## ANTIBACTERIAL ACTIVITY OF SPONGE ASSOCIATED-BACTERIA ISOLATED FROM NORTH JAVA SEA

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### ABSTRACT

A total of 90 bacterial isolates were obtained from association with sponges collected from Bandengan water, Jepara and Karimun island of Karimunjawa islands in the north java sea. Antibacterial screening by using a pathogenic Escherichia coli indicated that two isolates BSP.12 and MKSP.5 inhihited the growth of tested strain. Molecular identification based on 16S rDNA approach revealed that isolate BSP.12 was closely related to Vibrio harveyi with a homology of 100% and isolate MKSP.5 showed highest similarity to Brachybacterium rhamnosum (99%), respectively.

A PCR-based approach by using specific primers targeting the occurrence of gene fragments necessary for the biosynthesis of major natural products, namely Non-ribosomal peptide synthetases (NRPS) and Polyketide synthases (PKS) was applied to estimate the genetic potential of these active strains. Both isolates were capable of amplifying the NRPS gene fragments but not the PKS gene fragments.

Key words: antibacterial, sponge associated-bacteria, PKS, NRPS, North Java Sea

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## INTRODUCTION

Marine organisms including those from coral reef ecosystems have become sources of great interest to natural product chemistry, since they provide a large proportion of bioactive metabolites with different biological activities (Faulkner 2000). In particular, marine invertebrates with high species diversity in the Indo-Pacific regions (Coll and Sammarco 1986) are often rich in secondary metabolites and are preferential targets in the search for bioactive natural products (Sammarco and Coll 1992). Sponges (phylum Porifera) are most primitive of the multicelled animals that have existed for 700–800 million years. Of the approximately 15,000 sponge species, most occur in marine environments. Only about 1% of the species inhabits freshwater (Belarbi et al, 2003).

Perhaps the most significant problem that has hampered the investigation of secondary metabolites produced by reef's invertebrates is their low concentration. In marine invertebrates

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many highly active compounds contribute  $to < 10^{-6}$  % of the body-wet weight. Providing sufficient amounts of these biologically active substances, hence, may be a difficult task (Proksch et al, 2002; Radjasa et al 2007a,b,c).

The present work is aimed at screening of marine bacteria associated with sponge for the production of secondary metabolites against pathogenic *Escherichia coli* coupled with PCR-based method for the occurrence of NRPS and PKS gene fragments for estimating the genetic potential of the biologically active strains.

### MATERIALS AND METHODS

### Sampling and isolation of spongeassociated bacteria

Colonies of sponges were collected from Bandengan water, Jepara, and Karimun island, Karimunjawa islands, North Java Sea, Indonesia by scuba diving from a depth of approximately 5 meters. Upon collection sponge colonies were put into sterile plastic bags (Whirl-Pak, Nasco, USA) The sponges were then rinsed with sterile seawater and 1 cubic centimeter of sponge tissue was excised from the middle of the whole sponge and sponge surface after it is peeled off (Radjasa et

**Table 1.** Number of isolate obtained from sponges

al, 2007c) with a sterile knife. The resultant tissues were serially diluted, spread on <sup>1</sup>/<sub>2</sub> strength ZoBell 2216E marine agar medium and incubated at room temperature for 48 hours. On the basis of morphological features, colonies were randomly picked and purified by making streak plates (Madigan et al, 2000).

## Screening of sponge bacteria with biological activity

Screening and antibacterial tests as well as molecular based-works were carried out at Marine Microbiology Laboratory, Diponegoro University, Semarang, Indonesia. To screen their biological activity, a total of 90 sponge isolates (Table 1) were tested against isolate pathogenic bacterium Escherichia coli. One 100 µl culture of indicator microorganism in the logarithmic phase (ca.  $10^9$  cells ml<sup>-1</sup>) was spread on to agar medium. Several paper disks ( 8 mm; Advantec, Toyo Roshi, Ltd, Japan) containing 30 µl of the coral bacterial strain were placed on the respective agar surface. The plates were then incubated at room temperature for 48 hours. Antibacterial activity was defined according to Radjasa et al (2007a) by the formation of inhibition zones greater than 9 mm around the paper disk.

Number of Number of Media Location Media Zobell Sponge Actinomycetes isolate 42 15 60 • Bandengan 6 • Karimun 4 25 5 30 Total 10 67 20 90

# PCR-based analysis of NRPS and PKS producing bacterial strains

To obtain genomic DNA of secondary metabolite producing-strains for PCR analysis, cell materials were taken from an agar plate, suspended in sterile water (Sigma, Germany) and subjected to five cycles of freeze (-80°C) and thaw (95°C). Amplification of peptide synthetase gene fragments was carried out with the NRPS degenerated primers A2gamF (5'-AAG

GCN GGC GSB GCS TAY STG CC-3') and A3gamR (5'-TTG GGB IKB CCG GTS GIN CCS GAG GTG-3') (Marahiel *et al.*, 1997) and PKS degenerated primers KSDPQQF (5'-MGN GAR GCN NWN SMN ATG GAY CCN CAR CAN MG-3') and KSHGTGR (5'-GGR TCN CCN ARN SWN GTN CCN GTN CCR TG -3') (Piel, 2002). All primers were manufactured by MWG-Biotech (Ebersberg, Germany).

PCR was performed with an ProgeneThermal cycler (Techne, Burkhardtsorf, Germany) as follows: 1 µl template DNA, 1 µl of each of the appropriate primers, and 23 µl DNA free water (Fluka, Sigma-Aldrich Chemie GmbH, Germany) were added to puReTaq Ready-To-Go PCR beads (Amersham Biosciences Europe GmbH, Germany). The NRPS-PCR run comprised 40 cycles with denaturing conditions for 1 min at 95°C, annealing for 1 min at 70°C and extension for 2 min at 72°C, respectively. Pseudomonas sp. DSM 50117 as positive control. was used The amplification of PKS gene fragments included an initial denaturating step at 94°C for 2 min, followed by 45 cycles at 94°C for 1 min, annealing at 55°C for 1 min and elongation at 72°C for 2 min. Bacillus subtilis 168 was utilized for positive control.

## PCR amplification and sequencing of 16S rRNA gene fragments.

Amplification was conducted according to method of Radjasa et al (2007a). Genomic DNA of secondary metabolite producingstrains for PCR analysis were obtained from cell materials taken from an agar plate, suspended in sterile water (Sigma, Germany) and subjected to five cycles of freeze (-80°C) and thaw (95°C). PCR amplification of partial 16S rRNA gene of sponge bacteria, purification of PCR products and subsequent sequencing analysis were performed according to the method of Radjasa et al (2007b). The determined DNA sequences of strains were then compared for homology to the BLAST database.

## **R**ESULTS AND **D**ISCUSSION

Inhibitory interactions among spongeassociated bacteria that occur within the sponge surface are of great interest to search for secondary metabolite-producing bacteria. Isolation and screening for secondary metabolite-producing bacteria in coral reef ecosystems have been strongly neglected until now in comparison with the invertebrate parts.

The present study indicated that 2 among 90 marine bacteria associated with sponges showed growth inhibition against indicator microorganism (**Table 1**). This offers the possibility to use sponge bacteria as the source of antibacterial compounds for controlling the pathogenic bacteria such as *Escherichia coli*.

No	Isolate	Zone of inhibition (mm)
1	BSP.12	8.9 ± 0,004
2	MKSP.5	10.3 ± 0,02

Table 2. Inhibitory interaction of sponge associated-bacteria agains E.coli

Molecular identification based on 16S rDNA approach showed that the two active

isolates are the member of genera *Vibrio* and *Brachybacterium* (**Table 2**).

No	Isolate	Closest relative	Homology(%)	Acc. number
1.	MKSP.5	Vibrio harveyi strain LB5	100	DQ146936
2.	BSP.12	Brachybacterium rhamnosum	99	AJ415376

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**Table 3.** Molecular identification of active isolates

As shown in the Table 2, isolate MKSP.5 has a high homology to Vibrio harveyi with (100%), on the other hand, isolate BSP.12 is Brachybacterium closely related to rhamnosum (99%). The detailed alignments of DNA sequences between isolate MKSP.5 and Vibrio harveyi LB5 (accession number DO146936) BSP.5 and isolate and Brachybacterium rhamnosum (AJ41537) are shown in the fig. 1 and 2.

The members of Alteromonadales and Vibrionales of the proteobacteria, such as *Pseudoalteromonas* and *Vibrio* have been known as the dominant antibiotics producers (Long and Azam, 2001; Grossart et al, 2004). Furthermore, a bacterium BSP1.12 isolated from sponge *Haliclona* sp. that closely related to *Vibrio parahaemolyticus* and inhibited only the growth of the tested bacterium *Aeromonas hydrophila* known as the causative agent of the disease *Motile Aeromonas Septicemia* (MAS) in many freshwater fishes (Radjasa et al, 2007c).

One of the active isolate BSP.12 showed close relativeness to the member of actinomycetes. The actinomycetes, although not all the Actinobacteria, are easy to isolate from the marine environment. However, their ecological role in the marine ecosystem is largely neglected and various assumptions meant there was little incentive to isolate strains for search and discovery of new drugs. However, the marine environment has become a prime resource in search and discovery for novel natural products and biological diversity, and marine actinomycetes turn out to be important contributors (Ward and Bora, 2006).

Among these five, the Class Actinobacteria, and more specifically, bacteria

belonging to the Order Actinomycetales (commonly called actinomycetes) account for approximately 7000 of the compounds reported in the Dictionary of Natural Products. Looking individually at the more than 140 currently described actinomycete genera, it becomes clear that even within this Order it is a few well-known soil genera that account for the vast majority of microbial natural products discovered. In the genus Streptomyces alone fact. accounts for a remarkable 80% of the actinomycete natural products reported to date, a biosynthetic capacity that remains without rival in the microbial world (Jensen et al, 2005).

Polyketides and non-ribosomal peptides are two of the largest groups of multifunctional proteins that create a multitude of secondary metabolites (Hutchinson, 2003), many of them are used as therapeutic agents (Piel et al, 2003). Products of the microbial non-ribosomal peptide synthesis include the immunosuppressant cyclosporine and other antibiotics such as gramicin S, tyrocin A and surfactins (Kleinkauf and von Doehren, 1996). clinically important Among polyketides are the antibiotics aunorubicin, erythromycin, lovastatin and rapamycin (Due et al, 2001).

With advanced techniques of molecular biology such as polymerase chain reaction (PCR), it is now become possible to carry out a screening on the presence of polyketides and non ribosomal peptides by using specific primers of polyketide synthases (PKS) (Piel, 2002)

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Score = 1604 bits (809), Expect = 0.0 Identities = 809/809 (100%), Gaps = 0/809 (0%) Strand=Plus/Minus						
Query	4	GCGTCCTCCCGAAGGTTAAACTACCTACTTCTTTTGCAGCCCACTCCCATGGTGTGACGG	63			
Sbjct	1435	GCGTCCTCCCGAAGGTTAAACTACCTACTTCTTTTGCAGCCCACTCCCATGGTGTGACGG	1376			
Query	64	GCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTGGCATTCTGATCCACGATTACTAGC	123			
Sbjct	1375	GCGGTGTGTACAAGGCCCGGGAACGTATTCACCGTGGCATTCTGATCCACGATTACTAGC	1316			
Query	124	GATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACGCACTTTTTGG	183			
Sbjct	1315	GATTCCGACTTCATGGAGTCGAGTTGCAGACTCCAATCCGGACTACGACGCACTTTTTGG	1256			
Query	184	GATTCGCTCACTATCGCTAGCTTGCTGCCCCTCTGTATGCGCCATTGTAGCACGTGTGTAG	243			
Sbjct	1255	GATTCGCTCACTATCGCTAGCTTGCTGCCCTCTGTATGCGCCATTGTAGCACGTGTGTAG	1196			
Query	244	CCCTACTCGTAAGGGCCATGATGACTTGACGTCGTCCCCACCTTCCTCCGGTTTATCACC	303			
Sbjct	1195	CCCTACTCGTAAGGGCCATGATGACTTGACGTCGTCCCCACCTTCCTCCGGTTTATCACC	1136			
Query	304	GGCAGTCTCCCTGGAGTTCCCGACATTACTCGCTGGCAAACAAGGATAAGGGTTGCGCTC	363			
Sbjct	1135	GGCAGTCTCCCTGGAGTTCCCCGACATTACTCGCTGGCAAACAAGGATAAGGGTTGCGCTC	1076			
Query	364	GTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGT	423			
Sbjct	1075	GTTGCGGGACTTAACCCAACATTTCACAACACGAGCTGACGACAGCCATGCAGCACCTGT	1016			
Query	424	CTCAGAGTTCCCGAAGGCACCAATCCATCTCTGGAAAGTTCTCTGGATGTCAAGAGTAGG	483			
Sbjct	1015	CTCAGAGTTCCCGAAGGCACCAATCCATCTCTGGAAAGTTCTCTGGATGTCAAGAGTAGG	956			
Query	484	TAAGGTTCTTCGCGTTGCATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCG	543			
Sbjct	955	TAAGGTTCTTCGCGTTGCATCGAATTAAACCACATGCTCCACCGCTTGTGCGGGCCCCCG	896			
Query	544	TCAATTCATTTGAGTTTTAATCTTGCGACCGTACTCCCCAGGCGGTCTACTTAACGCGTT	603			
Sbjct	895	TCAATTCATTTGAGTTTTAATCTTGCGACCGTACTCCCCAGGCGGTCTACTTAACGCGTT	836			
Query	604	AGCTCCGAAAGCCACGGCTCAAGGCCACAACCTCCAAGTAGACATCGTTTACGGCGTGGA	663			
Sbjct	835	AGCTCCGAAAGCCACGGCTCAAGGCCACAACCTCCAAGTAGACATCGTTTACGGCGTGGA	776			
Query	664	CTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGCATCTGAGTGTCAGTATCTG	723			
Sbjct	775	CTACCAGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCGCATCTGAGTGTCAGTATCTG	716			
Query	724	TCCAGGGGGCCGCCTTCGCCACCGGTATTCCTTCAGATCTCTACGCATTTCACCGCTACA	783			
Sbjct	715	TCCAGGGGGCCGCCTTCGCCACCGGTATTCCTTCAGATCTCTACGCATTTCACCGCTACA	656			
Query	784	CCTGAAATTCTACCCCCCTCTACAGTACT 812				
Sbjct	655	CCTGAAATTCTACCCCCCTCTACAGTACT 627				

Fig1. The DNA alignment showing the homology of isolate MKSP.5 and *Vibrio harveyi* based on BLAST system.

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Score = 1092 bits (551), Expect = 0.0
Identities = 554/555 (99%), Gaps = 0/555 (0%)
Strand=Plus/Minus
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Query	1	GTTACCGACTTTCGTGACTTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGC	60
Sbjct	1378	GTTACCGACTTTCGTGACTTGACGGGCGGTGTGTACAAGGCCCGGGAACGTATTCACCGC	1319
Query	61	AGCGTTGCTGATCTGCGATTACTAGCGACTCCGACTTCATGGGGTCGAGTTGCAGACCCC	120
Sbjct	1318	AGCGTTGCTGATCTGCGATTACTAGCGACTCCGACTTCATGGGGTCGAGTTGCAGACCCC	1259
Query	121	AATCCGAACTGAGACCGGCTTTTTGGGATTCGCTCCACCTCACAGTTTCGCAACCCATTG	180
Sbjct	1258	AATCCGAACTGAGACCGGCTTTTTGGGATTCGCTCCACCCTCACAGTTTCGCAACCCTTTG	1199
Query	181	TACCGGCCATTGTAGCATGCGTGAAGCCCAAGACATAAGGGGCATGATGATTTGACGTCG	240
Sbjct	1198	TACCGGCCATTGTAGCATGCGTGAAGCCCAAGACATAAGGGGCATGATTTGACGTCG	1139
Query	241	TCCCCACCTTCCTCCGAGTTGACCCCGGCAGTCTCCCATGAGTCCCCGCCATTACGCGCT	300
Sbjct	1138	TCCCCACCTTCCTCCGAGTTGACCCCGGCAGTCTCCCATGAGTCCCCGCCATTACGCGCT	1079
Query	301	GGCAACATGGAACGAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGA	360
Sbjct	1078	GGCAACATGGAACGAGGGTTGCGCTCGTTGCGGGACTTAACCCAACATCTCACGACACGA	1019
Query	361	GCTGACGACAACCATGCACCACCTGTGCACCAGTCCGAAGAAAACCCCATCTCTGGAGTC	420
Sbjct	1018	GCTGACGACAACCATGCACCACCTGTGCACCAGTCCGAAGAAAACCCCATCTCTGGAGTC	959
Query	421	GTCCGGTGCATGTCAAGCCTTGGTAAGGTTCTTCGCGTTGCATCGAATTAATCCGCATGC	480
Sbjct	958	GTCCGGTGCATGTCAAGCCTTGGTAAGGTTCTTCGCGTTGCATCGAATTAATCCGCATGC	899
Query	481	TCCGCCGCTTGTGCGGGCCCCCGTCAATTCCTTTGAGTTTTAGCCTTGCGGCCGTACTCC	540
Sbjct	898	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	839
Query	541	CCAGGCGGGGCACTT 555	
Sbjct	838	 CCAGGCGGGGCACTT 824	

Fig 2. The DNA alignment showing the homology of isolate BSP.12 and *Brachybacterium rhamnosum* based on BLAST system.

and non ribosomal polypeptide synthetases (NRPS) (Marahiel *et al.*, 1997).

The present study revealed that both active isolates were able to amplify the NRPS gene fragments that are essential in the biosynthesis of peptide bioactive products. Vibrio is among the dominant producers of peptide bioactive products. Liu et al (2005) reported that *Vibrio anguillaum* produced substance as virulent factor that was synthesized by a non-ribosomal peptide synthetases (NRPS). Two member of Vibrio, namely *V. coralliitycus* MJ.5 and *V.* 

parahaemolyticus MJ.11 were obtained from coral *Porites lutea* that have antibacterial activity against *Bacillus subtilis* and *Staphylococcus lentus*. Interestingly, isolate *V. coralliitycus* MJ.5 was also amplified NRPS gene fragments (Radjasa *et al*, unpublished).

Ayuso-Sacido and Genilloud (2004) reported that the members of Actinomycetes have been reported to produce various antibacterial compounds which are also synthesized by non-ribosomal peptide synthetases (NRPS). In this study, an

occurrence of NRPS gene fragment within *Brachybacterium rhamnosum* is reported for the first time. It is indicated that there are more genera within the Actinomycetes that offer possibility as the source of antibacterial compounds.

## CONCLUSION

In conclusion, sponges from North Java Sea exhibited secondary metabolite producingmarine bacteria with antibacterial potential against Ε. coli. The present study highlighted the PCR-based method by using specific degenerated primers NRPS and PKS as a powerful tool in estimating the genetic potential of sponge associatedbacteria that is essential in the search for secondary metabolite-producers among sponge colonizers.

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## REFERENCES

- Ayuso-Sacido A, and O. Genilloud, 2004. New PCR primers for the screening of NRPS and PKS-I systems in actinomycetes: Detection and distribution of these biosynthetic gene sequences in major taxonomic groups. *Microbial Ecol* 49: 10-24
- Belarbi E.H, A. C. Go'mez, Y. Chisti, F. G. Camacho, and E. M. Grima. 2003.

Producing drugs from marine sponges. *Biotechnol. Adv.* 21: 585–598

- Coll J.C, and P.W Sammarco, 1986. Soft corals: Chemistry and ecology. *Oceanus* 29 (2): 33-37
- Due L, Sanchez C, Shen B. 2001. Hybrid peptide-polyketide natural products: biosynthesis and prospects toward engineering novel molecules. *Metabol Engineer* 3:78-95
- Faulkner D.J, 2000. Marine pharmacology. Anton Leeuw Int J G. 77:135-145
- Grossart HP, A. Schlingloff, M. Bernhard, M. Simon, and T. Brinkhoff, 2004. Antagonistic activity of bacteria isolated from organic aggregates of the German Wadden Sea. *FEMS Microbiol Ecol* 47:387-396
- Kleinkauf H, von Doehren H. 1996. A nonribosomal system of peptide biosynthesis. *Eur J Biochem* 236:335-351
- Madigan M.T, J.M. Martinko, J. Parker, and T.D. Brock, 2000. Biology of microorganisms. Prentice-Hall, Inc., New Jersey, USA
- Marahiel MA, Stachelhaus T, Mootz HD.1997. Modular peptide synthetases involved in nonribosomal peptide synthesis. *Chem Rev* 97:2651-2673
- Jensen, PR., T.J Mincer., P.G Williams and P. Fenical. 2005. Marine actinomycete diversity and natural product discovery. *Ant. Leeuw.* 87:43-48.
- Liu, Q., Y Ma, H Wu, M Shao, H Liu, Y Zhang . 2004. Cloning, identification and expression of an *entE* homologue *angE* from *Vibrio anguillarum* serotype O1. *Arch. Microbiol.* 181: 287-293

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- Piel J. 2002. A polyketide synthase-peptide synthetase gene cluster from an uncultured bacterial symbiont of Paederus beetles. *PNAS* 29:14002-14007
- Piel J, Hui D, Fusetani N, Matsunaga S. 2003. Targeting modular polyketide synthetase with iteratively acting acyltransferases from metagenomes of uncultured bacterial consortia. *Environ Microbiol* 6:921-927
- Proksch P, R.A. Edrada, R. Ebel, 2002. Drugs from the seas-current status and microbiological implications. *Appl Microbiol Biotechnol*. 59:125-134
- Radjasa, O.K., T. Martens., H-P. Grossart, T Brinkoff., A Sabdono., and M. Simon. 2007a. Antagonistic activity of a marine bacterium *Pseudoalteromonas luteoviolacea* TAB4.2 associated with coral *Acropora* sp. J. Biol. Sci. 7(2):239-246.

- Radjasa, O.K., S.I.O. Salasia, A. Sabdono, J. Weise, J. F. Imhoff, C. Lämmler and M. J. Risk. 2007b. Antibacterial activity of marine bacterium *Pseudomonas* sp. associated with soft coral *Sinularia polydactyla* against *Streptococcus equi* subsp. *zooepidemicus. Int. J. Pharmacol.* 3(2):170-174.
- Radjasa, O.K., A. Sabdono, Junaidi and E.
  Zocchi. 2007. Richness of secondary metabolite-producing marine bacteria associated with sponge *Haliclona* sp. *Int. J. Pharmacol.* (*In press*).3 (3) : 275-279
- Sammarco P.W., J.C. Coll, 1992. Chemical adaptation in the Octocorallia: Evolutionary considerations. *Mar. Ecol. Prog. Ser.* 88:93-104
- Ward, A.C and N. Bora. 2006. Diversity and biogeography of marine actinobacteria. *Curr. Opini. Microbiol.* 9:279-286.