75	-	EYE922 10.1	hypothetical protein EURHEDRAFT_506915
							Eurhe1_41 5628	EURHEDRAFT_ 415628	1513 13	1517 51	+	EYE922 11.1	hypothetical protein EURHEDRAFT_415628
							Eurhe1_51 7778	EURHEDRAFT_ 517778	1530 46	1541 86	-	EYE922 12.1	aryl-alcohol dehydrogenase
							Eurhe1_41 5629	EURHEDRAFT_ 415629	1551 65	1559 66	-	EYE922 13.1	carbonic anhydrase family protein
							Eurhe1_41 5632	EURHEDRAFT_ 415632	1567 51	1612 01	-	EYE922 14.1	L-aminoadipate-semialdehyde dehydrogenase large subunit
							Eurhe1_41 5634	EURHEDRAFT_ 415634	1616 55	1634 77	+	EYE922 15.1	hypothetical protein EURHEDRAFT_415634
							Eurhe1_46 3041	EURHEDRAFT_ 463041	1639 23	1681 47	+	EYE922 16.1	xanthine dehydrogenase
							Eurhe1_46 2984	EURHEDRAFT_ 462984	1684 12	1706 11	-	EYE922 17.1	plasma membrane fusion protein prm1
							Eurhe1_46 3209	EURHEDRAFT_ 463209	1723 64	1738 04	-	EYE922 18.1	putative amino acid transporter

							Eurhe1_51 7785	EURHEDRAFT_ 517785	1757 06	1775 32	-	EYE922 19.1	putative succinate-semialdehyde dehydrogenase
							Eurhe1_40 5336	EURHEDRAFT_ 405336	1779 98	1786 01	+	EYE922 20.1	YjgF-like protein
							Eurhe1_19 8382	EURHEDRAFT_ 198382	1801 03	1810 24	-	EYE922 21.1	class II aldolase and Adducin N-terminal domain protein
EruBG C29	KK0884 50.1	scaffold0 0040	1	35,84 8	35,8 48	9	Eurhe1_38 1440	EURHEDRAFT_ 381440	2363	4438	+	EYE909 51.1	hypothetical protein EURHEDRAFT_381440
							Eurhe1_41 6866	EURHEDRAFT_ 416866	4710	5523	-	EYE909 52.1	hypothetical protein EURHEDRAFT_416866
							Eurhe1_51 8721	EURHEDRAFT_ 518721	6288	8328	-	EYE909 53.1	hypothetical protein EURHEDRAFT_518721
							Eurhe1_38 9890	EURHEDRAFT_ 389890	1023 9	1164 3	-	EYE909 54.1	lipase
							Eurhe1_41 6869	EURHEDRAFT_ 416869	1200 5	1584 8	-	EYE909 55.1	putative NRPS-like enzyme
							Eurhe1_51 8724	EURHEDRAFT_ 518724	1980 5	2176 5	-	EYE909 56.1	hypothetical protein EURHEDRAFT_518724
							Eurhe1_52 6591	EURHEDRAFT_ 526591	2533 7	2629 6	-	EYE909 57.1	hypothetical protein EURHEDRAFT_526591
							Eurhe1_50 9489	EURHEDRAFT_ 509489	2998 5	3214 6	-	EYE909 58.1	amidase
							Eurhe1_53 3958	EURHEDRAFT_ 533958	3313 9	3528 4	-	EYE909 59.1	copper amine oxidase

EruBG C31	KK0884 64.1	scaffold0 0054	29,65 8	71,38 5	41,7 28	12	Eurhe1_41 7612	EURHEDRAFT_ 417612	3383 8	3421 6	-	EYE902 57.1	hypothetical protein EURHEDRAFT_417612
							Eurhe1_51 9285	EURHEDRAFT_ 519285	3500 3	3575 1	-	EYE902 58.1	hypothetical protein EURHEDRAFT_519285
							Eurhe1_51 9286	EURHEDRAFT_ 519286	3673 0	3857 9	+	EYE902 59.1	hypothetical protein EURHEDRAFT_519286
							Eurhe1_38 2136	EURHEDRAFT_ 382136	4043 4	4087 2	+	EYE902 60.1	hypothetical protein EURHEDRAFT_382136
							Eurhe1_46 7629	EURHEDRAFT_ 467629	4127 9	4292 0	-	EYE902 61.1	general substrate transporter
							Eurhe1_40 7055	EURHEDRAFT_ 407055	4729 1	4783 3	-	EYE902 62.1	ribonuclease U2
							Eurhe1_46 7614	EURHEDRAFT_ 467614	4839 2	4931 3	+	EYE902 63.1	hypothetical protein EURHEDRAFT_467614
							Eurhe1_38 2140	EURHEDRAFT_ 382140	4965 7	5138 5	-	EYE902 64.1	acetyl-CoA synthetase-like protein
							Eurhe1_46 7609	EURHEDRAFT_ 467609	5362 7	5594 0	-	EYE902 65.1	amino acid transporter
							Eurhe1_53 4467	EURHEDRAFT_ 534467	5876 0	6419 8	-	EYE902 66.1	hypothetical protein EURHEDRAFT_534467
							Eurhe1_39 0509	EURHEDRAFT_ 390509	6536 8	6746 3	+	EYE902 67.1	hypothetical protein EURHEDRAFT_390509
							Eurhe1_41 7624	EURHEDRAFT_ 417624	6977 4	7083 6	-	EYE902 68.1	NAD(P)-binding protein

EruBG C34	KK0884 74.1	scaffold0 0064	607	30,88 4	30,2 78	7	Eurhe1_51 9395	EURHEDRAFT_ 519395	4441	8228	-	EYE900 78.1	hypothetical protein EURHEDRAFT_519395
							Eurhe1_55 2159	EURHEDRAFT_ 552159	8804	9053	-	EYE900 79.1	hypothetical protein EURHEDRAFT_552159, partial
							Eurhe1_46 8048	EURHEDRAFT_ 468048	9055	9313	-	EYE900 80.1	hypothetical protein EURHEDRAFT_468048, partial
							Eurhe1_33 3675	EURHEDRAFT_ 333675	1108 5	1183 6	-	EYE900 81.1	hypothetical protein EURHEDRAFT_333675
							Eurhe1_33 3683	EURHEDRAFT_ 333683	1362 6	1387 5	+	EYE900 82.1	hypothetical protein EURHEDRAFT_333683
							Eurhe1_55 2178	EURHEDRAFT_ 552178	2060 6	2603 8	+	EYE900 83.1	acetyl-CoA synthetase-like protein
							Eurhe1_38 2301	EURHEDRAFT_ 382301	2798 9	2913 7	-	EYE900 84.1	hypothetical protein EURHEDRAFT_382301

*Core gene is marked by Bold letters

Table 3. Overview of T1pks-producing BGCs, their genes and proteins.

BGC ID	Scaffold ID	Scaffold	From	To	Size (bp)	Total genes	Most similar BGC	known BGC	Similarity	JGIDB ID*	Gene ID	Gene start	Gene end	Strand	Protein ID	Protein Description
EruBGC3	KK088412.1	scaffold0002	13,99,017	14,46,851	47,835	18	cornexistin	P	9%	Eurhe1_374348	EURHEDRAFT_374348	1401450	1402178	+	EYE99285.1	hypothetical protein EURHEDRAFT_374348

										Eurhe1_4470 18	EURHEDRAFT_4470 18	140254 7	1403809	+	EYE99286 .1	hypothetical protein EURHEDRAFT_44701 8
										Eurhe1_5411 69	EURHEDRAFT_5411 69	140417 1	1405353	-	EYE99287 .1	hypothetical protein EURHEDRAFT_54116 9
										Eurhe1_4085 66	EURHEDRAFT_4085 66	140621 5	1408370	-	EYE99288 .1	hypothetical protein EURHEDRAFT_40856 6
										Eurhe1_5125 39	EURHEDRAFT_5125 39	140968 4	1411243	+	EYE99289 .1	MFS general substrate transporter
										Eurhe1_3743 53	EURHEDRAFT_3743 53	141206 9	1412490	+	EYE99290 .1	putative ATPase inhibitor mitochondrial precursor
										Eurhe1_3995 65	EURHEDRAFT_3995 65	141295 6	1413271	-	EYE99291 .1	hypothetical protein EURHEDRAFT_39956 5
										Eurhe1_5282 40	EURHEDRAFT_5282 40	141444 7	1418747	+	EYE99292 .1	hypothetical protein EURHEDRAFT_52824 0
										Eurhe1_5411 71	EURHEDRAFT_541 171	141901 6	1426851	-	EYE99293 .1	putative polyketide synthase
										Eurhe1_1350 86	EURHEDRAFT_1350 86	142722 6	1427820	-	EYE99294 .1	putative DUF341 family oxidoreductase

										Eurhe1_4085 75	EURHEDRAFT_4085 75	142852 6	1429162	+	EYE99295 .1	benzodiazepine receptor family protein
										Eurhe1_4085 79	EURHEDRAFT_4085 79	142997 6	1432559	+	EYE99296 .1	DUF1212-domain- containing protein
										Eurhe1_4198 96	EURHEDRAFT_4198 96	143293 0	1433245	-	EYE99297 .1	hypothetical protein EURHEDRAFT_41989 6, partial
										Eurhe1_5282 45	EURHEDRAFT_5282 45	143486 1	1435988	-	EYE99298 .1	mitochondrial DNA replication protein
										Eurhe1_3743 62	EURHEDRAFT_3743 62	143626 1	1437343	+	EYE99299 .1	hypothetical protein EURHEDRAFT_37436 2
										Eurhe1_4926 25	EURHEDRAFT_4926 25	143766 9	1439684	+	EYE99300 .1	hypothetical protein EURHEDRAFT_49262 5
										Eurhe1_3995 72	EURHEDRAFT_3995 72	143983 0	1441495	-	EYE99301 .1	general substrate transporter
										Eurhe1_4085 82	EURHEDRAFT_4085 82	144178 9	1443025	+	EYE99302 .1	DUF453-domain- containing protein
EruBGC5	KK088413 .1	scaffold000 03	5,28,555	5,75,235	46,68 1	14	naphthopyro ne	P	100 %	Eurhe1_4483 13	EURHEDRAFT_4483 13	528817	530036	-	EYE98502 .1	structure-specific endonuclease subunit slx1
										Eurhe1_3745 83	EURHEDRAFT_3745 83	531903	537421	+	EYE98503 .1	PHD transcription factor

										Eurhe1_3997 90	EURHEDRAFT_3997 90	538067	539270	-	EYE98504 .1	putative 1-aminocyclopropane-1-carboxylate deaminase
										Eurhe1_3745 85	EURHEDRAFT_3745 85	539516	540914	+	EYE98505 .1	DHH phosphoesterase
										Eurhe1_4480 02	EURHEDRAFT_4480 02	541397	545618	-	EYE98506 .1	putative SH3 domain protein
										Eurhe1_2137 58	EURHEDRAFT_213 758	548554	555235	+	EYE98507 .1	polyketide synthetase PksP
										Eurhe1_4088 47	EURHEDRAFT_4088 47	555539	556972	-	EYE98508 .1	amidase
										Eurhe1_3745 89	EURHEDRAFT_3745 89	557304	559703	-	EYE98509 .1	HDA1 complex subunit
										Eurhe1_3745 90	EURHEDRAFT_3745 90	559949	561150	-	EYE98510 .1	hypothetical protein EURHEDRAFT_374590
										Eurhe1_4088 49	EURHEDRAFT_4088 49	561509	563043	-	EYE98511 .1	putative flavin dependent monooxygenase
										Eurhe1_3745 92	EURHEDRAFT_3745 92	563606	567894	+	EYE98512 .1	hypothetical protein EURHEDRAFT_374592
										Eurhe1_4088 50	EURHEDRAFT_4088 50	568136	569458	-	EYE98513 .1	hypothetical protein EURHEDRAFT_408850

										Eurhe1_4088 51	EURHEDRAFT_4088 51	570146	573004	+	EYE98514 .1	glutamine-dependent NAD(+) synthetase
										Eurhe1_2140 03	EURHEDRAFT_2140 03	573294	574647	-	EYE98515 .1	hypothetical protein EURHEDRAFT_21400 3
EruBGC8	KK088414 .1	scaffold000 04	11,04,40 3	11,49,85 9	45,45 7	20	TAN-1612-\$	P	60%	Eurhe1_4491 86	EURHEDRAFT_4491 86	110463 0	1106660	-	EYE98249 .1	hypothetical protein EURHEDRAFT_44918 6
										Eurhe1_2749 54	EURHEDRAFT_2749 54	110729 8	1109351	-	EYE98250 .1	electron transfer flavo protein-ubiquinone oxidoreductase mitochondrial precursor
										Eurhe1_4095 87	EURHEDRAFT_4095 87	111186 4	1112146	+	EYE98251 .1	hypothetical protein EURHEDRAFT_40958 7
										Eurhe1_4095 88	EURHEDRAFT_4095 88	111240 7	1112874	+	EYE98252 .1	TBP-domain- containing protein
										Eurhe1_4095 89	EURHEDRAFT_4095 89	111454 0	1115981	-	EYE98253 .1	fructosyl amino acid oxidasesarcosine oxidase
										Eurhe1_4095 90	EURHEDRAFT_4095 90	111622 2	1117313	+	EYE98254 .1	ubiquinone/menaquin one biosynthesis- related protein

										Eurhe1_3752 07	EURHEDRAFT_3752 07	111778 4		1119151	+	EYE98255 .1	hypothetical protein EURHEDRAFT_37520 7
										Eurhe1_4095 92	EURHEDRAFT_4095 92	111971 2		1121842	+	EYE98256 .1	hypothetical protein EURHEDRAFT_40959 2
										Eurhe1_5132 79	EURHEDRAFT_5132 79	112212 1		1123122	+	EYE98257 .1	NADH-cytochrome b5 reductase-like protein
										Eurhe1_4095 94	EURHEDRAFT_4095 94	112322 9		1123898	-	EYE98258 .1	S-adenosyl-L- methionine dependent methyltransferase
										Eurhe1_5211 62	EURHEDRAFT_521 162	112440 2		1129859	-	EYE98259 .1	putative polyketide synthase
										Eurhe1_4730 94	EURHEDRAFT_4730 94	113034 6		1131332	-	EYE98260 .1	putative metallo-beta- lactamase domain protein
										Eurhe1_2752 73	EURHEDRAFT_2752 73	113184 1		1132060	-	EYE98261 .1	hypothetical protein EURHEDRAFT_27527 3
										Eurhe1_4730 96	EURHEDRAFT_4730 96	113258 8		1134362	-	EYE98262 .1	pisatin demethylase
										Eurhe1_5132 84	EURHEDRAFT_5132 84	113473 5		1136478	+	EYE98263 .1	putative cytochrome P450
										Eurhe1_4095 98	EURHEDRAFT_4095 98	113704 8		1138271	+	EYE98264 .1	NAD(P)-binding protein

										Eurhe1_4095 99	EURHEDRAFT_4095 99	113856 3		1139916	+	EYE98265 .1	hypothetical protein EURHEDRAFT_40959 9
										Eurhe1_4731 03	EURHEDRAFT_4731 03	114270 3		1144236	+	EYE98266 .1	hypothetical protein EURHEDRAFT_47310 3
										Eurhe1_4096 01	EURHEDRAFT_4096 01	114439 5		1144635	+	EYE98267 .1	hypothetical protein EURHEDRAFT_40960 1
										Eurhe1_5132 86	EURHEDRAFT_5132 86	114511 5		1147893	+	EYE98268 .1	hypothetical protein EURHEDRAFT_51328 6
EruBGC1 1	KK088415 .1	scaffold000 05	9,29,173	9,75,269	46,09 7	18				Eurhe1_4099 93	EURHEDRAFT_4099 93	930171 930369		930369	+	EYE97757 .1	hypothetical protein EURHEDRAFT_40999 3
										Eurhe1_4099 94	EURHEDRAFT_4099 94	930833 932105		932105	+	EYE97758 .1	hypothetical protein EURHEDRAFT_40999 4
										Eurhe1_4007 50	EURHEDRAFT_4007 50	932848 933262		933262	-	EYE97759 .1	hypothetical protein EURHEDRAFT_40075 0
										Eurhe1_4007 51	EURHEDRAFT_4007 51	933895 938024		938024	-	EYE97760 .1	WD40 repeat-like protein

										Eurhe1_4505 48	EURHEDRAFT_4505 48	938452	938967	+	EYE97761 .1	putative peptidyl prolyl cis-trans isomerase cyclophilin
										Eurhe1_4501 62	EURHEDRAFT_4501 62	939203	939800	-	EYE97762 .1	hypothetical protein EURHEDRAFT_45016 2
										Eurhe1_4739 95	EURHEDRAFT_4739 95	940074	940739	+	EYE97763 .1	cytochrome c oxidase polypeptide vib
										Eurhe1_4099 99	EURHEDRAFT_4099 99	941301	942421	-	EYE97764 .1	dicarboxylate transporter
										Eurhe1_4100 00	EURHEDRAFT_4100 00	943086	944640	+	EYE97765 .1	phenylalanyl-tRNA synthetase alpha subunit
										Eurhe1_5135 99	EURHEDRAFT_5135 99	944893	946023	+	EYE97766 .1	tartrate dehydrogenase
										Eurhe1_5136 00	EURHEDRAFT_5136 00	946398	947486	+	EYE97767 .1	NAD(P)-binding protein
										Eurhe1_5501 55	EURHEDRAFT_550 155	949172	955269	+	EYE97768 .1	polyketide synthase
										Eurhe1_3755 87	EURHEDRAFT_3755 87	956564	957299	-	EYE97769 .1	hypothetical protein EURHEDRAFT_37558 7
										Eurhe1_5136 02	EURHEDRAFT_5136 02	962277	963428	-	EYE97770 .1	RNA polymerase II subunit 3

										Eurhe1_4500 46	EURHEDRAFT_4500 46	964461	965094	-	EYE97771 .1	hypothetical protein EURHEDRAFT_45004 6
										Eurhe1_4100 07	EURHEDRAFT_4100 07	970170	972051	+	EYE97772 .1	arginine-tRNA-protein transferase
										Eurhe1_4100 08	EURHEDRAFT_4100 08	972308	973128	-	EYE97773 .1	Calciopressin, partial
										Eurhe1_4100 10	EURHEDRAFT_4100 10	974274	975237	-	EYE97774 .1	hypothetical protein EURHEDRAFT_41001 0
EruBGC1 3	KK088417 .1	scaffold000 07	3,87,526	4,33,826	46,30 1	15				Eurhe1_5140 53	EURHEDRAFT_5140 53	388641	390143	+	EYE96814 .1	hypothetical protein EURHEDRAFT_51405 3
										Eurhe1_4106 04	EURHEDRAFT_4106 04	390594	392700	-	EYE96815 .1	hypothetical protein EURHEDRAFT_41060 4
										Eurhe1_5140 55	EURHEDRAFT_5140 55	394110	395952	+	EYE96816 .1	hypothetical protein EURHEDRAFT_51405 5
										Eurhe1_3398 63	EURHEDRAFT_3398 63	396584	396926	+	EYE96817 .1	hypothetical protein EURHEDRAFT_33986 3
										Eurhe1_4521 32	EURHEDRAFT_4521 32	400635	402375	-	EYE96818 .1	tannase and feruloyl esterase

										Eurhe1_3850 32	EURHEDRAFT_3850 32	403442	405164	-	EYE96819 .1	cytochrome P450
										Eurhe1_3761 02	EURHEDRAFT_3761 02	405642	405968	-	EYE96820 .1	hypothetical protein EURHEDRAFT_37610 2
										Eurhe1_4968 03	EURHEDRAFT_496 803	407525	413826	+	EYE96821 .1	PKS16 protein
										Eurhe1_5527 33	EURHEDRAFT_5527 33	414036	416270	-	EYE96822 .1	hydrolase
										Eurhe1_4106 11	EURHEDRAFT_4106 11	419072	420021	+	EYE96823 .1	putative AhpC/TSA family thioredoxin peroxidase
										Eurhe1_4520 70	EURHEDRAFT_4520 70	420541	421906	-	EYE96824 .1	hypothetical protein EURHEDRAFT_45207 0
										Eurhe1_4106 13	EURHEDRAFT_4106 13	423335	424593	-	EYE96825 .1	hypothetical protein EURHEDRAFT_41061 3
										Eurhe1_4106 15	EURHEDRAFT_4106 15	425595	427243	+	EYE96826 .1	putative MFS sugar transporter
										Eurhe1_4520 03	EURHEDRAFT_4520 03	427576	429081	-	EYE96827 .1	hypothetical protein EURHEDRAFT_45200 3

										Eurhe1_5140 71	EURHEDRAFT_5140 71	431942	433349	+	EYE96828 .1	hypothetical protein EURHEDRAFT_51407 1
EruBGC2 3	KK088442 .1	scaffold000 32	12,507	60,060	47,55 4	14				Eurhe1_4161 45	EURHEDRAFT_4161 45	12506	15089	+	EYE91644 .1	alanyl dipeptidyl peptidase
										Eurhe1_4161 46	EURHEDRAFT_4161 46	16970	19154	-	EYE91645 .1	hypothetical protein EURHEDRAFT_41614 6
										Eurhe1_5181 84	EURHEDRAFT_5181 84	19494	20418	+	EYE91646 .1	NAD(P)-binding protein
										Eurhe1_4161 49	EURHEDRAFT_4161 49	21921	23413	+	EYE91647 .1	hypothetical protein EURHEDRAFT_41614 9
										Eurhe1_5260 39	EURHEDRAFT_5260 39	26050	26455	+	EYE91648 .1	hypothetical protein EURHEDRAFT_52603 9
										Eurhe1_3893 21	EURHEDRAFT_3893 21	26763	27091	+	EYE91649 .1	hypothetical protein EURHEDRAFT_38932 1
										Eurhe1_3807 96	EURHEDRAFT_3807 96	29146	29451	+	EYE91650 .1	hypothetical protein EURHEDRAFT_38079 6
										Eurhe1_5080 17	EURHEDRAFT_508 017	31969	41022	+	EYE91651 .1	hypothetical protein EURHEDRAFT_50801 7

										Eurhe1_3807 98	EURHEDRAFT_3807 98	41582	42984	-	EYE91652 .1	putative dihydrofolate synthase
										Eurhe1_2309 01	EURHEDRAFT_2309 01	43666	46512	-	EYE91653 .1	vacuolar transporter chaperone 4
										Eurhe1_4161 56	EURHEDRAFT_4161 56	47405	50563	-	EYE91654 .1	DNA replication licensing factor MCM4
										Eurhe1_4644 58	EURHEDRAFT_4644 58	53015	56776	+	EYE91655 .1	DUF221-domain- containing protein
										Eurhe1_4161 58	EURHEDRAFT_4161 58	57462	58761	+	EYE91656 .1	arginine N- methyltransferase 2
										Eurhe1_4161 59	EURHEDRAFT_4161 59	58952	60060	-	EYE91657 .1	prohibitin-2
EruBGC2 4	KK088442 .1	scaffold000 32	1,26,039	1,73,940	47,90 2	21	asperfuranon e	P	18%	Eurhe1_4161 77	EURHEDRAFT_4161 77	127208	128043	-	EYE91683 .1	hypothetical protein EURHEDRAFT_41617 7
										Eurhe1_4058 22	EURHEDRAFT_4058 22	128301	130110	+	EYE91684 .1	P450 monooxygenase
										Eurhe1_4644 12	EURHEDRAFT_4644 12	130305	131241	-	EYE91685 .1	putative NAD dependent epimerase/dehydratas e
										Eurhe1_4643 84	EURHEDRAFT_4643 84	131502	132846	+	EYE91686 .1	hypothetical protein EURHEDRAFT_46438 4

										Eurhe1_5182 17	EURHEDRAFT_5182 17	132939	134271	+	EYE91687 .1	hypothetical protein EURHEDRAFT_51821 7
										Eurhe1_3893 58	EURHEDRAFT_3893 58	134364	135408	+	EYE91688 .1	hypothetical protein EURHEDRAFT_38935 8
										Eurhe1_2345 19	EURHEDRAFT_2345 19	135426	136779	-	EYE91689 .1	hypothetical protein EURHEDRAFT_23451 9
										Eurhe1_4643 40	EURHEDRAFT_4643 40	136908	138568	+	EYE91690 .1	FAD-binding domain- containing protein
										Eurhe1_4644 31	EURHEDRAFT_4644 31	138899	140470	+	EYE91691 .1	MFS general substrate transporter
										Eurhe1_5182 20	EURHEDRAFT_5182 20	140498	141398	-	EYE91692 .1	putative short-chain dehydrogenase/reduct ase
										Eurhe1_4644 43	EURHEDRAFT_4644 43	141605	142971	+	EYE91693 .1	putative salicylate hydroxylase
										Eurhe1_5182 22	EURHEDRAFT_5182 22	142990	144367	-	EYE91694 .1	hypothetical protein EURHEDRAFT_51822 2
										Eurhe1_4161 81	EURHEDRAFT_4161 81	144527	145637	+	EYE91695 .1	putative zinc-binding oxidoreductase ToxD
										Eurhe1_3808 44	EURHEDRAFT_380 844	146038	153940	+	EYE91696 .1	putative polyketide synthase

										Eurhe1_4058 35	EURHEDRAFT_4058 35	154100	155780	-	EYE91697 .1	hypothetical protein EURHEDRAFT_40583 5
										Eurhe1_3808 46	EURHEDRAFT_3808 46	157496	159347	+	EYE91698 .1	putative amino acid permease
										Eurhe1_5081 26	EURHEDRAFT_5081 26	159445	161125	-	EYE91699 .1	hypothetical protein EURHEDRAFT_50812 6
										Eurhe1_4058 38	EURHEDRAFT_4058 38	161564	163785	-	EYE91700 .1	hypothetical protein EURHEDRAFT_40583 8
										Eurhe1_5260 86	EURHEDRAFT_5260 86	164953	165901	-	EYE91701 .1	short-chain dehydrogenase/reduct ase SDR
										Eurhe1_4058 40	EURHEDRAFT_4058 40	169399	170445	-	EYE91702 .1	NAD(P)-binding protein
										Eurhe1_4642 92	EURHEDRAFT_4642 92	170663	172442	+	EYE91703 .1	cytochrome P450
EruBGC3 5	KK088487 .1	scaffold000 79	1	19,330	19,330 0	8				Eurhe1_4358 99	EURHEDRAFT_4358 99	5	767	-	EYE89960 .1	hypothetical protein EURHEDRAFT_43589 9, partial
										Eurhe1_4364 00	EURHEDRAFT_4364 00	977	1388	-	EYE89961 .1	hypothetical protein EURHEDRAFT_43640 0, partial

										Eurhe1_3823 86	EURHEDRAFT_3823 86	4299	6537	-	EYE89962 .1	oxidoreductase
										Eurhe1_3906 96	EURHEDRAFT_3906 96	6801	8061	+	EYE89963 .1	hypothetical protein EURHEDRAFT_39069 6
										Eurhe1_5346 10	EURHEDRAFT_5346 10	8303	9121	+	EYE89964 .1	hypothetical protein EURHEDRAFT_53461 0
										Eurhe1_4683 12	EURHEDRAFT_4683 12	9705	10875	+	EYE89965 .1	NAD(P)-binding protein
										Eurhe1_5346 13	EURHEDRAFT_5346 13	11449	13387	-	EYE89966 .1	NAD(P)-binding protein
										Eurhe1_5115 27	EURHEDRAFT_511 527	14052	16410	+	EYE89967 .1	thiolase-like protein

*P- Polyketide: Iterative type I; **Core gene is marked by Bold letters; TAN-1612-\$ - TAN-1612 / 1-(2,3,5,10-tetrahydroxy-7-methoxy-4-oxo-1,2,3,4-tetrahydro-anthracen-2-yl)pentane-2,4-dione / desmethyl TAN-1612

Table 4. Summary of terpene BGCs, their genes and proteins.

BGC ID	Scaffold ID	Scaffold	From	To	Size (bp)	Total genes	Most similar BGC	known BGC type	Similarity	JGIDB ID*	Gene ID	Gene start	Gene end	Strand	Protein ID	Protein Description

EruBGC1	KK088412.1	scaffold00002	1	11,815	11,815	2				Eurhe1_40796 8	EURHEDRAFT_4079 68	696	1815	+	EYE98762.1	terpenoid synthase
										Eurhe1_40797 0	EURHEDRAFT_4079 70	4704	9097	-	EYE98763.1	ARM repeat- containing protein
EruBGC6	KK088413.1	scaffold00003	8,68,883	8,90,032	21,150	9				Eurhe1_54530 4	EURHEDRAFT_5453 04	86909 8	87075 8	+	EYE98611.1	FAD/NAD(P)-binding domain-containing protein
										Eurhe1_40895 6	EURHEDRAFT_4089 56	87217 2	87322 5	-	EYE98612.1	nmrA-like family protein
										Eurhe1_54530 9	EURHEDRAFT_5453 09	87427 2	87453 3	+	EYE98613.1	hypothetical protein EURHEDRAFT_54530 9
										Eurhe1_40895 8	EURHEDRAFT_4089 58	87504 8	87527 2	-	EYE98614.1	hypothetical protein EURHEDRAFT_40895 8, partial
										Eurhe1_39988 2	EURHEDRAFT_3998 82	87563 8	87746 8	-	EYE98615.1	putative aryl-alcohol dehydrogenase
										Eurhe1_37468 2	EURHEDRAFT_3746 82	87888 2	88003 2	+	EYE98616.1	terpenoid synthase
										Eurhe1_38373 7	EURHEDRAFT_3837 37	88072 8	88184 2	-	EYE98617.1	terpenoid synthase
										Eurhe1_47179 1	EURHEDRAFT_4717 91	88276 9	88457 2	+	EYE98618.1	cytochrome P450

										Eurhe1_37468 5	EURHEDRAFT_3746 85	88482 5	88550 0	-	EYE98619.1	hypothetical protein EURHEDRAFT_37468 5
EruBGC1 6	KK088420. 1	scaffold00008	1,52,089	1,74,460	22,372	11	CA	Terpen e	100 %	Eurhe1_41156 4	EURHEDRAFT_4115 64	15509 7	15592 2	-	EYE95846.1	hypothetical protein EURHEDRAFT_41156 4
										Eurhe1_41156 5	EURHEDRAFT_4115 65	15610 4	15656 0	+	EYE95847.1	hypothetical protein EURHEDRAFT_41156 5
										Eurhe1_53031 8	EURHEDRAFT_5303 18	15700 0	15873 7	+	EYE95848.1	Scramblase-domain- containing protein
										Eurhe1_41156 8	EURHEDRAFT_4115 68	15914 4	15973 3	+	EYE95849.1	ubiquitin-conjugating enzyme E2
										Eurhe1_45460 6	EURHEDRAFT_4546 06	15998 6	16148 1	-	EYE95850.1	meiotic recombination protein spo11
										Eurhe1_41157 4	EURHEDRAFT_4115 74	16208 8	16446 0	+	EYE95851.1	lanosterol synthase
										Eurhe1_45428 9	EURHEDRAFT_4542 89	16486 7	16631 8	+	EYE95852.1	SGS-domain- containing protein
										Eurhe1_41157 7	EURHEDRAFT_4115 77	16652 1	16762 5	-	EYE95853.1	PQ loop repeat protein
										Eurhe1_41157 9	EURHEDRAFT_4115 79	16817 8	16933 6	+	EYE95854.1	DHS-like NAD/FAD- binding domain- containing protein

										Eurhe1_411580	EURHEDRAFT_411580	169847	170994	+	EYE95855.1	Pkinase-domain-containing protein
										Eurhe1_411581	EURHEDRAFT_411581	171525	171795	+	EYE95856.1	hypothetical protein EURHEDRAFT_411581
EruBGC19	KK088424.1	scaffold00014	8,442	30,059	21,618	12	SQ	Terpene	60%	Eurhe1_515537	EURHEDRAFT_515537	9069	9576	-	EYE94767.1	acyl-CoA N-acyltransferase
										Eurhe1_479185	EURHEDRAFT_479185	9639	11586	-	EYE94768.1	putative extracellular lipase
										Eurhe1_537881	EURHEDRAFT_537881	11964	13899	+	EYE94769.1	MFS general substrate transporter
										Eurhe1_420232	EURHEDRAFT_420232	14695	15140	+	EYE94770.1	hypothetical protein EURHEDRAFT_420232, partial
										Eurhe1_456526	EURHEDRAFT_456526	15317	16133	-	EYE94771.1	putative aspergillopepsin-2 precursor
										Eurhe1_456627	EURHEDRAFT_456627	17111	17704	-	EYE94772.1	hypothetical protein EURHEDRAFT_456627
										Eurhe1_412589	EURHEDRAFT_412589	18441	20059	-	EYE94773.1	farnesyl-diphosphate farnesyltransferase
										Eurhe1_456467	EURHEDRAFT_456467	20753	22406	+	EYE94774.1	DnaJ domain protein

										Eurhe1_45668 7	EURHEDRAFT_4566 87	23560	26803	+	EYE94775.1	hypothetical protein EURHEDRAFT_45668 7
										Eurhe1_37778 9	EURHEDRAFT_3777 89	26979	27392	-	EYE94776.1	hypothetical protein EURHEDRAFT_37778 9
										Eurhe1_41259 1	EURHEDRAFT_4125 91	27806	28274	+	EYE94777.1	hypothetical protein EURHEDRAFT_41259 1
										Eurhe1_51554 6	EURHEDRAFT_5155 46	28421	30023	-	EYE94778.1	CaaX prenyl protease Ste24
EruBGC2 1	KK088437. 1	scaffold00027	1,86,829	2,07,933	21,105	10				Eurhe1_41549 8	EURHEDRAFT_4154 98	18983 7	19034 7	+	EYE92372.1	DUF543 domain protein
										Eurhe1_46258 9	EURHEDRAFT_4625 89	19099 0	19266 1	-	EYE92373.1	hypothetical protein EURHEDRAFT_46258 9
										Eurhe1_41550 0	EURHEDRAFT_4155 00	19325 5	19426 1	+	EYE92374.1	putative mitochondrial outer membrane protein
										Eurhe1_38017 7	EURHEDRAFT_3801 77	19488 1	19577 8	-	EYE92375.1	cell division control protein 14
										Eurhe1_46284 8	EURHEDRAFT_4628 48	19682 8	19793 3	+	EYE92376.1	terpenoid synthase
										Eurhe1_48505 7	EURHEDRAFT_4850 57	19827 6	19921 3	-	EYE92377.1	smr family protein

										Eurhe1_46277 6	EURHEDRAFT_4627 76	20213 5	20336 5	+	EYE92378.1	guanine nucleotide-binding protein subunit alpha
										Eurhe1_51765 8	EURHEDRAFT_5176 58	20418 4	20526 8	-	EYE92379.1	hypothetical protein EURHEDRAFT_51765 8
										Eurhe1_41550 6	EURHEDRAFT_4155 06	20566 8	20620 4	-	EYE92380.1	hypothetical protein EURHEDRAFT_41550 6
										Eurhe1_19201 6	EURHEDRAFT_1920 16	20694 4	20728 0	-	EYE92381.1	hypothetical protein EURHEDRAFT_19201 6
EruBGC2 6	KK088445. 1	scaffold00035	1,12,483	1,36,782	24,300	7				Eurhe1_50866 2	EURHEDRAFT_5086 62	11543 2	11734 7	+	EYE91405.1	putative MFS sugar transporter
										Eurhe1_48708 7	EURHEDRAFT_4870 87	11798 0	12211 9	-	EYE91406.1	P-loop containing nucleoside triphosphate hydrolase protein
										Eurhe1_53368 2	EURHEDRAFT_5336 82	12248 2	12678 2	-	EYE91407.1	squalene cyclase
										Eurhe1_38957 7	EURHEDRAFT_3895 77	12774 7	12919 6	+	EYE91408.1	cytochrome P450
										Eurhe1_40607 1	EURHEDRAFT_4060 71	13146 6	13191 1	+	EYE91409.1	hypothetical protein EURHEDRAFT_40607 1

										Eurhe1_51842 5	EURHEDRAFT_5184 25	13220 3	13359 6	-	EYE91410.1	hypothetical protein EURHEDRAFT_51842 5
										Eurhe1_50867 3	EURHEDRAFT_5086 73	13470 1	13657 0	-	EYE91411.1	hypothetical protein EURHEDRAFT_50867 3
EruBGC2 7	KK088446. 1	scaffold00036	2,18,616	2,33,710	15,095	6				Eurhe1_38121 5	EURHEDRAFT_3812 15	22021 3	22095 9	-	EYE91361.1	hypothetical protein EURHEDRAFT_38121 5
										Eurhe1_50895 0	EURHEDRAFT_5089 50	22219 7	22329 2	+	EYE91362.1	alpha/beta-hydrolase
										Eurhe1_38121 7	EURHEDRAFT_3812 17	22385 0	22485 9	+	EYE91363.1	hypothetical protein EURHEDRAFT_38121 7
										Eurhe1_52640 2	EURHEDRAFT_5264 02	22592 7	22680 3	+	EYE91364.1	DUF829-domain- containing protein
										Eurhe1_46521 1	EURHEDRAFT_4652 11	22861 5	22972 2	-	EYE91365.1	terpenoid synthase
										Eurhe1_46517 8	EURHEDRAFT_4651 78	23096 8	23247 2	+	EYE91366.1	cytochrome P450
EruBGC3 3	KK088470. 1	scaffold00060	1	19,714	19,714	7				Eurhe1_46789 9	EURHEDRAFT_4678 99	1881	3363	+	EYE90125.1	hypothetical protein EURHEDRAFT_46789 9
										Eurhe1_38224 5	EURHEDRAFT_3822 45	5446	7374	-	EYE90126.1	putative lignostilbene dioxygenase

										Eurhe1_55202 1	EURHEDRAFT_5520 21	7721	9714	+	EYE90127.1	phytoene synthase
										Eurhe1_40715 3	EURHEDRAFT_4071 53	10020	11797	-	EYE90128.1	phytoene dehydrogenase
										Eurhe1_55202 9	EURHEDRAFT_5520 29	11928	12822	-	EYE90129.1	family A G protein- coupled receptor-like protein
										Eurhe1_53453 7	EURHEDRAFT_5345 37	13253	14405	+	EYE90130.1	NAD(P)-binding protein
										Eurhe1_46789 3	EURHEDRAFT_4678 93	17919	18831	-	EYE90131.1	hypothetical protein EURHEDRAFT_46789 3, partial
EruBGC3 6	KK088489. 1	scaffold00079	1	16,462	16,462	9				Eurhe1_55342 8	EURHEDRAFT_5534 28	325	682	+	EYE89947.1	hypothetical protein EURHEDRAFT_55342 8
										Eurhe1_38239 7	EURHEDRAFT_3823 97	741	2825	+	EYE89948.1	hypothetical protein EURHEDRAFT_38239 7
										Eurhe1_46834 8	EURHEDRAFT_4683 48	4433	6485	-	EYE89949.1	squalene cyclase
										Eurhe1_51154 9	EURHEDRAFT_5115 49	6798	8709	+	EYE89950.1	cytochrome P450
										Eurhe1_51155 2	EURHEDRAFT_5115 52	8903	9652	-	EYE89951.1	hypothetical protein EURHEDRAFT_51155 2

										Eurhe1_39070 7	EURHEDRAFT_3907 07	11170	13192	-	EYE89952.1	alpha/beta-hydrolase
										Eurhe1_51946 6	EURHEDRAFT_5194 66	13968	14641	+	EYE89953.1	hypothetical protein EURHEDRAFT_51946 6
										Eurhe1_41794 7	EURHEDRAFT_4179 47	14917	15406	+	EYE89954.1	hypothetical protein EURHEDRAFT_41794 7
										Eurhe1_43682 3	EURHEDRAFT_4368 23	16189	16441	-	EYE89955.1	hypothetical protein EURHEDRAFT_43682 3, partial
EruBGC1 5	KK088420. 1	scaffold00008	64,748	89,265	24,518	10				Eurhe1_47704 7	EURHEDRAFT_4770 47	67681	69254	+	EYE95805.1	acyl-CoA dehydrogenase NM domain-like protein
										Eurhe1_40198 7	EURHEDRAFT_4019 87	69508	70105	-	EYE95806.1	hypothetical protein EURHEDRAFT_40198 7
										Eurhe1_37686 8	EURHEDRAFT_3768 68	70530	71968	-	EYE95807.1	hypothetical protein EURHEDRAFT_37686 8
										Eurhe1_45412 9	EURHEDRAFT_4541 29	72409	74434	-	EYE95808.1	ClpP/crotonase
										Eurhe1_45446 4	EURHEDRAFT_4544 64	74747	76696	+	EYE95809.1	acetyl-CoA synthetase-like protein

										Eurhe1_37687 1	EURHEDRAFT_3768 71	77372	79265	+	EYE95810.1	aldolase
										Eurhe1_53568 1	EURHEDRAFT_5356 81	83433	83628	+	EYE95811.1	hypothetical protein EURHEDRAFT_53568 1
										Eurhe1_51475 0	EURHEDRAFT_5147 50	83748	85723	-	EYE95812.1	hypothetical protein EURHEDRAFT_51475 0
										Eurhe1_45434 5	EURHEDRAFT_4543 45	86581	87658	-	EYE95813.1	hypothetical protein EURHEDRAFT_45434 5
										Eurhe1_35954	EURHEDRAFT_3595 4	87976	88345	-	EYE95814.1	hypothetical protein EURHEDRAFT_35954

CA- clavaric acid; SQ - squalastatin S1;

*Core gene is marked by Bold letters

Table 5. Summary of hybrid BGCs, their genes and proteins.

BGC ID	BGC Type	Scaffold ID	Scaffold	From	To	Size (bp)	Total genes	Most similar BGC	known BGC type	Similarity	JGIDB ID*	Gene ID	Protein ID	Protein Description
EruBGC 7	NRPS,indole	KK08841 3.1	scaffold000 03	11,83,6 05	12,27,7 76	44,17 2	17				Eurhe1_447 902	EURHEDRAFT_44 7902	EYE9873 5.1	hypothetical protein EURHEDRAFT_447902

											Eurhe1_409 070	EURHEDRAFT_40 9070	EYE9873 6.1	sterol glucosyltransferase
											Eurhe1_448 757	EURHEDRAFT_44 8757	EYE9873 7.1	RTA1 like protein
											Eurhe1_448 668	EURHEDRAFT_44 8668	EYE9873 8.1	pectate lyase
											Eurhe1_374 793	EURHEDRAFT_37 4793	EYE9873 9.1	hypothetical protein EURHEDRAFT_374793
											Eurhe1_222 453	EURHEDRAFT_22 2453	EYE9874 0.1	hypothetical protein EURHEDRAFT_222453
											Eurhe1_409 074	EURHEDRAFT_40 9074	EYE9874 1.1	BNR/Asp-box repeat domain protein
											Eurhe1_448 612	EURHEDRAFT_44 8612	EYE9874 2.1	aromatic prenyl- transferase
											Eurhe1_383 835	EURHEDRAFT_38 3835	EYE9874 3.1	general substrate transporter
											Eurhe1_472 053	EURHEDRAFT_47 2053	EYE9874 4.1	acetyl-CoA synthetase- like protein, partial
											Eurhe1_409 075	EURHEDRAFT_40 9075	EYE9874 5.1	cytochrome P450
											Eurhe1_448 141	EURHEDRAFT_44 8141	EYE9874 6.1	putative dimethylallyl tryptophan synthase, partial
											Eurhe1_528 589	EURHEDRAFT_52 8589	EYE9874 7.1	hypothetical protein EURHEDRAFT_528589

											Eurhe1_409 077	EURHEDRAFT_40 9077	EYE9874 8.1	putative NADH- dependent flavin oxidoreductase
											Eurhe1_374 803	EURHEDRAFT_37 4803	EYE9874 9.1	GroES-like protein
											Eurhe1_383 841	EURHEDRAFT_38 3841	EYE9875 0.1	salicylate hydroxylase
											Eurhe1_400 000	EURHEDRAFT_40 0000	EYE9875 1.1	fatty-acyl coenzyme A oxidase
EruBGC 17	T1PKS,ind ole	KK08842 2.1	scaffold000 12	1,59,19 2	2,52,50 0	93,30 9	36	epipyricul ol	Polyketi de	17%	Eurhe1_550 27	EURHEDRAFT_55 027	EYE9531 1.1	hypothetical protein EURHEDRAFT_55027
											Eurhe1_530 712	EURHEDRAFT_53 0712	EYE9531 2.1	FAD/NAD(P)-binding domain-containing protein
											Eurhe1_377 401	EURHEDRAFT_37 7401	EYE9531 3.1	hypothetical protein EURHEDRAFT_377401
											Eurhe1_377 402	EURHEDRAFT_37 7402	EYE9531 4.1	putative vesicle- mediated transport protein Vid24
											Eurhe1_377 403	EURHEDRAFT_37 7403	EYE9531 5.1	hypothetical protein EURHEDRAFT_377403
											Eurhe1_386 218	EURHEDRAFT_38 6218	EYE9531 6.1	hypothetical protein EURHEDRAFT_386218

											Eurhe1_530 714	EURHEDRAFT_53 0714	EYE9531 7.1	drug resistance transporter EmrB/QacA subfamily
											Eurhe1_523 084	EURHEDRAFT_52 3084	EYE9531 8.1	hypothetical protein EURHEDRAFT_523084
											Eurhe1_455 324	EURHEDRAFT_45 5324	EYE9531 9.1	cytochrome P450
											Eurhe1_455 338	EURHEDRAFT_45 5338	EYE9532 0.1	ketoacyl-synt-domain- containing protein
											Eurhe1_455 544	EURHEDRAFT_45 5544	EYE9532 1.1	KR-domain-containing protein
											Eurhe1_412 135	EURHEDRAFT_41 2135	EYE9532 2.1	hypothetical protein EURHEDRAFT_412135
											Eurhe1_551 33	EURHEDRAFT_55 133	EYE9532 3.1	hypothetical protein EURHEDRAFT_55133
											Eurhe1_402 523	EURHEDRAFT_40 2523	EYE9532 4.1	hypothetical protein EURHEDRAFT_402523
											Eurhe1_551 41	EURHEDRAFT_55 141	EYE9532 5.1	hypothetical protein EURHEDRAFT_55141
											Eurhe1_377 410	EURHEDRAFT_37 7410	EYE9532 6.1	hypothetical protein EURHEDRAFT_377410
											Eurhe1_412 141	EURHEDRAFT_41 2141	EYE9532 7.1	hypothetical protein EURHEDRAFT_412141, partial

											Eurhe1_412 142	EURHEDRAFT_41 2142	EYE9532 8.1	UDP- Glycosyltransferase/gly cogen phosphorylase
											Eurhe1_412 143	EURHEDRAFT_41 2143	EYE9532 9.1	hypothetical protein EURHEDRAFT_412143
											Eurhe1_523 089	EURHEDRAFT_52 3089	EYE9533 0.1	hypothetical protein EURHEDRAFT_523089
											Eurhe1_412 144	EURHEDRAFT_41 2144	EYE9533 1.1	hypothetical protein EURHEDRAFT_412144
											Eurhe1_537 038	EURHEDRAFT_53 7038	EYE9533 2.1	hypothetical protein EURHEDRAFT_537038
											Eurhe1_455 472	EURHEDRAFT_45 5472	EYE9533 3.1	putative MAP kinase
											Eurhe1_455 859	EURHEDRAFT_45 5859	EYE9533 4.1	ammonium transporter MEP2
											Eurhe1_412 148	EURHEDRAFT_41 2148	EYE9533 5.1	hypothetical protein EURHEDRAFT_412148
											Eurhe1_499 888	EURHEDRAFT_49 9888	EYE9533 6.1	polyketide synthase
											Eurhe1_377 419	EURHEDRAFT_37 7419	EYE9533 7.1	NAD(P)-binding protein
											Eurhe1_455 854	EURHEDRAFT_45 5854	EYE9533 8.1	NAD(P)-binding protein
											Eurhe1_455 792	EURHEDRAFT_45 5792	EYE9533 9.1	cytochrome P450

											Eurhe1_412 154	EURHEDRAFT_41 2154	EYE9534 0.1	FAD-binding domain- containing protein
											Eurhe1_515 220	EURHEDRAFT_51 5220	EYE9534 1.1	NAD(P)-binding protein
											Eurhe1_530 727	EURHEDRAFT_53 0727	EYE9534 2.1	aromatic prenyltransferase
											Eurhe1_402 538	EURHEDRAFT_40 2538	EYE9534 3.1	hypothetical protein EURHEDRAFT_402538
											Eurhe1_412 157	EURHEDRAFT_41 2157	EYE9534 4.1	beta-1 and beta-2 tubulin
											Eurhe1_499 916	EURHEDRAFT_49 9916	EYE9534 5.1	hypothetical protein EURHEDRAFT_499916
											Eurhe1_402 541	EURHEDRAFT_40 2541	EYE9534 6.1	hypothetical protein EURHEDRAFT_402541
EruBGC 28	T1PKS,NR PS-like	KK08844 7.1	scaffold000 36	1,73,97 9	2,24,25 4	50,27 6	19	asperlacto ne	Polyketi de	100 %	Eurhe1_416 682	EURHEDRAFT_41 6682	EYE9123 9.1	37S ribosomal protein S11
											Eurhe1_406 264	EURHEDRAFT_40 6264	EYE9124 0.1	TIM44 subunit of mitochondria import inner membrane translocase
											Eurhe1_416 684	EURHEDRAFT_41 6684	EYE9124 1.1	TPR-like protein
											Eurhe1_416 685	EURHEDRAFT_41 6685	EYE9124 2.1	hypothetical protein EURHEDRAFT_416685

											Eurhe1_251 045	EURHEDRAFT_25 1045	EYE9124 3.1	hypothetical protein EURHEDRAFT_251045
											Eurhe1_518 589	EURHEDRAFT_51 8589	EYE9124 4.1	GTP-binding protein YchF
											Eurhe1_381 296	EURHEDRAFT_38 1296	EYE9124 5.1	Hira-domain-containing protein
											Eurhe1_547 227	EURHEDRAFT_54 7227	EYE9124 6.1	6-methylsalicylic acid synthase MsaS
											Eurhe1_406 270	EURHEDRAFT_40 6270	EYE9124 7.1	ochratoxin A non- ribosomal peptide synthetase
											Eurhe1_416 691	EURHEDRAFT_41 6691	EYE9124 8.1	hypothetical protein EURHEDRAFT_416691
											Eurhe1_509 132	EURHEDRAFT_50 9132	EYE9124 9.1	PAP2 domain protein
											Eurhe1_389 761	EURHEDRAFT_38 9761	EYE9125 0.1	NADP(+) coupled glycerol dehydrogenase
											Eurhe1_416 698	EURHEDRAFT_41 6698	EYE9125 1.1	hypothetical protein EURHEDRAFT_416698
											Eurhe1_416 702	EURHEDRAFT_41 6702	EYE9125 2.1	hypothetical protein EURHEDRAFT_416702
											Eurhe1_416 703	EURHEDRAFT_41 6703	EYE9125 3.1	hypothetical protein EURHEDRAFT_416703
											Eurhe1_509 144	EURHEDRAFT_50 9144	EYE9125 4.1	hypothetical protein EURHEDRAFT_509144

											Eurhe1_509 149	EURHEDRAFT_50 9149	EYE9125 5.1	RmlC-like cupin
											Eurhe1_430 683	EURHEDRAFT_43 0683	EYE9125 6.1	hypothetical protein EURHEDRAFT_430683, partial
											Eurhe1_416 707	EURHEDRAFT_41 6707	EYE9125 7.1	hypothetical protein EURHEDRAFT_416707
EruBGC 30	T1PKS,NR PS	KK08845 3.1	scaffold000 43		1,59,98 7	66,90 6	22				Eurhe1_526 771	EURHEDRAFT_52 6771	EYE9079 8.1	Cloroperoxidase
											Eurhe1_417 104	EURHEDRAFT_41 7104	EYE9079 9.1	hypothetical protein EURHEDRAFT_417104
											Eurhe1_466 350	EURHEDRAFT_46 6350	EYE9080 0.1	hypothetical protein EURHEDRAFT_466350
											Eurhe1_417 106	EURHEDRAFT_41 7106	EYE9080 1.1	putative trans-aconitate 2-methyltransferase
											Eurhe1_417 107	EURHEDRAFT_41 7107	EYE9080 2.1	putative fungal-specific transcription factor
											Eurhe1_417 108	EURHEDRAFT_41 7108	EYE9080 3.1	putative arabinan endo- 1,5-alpha-L- arabinosidase A
											Eurhe1_518 906	EURHEDRAFT_51 8906	EYE9080 4.1	hypothetical protein EURHEDRAFT_518906
											Eurhe1_466 336	EURHEDRAFT_46 6336	EYE9080 5.1	alcohol oxidase

											Eurhe1_406 621	EURHEDRAFT_40 6621	EYE9080 6.1	lysophospholipase Plb1
											Eurhe1_548 861	EURHEDRAFT_54 8861	EYE9080 7.1	MFS general substrate transporter
											Eurhe1_381 680	EURHEDRAFT_38 1680	EYE9080 8.1	hypothetical protein EURHEDRAFT_381680
											Eurhe1_466 320	EURHEDRAFT_46 6320	EYE9080 9.1	NAD(P)-binding protein
											Eurhe1_406 625	EURHEDRAFT_40 6625	EYE9081 0.1	putative vitamin H transporter
											Eurhe1_510 001	EURHEDRAFT_51 0001	EYE9081 1.1	Zn(II)2Cys6 transcription factor
											Eurhe1_466 329	EURHEDRAFT_46 6329	EYE9081 2.1	putative fructose- bisphosphate aldolase
											Eurhe1_466 314	EURHEDRAFT_46 6314	EYE9081 3.1	putative pantothenate transporter
											Eurhe1_390 106	EURHEDRAFT_39 0106	EYE9081 4.1	hypothetical protein EURHEDRAFT_390106
											Eurhe1_510 009	EURHEDRAFT_51 0009	EYE9081 5.1	MFS transporter
											Eurhe1_466 361	EURHEDRAFT_46 6361	EYE9081 6.1	FAD binding domain protein
											Eurhe1_417 116	EURHEDRAFT_41 7116	EYE9081 7.1	hypothetical protein EURHEDRAFT_417116

											Eurhe1_466 393	EURHEDRAFT_46 6393	EYE9081 8.1	cytochrome P450 oxidoreductase
											Eurhe1_466 446	EURHEDRAFT_46 6446	EYE9081 9.1	acetyl-CoA synthetase- like protein

*Core gene is marked by Bold letters

Table S6. Overview of siderophore BGCs, their genes and proteins.

BGC ID	Scaffold ID	Scaffold	From	To	Size (bp)	Total genes	JGIDB ID*	Gene ID	Gene start	Gene end	Strand	Protein ID	Protein Description
EruBGC9	KK088415. 1	scaffold0000 5	1,10,568	1,22,685	12,118	2	Eurhe1_51333 5	EURHEDRAFT_51333 5	115567	117685	+	EYE97444. 1	hypothetical protein EURHEDRAFT_513335
							Eurhe1_52898 6	EURHEDRAFT_52898 6				EYE97445. 1	hypothetical protein EURHEDRAFT_528986
EruBGC1 2	KK088417. 1	scaffold0000 7	3,72,420	3,84,556	12,137	5	Eurhe1_52964 7	EURHEDRAFT_52964 7	374939	376088	-	EYE96807. 1	Clavamate synthase-like protein
							Eurhe1_51405 1	EURHEDRAFT_51405 1	377419	379556	+	EYE96808. 1	hypothetical protein EURHEDRAFT_514051
							Eurhe1_37609 4	EURHEDRAFT_37609 4	379629	380190	-	EYE96809. 1	hypothetical protein EURHEDRAFT_376094
							Eurhe1_55268 5	EURHEDRAFT_55268 5	380375	381109	-	EYE96810. 1	hypothetical protein EURHEDRAFT_552685
							Eurhe1_41059 6	EURHEDRAFT_41059 6	383661	384519	-	EYE96811. 1	hypothetical protein EURHEDRAFT_410596

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*Core gene is marked by Bold letter.