SAJ NEWS

Vol. 26, No. 2, 2012

Contents

Outline of SAJ: Activities and Membership

The Society for Actinomycete Japan (SAJ) was established in 1955 and authorized as a scientific organization by Science Council of Japan in 1985. The Society for Applied Genetics of Actinomycetes, which was established in 1972, merged in SAJ in 1990. SAJ aims at promoting actinomycete researches as well as social and scientific exchanges between members domestically and internationally. The **Activities of SAJ** have included annual and regular scientific meetings, workshops and publications of The Journal of Antibiotics (the official journal, joint publication with Japan Antibiotics Research Association), Actinomycetologica (Newsletter) and laboratory manuals. Contributions to International Streptomyces Project (ISP) and International Symposium on Biology of Actinomycetes (ISBA) have also been SAJ's activities. In addition, SAJ have occasional special projects such as the publication of books related to actinomycetes: "Atlas of Actinomycetes, 1997", "Identification Manual of Actinomycetes, 2001" and "Digital Atlas of Actinomycetes, 2002" (http://www.nih.go.jp/saj/ DigitalAtlas/). These activities have been planned and organized by the board of directors with association of executive committees consisting of active members who belong to academic and nonacademic organizations.

The **SAJ Memberships** comprise **active members, student members, supporting members and honorary members**. Currently (as of Mar. 31, 2012), SAJ has about 330 active members including student members, 22 oversea members, 11 honorary members, 5 oversea honorary members, 1 special member and 12 supporting members. The SAJ members are allowed to join the scientific and social meetings or projects (regular and specific) of SAJ on a membership basis and to browse The Journal of Antibiotics from a link on the SAJ website and will receive each issue of Actinomycetologica, currently published in June and December. Actinomycete researchers in foreign countries are welcome to join SAJ. For application of SAJ membership, please contact the SAJ secretariat (see below). Annual membership fees are currently 5,000 yen for active members, 3,000 yen for student members and 20,000 yen or more for supporting members (mainly companies), provided that the fees may be changed without advance announcement.

The current members (April 2012 - March 2014) of the Board of Directors are: Hiroyuki Osada (Chairperson; RIKEN), Masayuki Hayakawa (Vice Chairperson; Yamanashi Univ.), Kenji Ueda (Secretary General; Nihon Univ.), Kenji Arakawa (Hiroshima Univ.), Koji Ichinose (Musashino Univ.), Masayuki Igarashi (Inst. Microb. Chem.), Haruo Ikeda (Kitasato Univ.), Fumio Kato (Toho Univ.), Masaaki Kizuka (Daiichi Sankyo RD Novare Co., Ltd.), Hideyuki Muramatsu (Astellas Res. Technol. Co., Ltd.), Susumu Okamoto (NFRI), Masahiro Sota (Nagase & Co., Ltd.), Ken-ichiro Suzuki (NITE), and Tomohiro Tamura (AIST).

The members of the Advisory Board are: Kunimoto Hotta, Kozo Ochi, Shinji Miyado, Yoko Takahashi, and Keiko Ochiai.

The SAJ Secretariat
c/o Kitasato Institute for Life Sciences
Kitasato University
5-9-1 Shirokane, Minato-ku,
Tokyo 108-8641, Japan
E-mail: saj@lisci.kitasato-u.ac.jp
Phone & Fax: +81-3-5791-6133

Award Lecture

Regulatory mechanisms of light-inducible transcription in non-phototrophic bacteria

Hideaki Takano

Life Science Research Center, College of Bioresource Sciences, Nihon University,
1866 Kameino, Fujisawa 252-0880, Japan
(Received Nov. 7, 2012)

INTRODUCTION

The ability of bacteria to respond and adapt to a variety of physiological and chemical stresses plays an important role in ensuring that they survive and thrive in their natural environments. Light is an environmental stress and stimulus that affects many living organisms, including many prokaryotes. In several bacteria, carotenoid production occurs in a light-dependent manner to protect cells from harmful oxygen radicals, thereby preventing oxidative stress[1]. Genetic studies of light-inducible carotenoid production in bacteria have been described only for *Myxococcus xanthus*[2-4]. Herein, I describe the molecular mechanism of light-inducible transcription by non-phototrophic bacteria, including *Streptomyces coelicolor* A3(2)[1,5] and *Thermus thermophilus* HB27[6]. I also describe the wide distribution of the LitR/CarH family, which acts as central regulators with photosensory functions in light-inducible carotenogenesis[7].

1. The regulatory mechanism of light-inducible carotenoid production in *Streptomyces coelicolor* A3(2)[5]

Originally, we discovered that *S. coelicolor* A3(2), a gram-positive soil bacterium renowned for its ability to produce a variety of secondary metabolites, produces carotenoids (*crt*) in response to illumination. The biosynthetic gene cluster of *S. coelicolor* consists of 2 convergent operon structures, *crtEIBV* and *crtYTU* (Fig. 1)[8]. The *crt* gene cluster is flanked by 2 transcriptional regulators, a MerR family transcriptional regulator *litR* (light-induced transcription; regulator), and an RNA polymerase ECF sigma factor, named *litS*. The LitR protein contains an *N*-terminal helix-turn-helix domain and a *C*-terminal cobalamin (Cbl, synonym, vitamin B12)-binding domain.

Our preliminary transcriptional analysis confirmed that transcription of the *crtE*, *crtY*, *litR*, and *litS* genes occurs in a light-inducible manner in *S. coelicolor* A3(2). This indicates that photoinducible carotenoid production is controlled at the transcriptional level. We then studied the role of LitR and LitS in the regulation of carotenoid production in *S. coelicolor* A3(2). The phenotypic and transcriptional analyses of *litR* and *litS* knockout mutants demonstrated that LitR acts as an essential transcriptional activator of the *litS* promoter in the light, whereas LitS serves as an RNA polymerase sigma factor that recognizes *crt* promoters. *In vitro* run-off transcriptional assays support the biochemical function of LitS; RNA polymerase containing σ^{LitS} directs the mRNA synthesis initiating from the *crt* promoters.

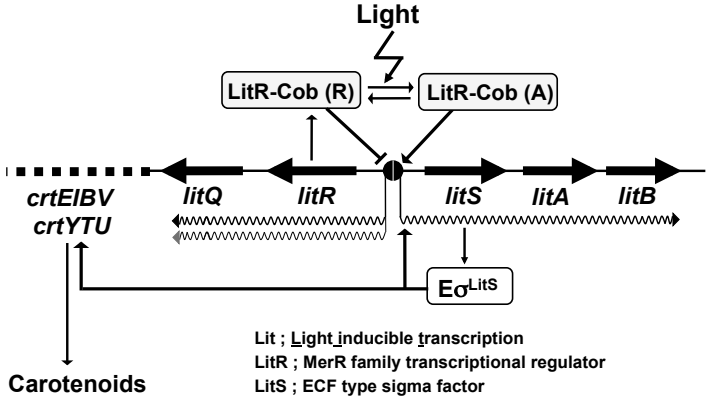

Fig. 1. Hypothetical model describing light-dependent transcriptional control of carotenoid production in *Streptomyces coelicolor* A3(2). LitR negatively regulates the transcription of both *litR* and *litS*. In the light, a change in the function of LitR from a repressor to an activator due to an unknown mechanism results in the expression of the RNA polymerase sigma factor LitS, which in turn activates the transcription of 2 convergent operons of the *crt* biosynthetic gene cluster.

Given that the activity of LitS is not affected by light, LitS does not have a photosensory function, and this is consistent with its high similarity to other sigma factors across its entire length.A minimal gene set required for light-inducible transcription was identified in *S. griseus* IFO13350 as a heterologous host because *S. griseus* encodes a *crt* biosynthesis gene cluster but does not produce carotenoids[9]. A melanin reporter plasmid, pQRS, which contains the *litR* and *litS* region, was used to monitor light-dependent transcription as melanin production. An *S. griseus* strain that harbored pQRS, produced the melanin pigment in light conditions, but not in dark conditions(7). This result showed that *litR* and *litS* constitute a minimal gene set sufficient for light-responsive transcription, and it suggests that LitR may also serve as a photosensor, given the end-to-end similarity of the LitS primary sequence with that of a typical sigma factor.

The MerR family proteins are known for their specific ligand binding, which affects their affinity for the target DNA[10]. Therefore, it is assumed that the activity of LitR depends on the binding of Cbl. We then generated a null mutant lacking *cobDQN*, which is involved in the early steps of Cbl biosynthesis. The *cob* mutant showed low-level production of carotenoids under both light and dark conditions. This phenotype was rescued by the addition of 10 nM methylcobalamin to the media. These results clearly showed that intracellular Cbl synthesis is essential for light-induced carotenoid production in this bacterium. In the course of the study on the role of Cbl, we found that a significant amount of Cbl was detected in the culture supernatant of *S. coelicolor* A3(2), which indicates that Cbl is a secondary metabolite, as discussed in the CONCLUSION. Taken together, our genetic study revealed that LitR is involved in the light-induced transcription of *litS*, which directs the transcription of the *crt* operon. Furthermore, LitR may serve as a photosensor by receiving light mediated by Cbl.

2. The molecular mechanism for photoresponses in a gram-negative bacterium, *Thermus thermophilus* HB27[6]

We found that the genome of the extremely thermophilic and gram-negative bacterium *T. thermophilus* HB27 encode a similar protein (TT_P0056 designated LitRtth) to LitR of *S. coelicolor*[11]. This information lead to our finding that this bacterium also shows light-inducible carotenoids production. We thus set out to elucidate the role of *litRtth* in the regulatory mechanism. As shown in Fig. 2, *litRtth* is flanked by the *crt* operon, and comprises a possible operon structure, with downstream coding sequences that encode a cyclic AMP receptor protein (CRP)/fumarate and a nitrate reduction regulator family transcriptional regulator LdrP (TT_P0055)[12]. The phenotypic and transcriptional analysis of knockout mutants for *litRtth* and *ldrP* showed that whereas LitRtth functions as a repressor, LdrP activates *crt* biosynthesis. We verified the biochemical function of the LitRtth and LdrP proteins of *T. thermophilus*, which were stably expressed and prepared as a soluble protein in an *Escherichia coli* expression system. DNase I footprint analysis revealed that LitRtth binds to the intergenic region of *litR* and *crtB*, corresponding to the positions -55 to -94 with respect to the transcriptional start point of *crtB*. The results of

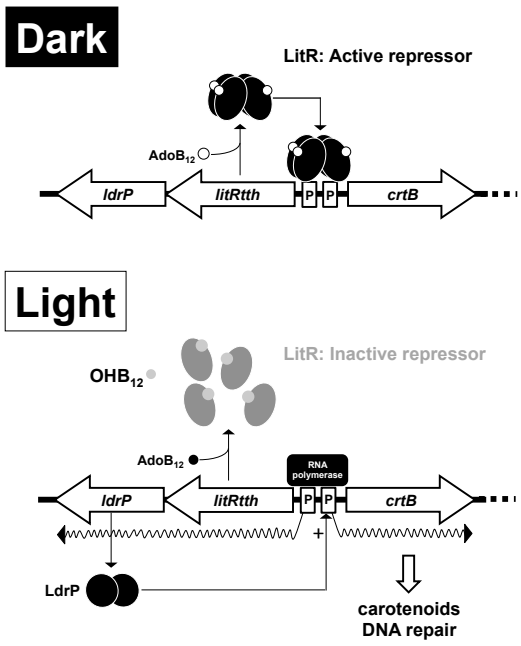

Fig. 2. Model of the light-inducible switch controlled by the light-sensitive regulator LitR. The tetrameric AdoB12-LitRtth complex binds the intergenic region of *litR-crtB* to repress divergent transcriptional initiation. The conversion of AdoB12 to OH12 of LitRtth caused by illumination induces a conformational change in LitRtth, which allows RNA polymerase to access the *litR* and *crtB* promoters. Substantial induction of *crtB* is required for the presence of LdrP, a CRP-like activator protein.

in vitro run-off transcriptional assays support the notion that LdrP activates *crt* biosynthesis; the RNA polymerase holoenzyme requires the LdrP protein to synthesize mRNA from the *crtB* promoter. This assay also demonstrated the function of LitRtth as a repressor: LitRtth prevented LdrP-mediated transcriptional initiation by the RNA polymerase holoenzyme (Fig. 2).

Recently, Ortiz-Guerrero *et al.* showed that CarH of *M. xanthus*, which is a homolog of LitR, is involved in light-inducible carotenoid production[13]. They also reported that a chimera protein, CTt2, which is composed of the N-terminal DNA-binding domain of CarH and the C-terminal Cbl-binding domain of LitRtth of *T. thermophilus* HB8, is an adenosyl B12 (AdoB12)-binding transcriptional regulator with light-sensitive DNA-binding activity. The light sensitivity of the CTt2 protein results from the photolysis of AdoB12 because of the light sensitivity of the Co-C bond of AdoB12. The photolysis of the AdoB12-bound CTt2 caused the conversion of AdoB12 into hydroxocobalamin (OHB12), which led to conformational changes in the subunit structures; AdoB12-bound CTt2 forms an oligomer in dark conditions, whereas illuminated AdoB12-bound CTt2 is monomeric in solution. The photolysis of AdoB12 upon illumination also resulted in the loss of its DNA-binding activity. Therefore, the conformation of AdoB12-bound CTt2 is changed upon receiving an illumination signal to control its DNA-binding affinity.

Fig. 2 shows the proposed molecular mechanism of light-inducible carotenogenesis in *T. thermophilus*, which is based on our study and the recent findings of Ortiz-Guerrero *et al*[13]. These studies strongly reinforce our view that the members of the LitR/CarH family of proteins are novel photosensors that are distributed in diverged bacterial genera as described further. Three-dimensional structures of the LitR/CarH family in both dark and light states will provide critical information about its ability to carry out $AdoB_{12}$-dependent photoregulation.

3. Wide distribution of the LitR/CarH family in non-phototrophic bacteria[7]

A genomic database search revealed that LitR/CarH family members are widely distributed among the phylogenetically diverged genera of non-phototrophic bacteria. These include not only *Actinobacteria* but also gram-negative bacteria such as *Pseudomonas*, *Shewanella*, and *Vibrio* spp., in which *litR* genes are frequently flanked by genes that are responsible for *crt* biosynthesis and DNA photolyase (Phr). In this paper, we focused on the distribution and redundancy of LitR/CarH family members in *Actinomycetes* on the basis of their genome information, as shown in Fig. 3. The completed genome sequences indicated that *Streptomyces* spp. have at least one copy of the *litR* homolog in their genome. In contrast to *S. coelicolor*, *litR* of *S. avermitilis* is encoded at a different locus within the *crt* gene cluster[14]. However, *S. avermitilis* exhibited light-inducible carotenoid production (our unpublished data), which implies that the LitR of *S. avermitilis* regulates other genes in addition to the *crt* genes. The LitR/CarH family is also found in the genomes of other *Actinomycetales* such as *Nocardia*, *Rhodococcus*, *Actinoplanes*, and *Micromonospora* spp. Interestingly, some *Actinomycetales* encode multiple *litR* homologs in their genomes: 2 homologs for *Actinosynnema mirum*, a nocardicin producer[15]; 3 homologs for *Kitasatospora setae*, a setamycin producer[16]; and 5 homologs for *Amycolatopsis mediterranei*, a rifamycin producer[17], were present in each genome. The multiplicity of the LitR/CarH family in the genome was also found in *Pseudomonas spp.*, which is a gram-negative bacterium that inhabits a wide variety of environments[18]. The multiplicity of photoreceptor indicates the importance of the photoresponse system with respect to their survival in each niche. Intriguingly, *Rhodococcus jostii*, *A. mirum*, *K. setae*, and *P. putida* did not produce pigmented compounds in response to illumination (our unpublished data), which suggests that the stress response system against illumination of these bacteria differ from that of *S. coelicolor* and *T. thermophilus*.

CONCLUSION

In this paper, I have summarized our studies of the regulatory mechanism of light-inducible transcription in non-phototrophic bacteria. Our genetic studies on bacterial light response showed that members of the LitR family are central regulators of light-inducible carotenoid production in the two different type bacteria, *S. coelicolor* and *T. thermophilus*. Biochemical studies based on our and other group have

indicated that LitR/CarH family is a light-responsive transcriptional regulator and that the light signal is received by the light-sensitive ligand, $AdoB_{12}$. $AdoB_{12}$ is an essential coenzyme for the activity of coenzyme B12-dependent enzymes such as methionine synthase in many organisms, including bacteria, archaea, algae, and animals, whereas $AdoB_{12}$ and its derivatives are produced only by some bacteria and archaea. Genomic information suggests that the distribution of *litR* and the *cbl* synthesis gene does not always occur as a pair in the genome. For example, the soil-dwelling *M. xanthus* partially encodes a biosynthesis gene for Cbl[19], which indicates that the activities of MetH and CarH are dependent on the presence of Cbl or its intermediate in the environment. Indeed, it was previously reported that the exogenous addition of Cbl is required for its photo-dependent carotenoid production in a minimal medium[20]. The co-existence of a Cbl-producer and its non-producer in soil indicates that bacteria such as *Streptomyces* spp. serve as suppliers for Cbl. In contrast, other bacteria such as *M. xanthus* require Cbl, which is necessary for light perception. This implies that Cbl may not only serve as a primary metabolite but also function as a secondary metabolite for symbiotic stress responses in bacteria. We assume that the

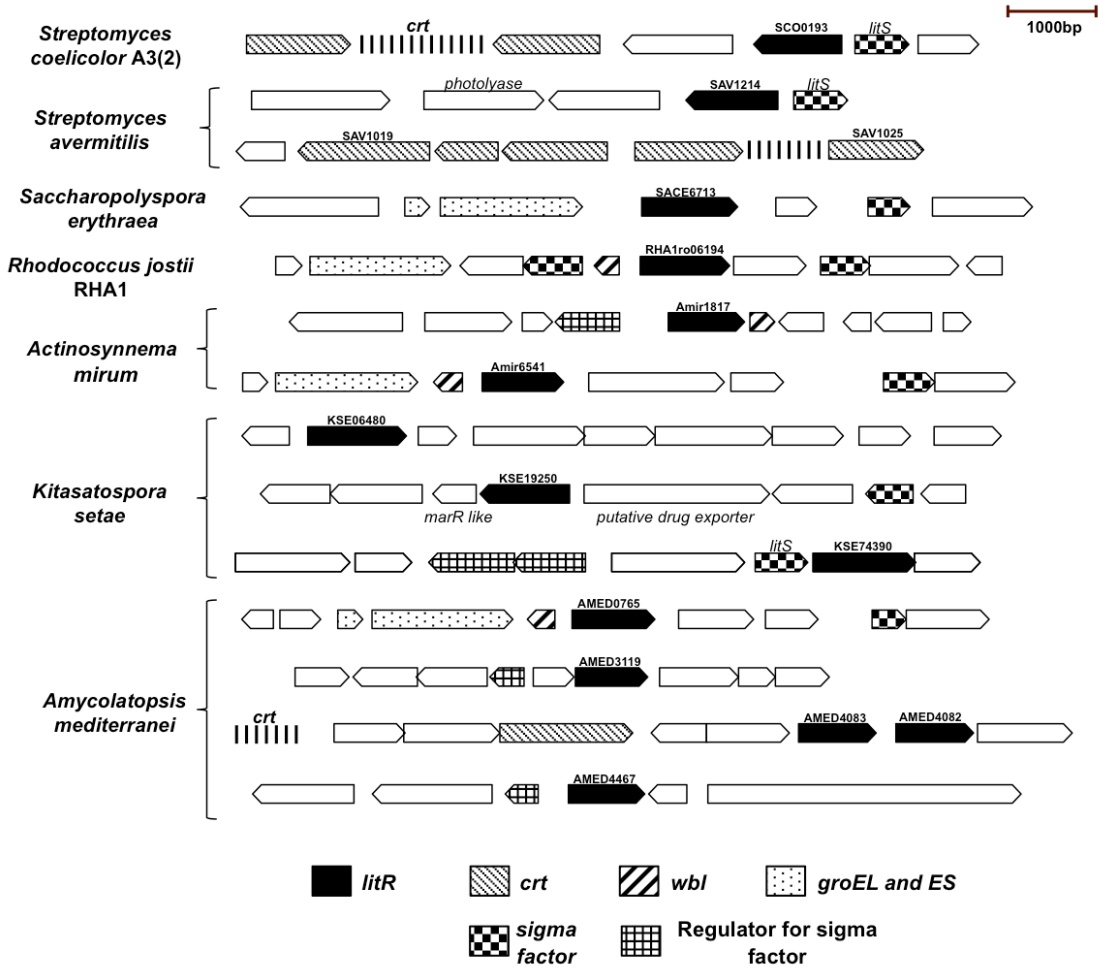

Fig. 3. Schematic representation of the genetic locus of *Actinomycetales* that possess CDSs of LitR/CarH family proteins. The lengths and orientations of the CDSs are indicated by the solid arrows. The multiple CDSs in the carotenoids biosynthesis clusters are shown as dashed lines. The *litRS* cluster exists in *S. avermitilis* at a locus that differs from that of *crt*. The Wbl (WhiB-like) family might function as transcription factors or disulphide reductases with an oxygen-sensitive [4Fe–4S] cluster, which is found exclusively within actinomycetes. Regulator of Sigma factor includes an anti-sigma factor and an anti-anti-sigma factor. For CarH/LitR homologs, the corresponding genome database IDs (the other nine organisms) are shown above the arrows. All the genomic data are available through the KEGG GENES database (http://www.genome.jp/kegg/genes.html).

utilization of Cbl as a vitamin may contribute to the wide distribution of the LitR/CarH family in non-phototrophic bacteria, as predicted from genomic information. The wide distribution of the LitR/CarH family indicates that the ability to sense and respond to light is distributed across a diverse range of non-phototrophic bacteria. The findings that were obtained from our study will provide new insights into the physiology and ecology of non-phototrophic bacteria.

ACKNOWLEDGMENTS

It is my great honor to receive the SAJ Hamada Award for 2012. I am most grateful to Prof. Emeritus Teruhiko Beppu and Associate Prof. Kenji Ueda for their insightful guidance. I would like to acknowledge their constant help and suggestions from late Prof. Sueharu Horinouchi and Prof. Yasuo Ohnishi (The University of Tokyo). I am deeply indebted to Prof. Haruo Ikeda (Kitasato University) for the teaching me many valuable experimental techniques. I would like to express my appreciation for support during this work to all members of the Laboratory of Biotechnology, Life Science Research Center, College of Bioresource Sciences, Nihon University.

REFERENCES

1. Takano, H., Asker, D., Beppu, T., and Ueda, K. (2006) Genetic control for light-induced carotenoid production in non-phototrophic bacteria. *J Ind Microbiol Biotechnol* **33**, 88-93
2. Gorham, H. C., McGowan, S. J., Robson, P. R., and Hodgson, D. A. (1996) Light-induced carotenogenesis in *Myxococcus xanthus*: light-dependent membrane sequestration of ECF sigma factor CarQ by anti-sigma factor CarR. *Mol Microbiol* **19**, 171-186
3. Whitworth, D. E., and Hodgson, D. A. (2001) Light-induced carotenogenesis in *Myxococcus xanthus*: evidence that CarS acts as an anti-repressor of CarA. *Mol Microbiol* **42**, 809-819
4. Pérez-Marín, M., Padmanabhan, S., Polanco, M., Murillo, F., and Elías-Arnanz, M. (2008) Vitamin B12 partners the CarH repressor to downregulate a photoinducible promoter in *Myxococcus xanthus*. *Mol Microbiol* **67**, 804-819
5. Takano, H., Obitsu, S., Beppu, T., and Ueda, K. (2005) Light-induced carotenogenesis in *Streptomyces coelicolor* A3(2): identification of an extracytoplasmic function sigma factor that directs photodependent transcription of the carotenoid biosynthesis gene cluster. *J Bacteriol* **187**, 1825-1832
6. Takano, H., Kondo, M., Usui, N., Usui, T., Ohzeki, H., Yamazaki, R., Washioka, M., Nakamura, A., Hoshino, T., Hakamata, W., Beppu, T., and Ueda, K. (2011) Involvement of CarA/LitR and CRP/FNR family transcriptional regulators in light-induced carotenoid production in *Thermus thermophilus*. *J Bacteriol* **193**, 2451-2459
7. Takano, H., Beppu, T., and Ueda, K. (2006) The CarA/LitR-family transcriptional regulator: Its possible role as a photosensor and wide distribution in non-phototrophic bacteria. *Biosci Biotechnol Biochem* **70**, 2320-2324
8. Bentley, S. D., Chater, K. F., Cerdeno-Tarraga, A. M., Challis, G. L., Thomson, N. R., James, K. D., Harris, D. E., Quail, M. A., Kieser, H., Harper, D., Bateman, A., Brown, S., Chandra, G., Chen, C. W., Collins, M., Cronin, A., Fraser, A., Goble, A., Hidalgo, J., Hornsby, T., Howarth, S., Huang, C. H., Kieser, T., Larke, L., Murphy, L., Oliver, K., O'Neil, S., Rabbinowitsch, E., Rajandream, M. A., Rutherford, K., Rutter, S., Seeger, K., Saunders, D., Sharp, S., Squares, R., Squares, S., Taylor, K., Warren, T., Wietzorrek, A., Woodward, J., Barrell, B. G., Parkhill, J., and Hopwood, D. A. (2002) Complete genome sequence of the model actinomycete *Streptomyces coelicolor* A3(2). *Nature* **417**, 141-147
9. Ohnishi, Y., Ishikawa, J., Hara, H., Suzuki, H., Ikenoya, M., Ikeda, H., Yamashita, A., Hattori, M., and Horinouchi, S. (2008) Genome sequence of the streptomycin-producing microorganism *Streptomyces griseus* IFO 13350. *J Bacteriol* **190**,

4050-4060

10. Brown, N. L., Stoyanov, J. V., Kidd, S. P., and Hobman, J. L. (2003) The MerR family of transcriptional regulators. *FEMS Microbiol Rev* **27**, 145-163
11. Henne, A., Brüggemann, H., Raasch, C., Wiezer, A., Hartsch, T., Liesegang, H., Johann, A., Lienard, T., Gohl, O., Martinez-Arias, R., Jacobi, C., Starkuviene, V., Schlenczeck, S., Dencker, S., Huber, R., Klenk, H. P., Kramer, W., Merkl, R., Gottschalk, G., and Fritz, H. J. (2004) The genome sequence of the extreme thermophile Thermus thermophilus. *Nat Biotechnol* **22**, 547-553
12. Agari, Y., Kuramitsu, S., and Shinkai, A. (2012) X-ray crystal structure of TTHB099, a CRP/FNR superfamily transcriptional regulator from Thermus thermophilus HB8, reveals a DNA-binding protein with no required allosteric effector molecule. *Proteins* **80**, 1490-1494
13. Ortiz-Guerrero, J. M., Polanco, M. C., Murillo, F. J., Padmanabhan, S., and Elías-Arnanz, M. (2011) Light-dependent gene regulation by a coenzyme B12-based photoreceptor. *Proc Natl Acad Sci U S A* **108**, 7565-7570
14. Ikeda, H., Ishikawa, J., Hanamoto, A., Shinose, M., Kikuchi, H., Shiba, T., Sakaki, Y., Hattori, M., and Omura, S. (2003) Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis. *Nat Biotechnol* **21**, 526-531
15. Land, M., Lapidus, A., Mayilraj, S., Chen, F., Copeland, A., Del Rio, T. G., Nolan, M., Lucas, S., Tice, H., Cheng, J. F., Chertkov, O., Bruce, D., Goodwin, L., Pitluck, S., Rohde, M., Göker, M., Pati, A., Ivanova, N., Mavromatis, K., Chen, A., Palaniappan, K., Hauser, L., Chang, Y. J., Jeffries, C. C., Brettin, T., Detter, J. C., Han, C., Chain, P., Tindall, B. J., Bristow, J., Eisen, J. A., Markowitz, V., Hugenholtz, P., Kyrpides, N. C., and Klenk, H. P. (2009) Complete genome sequence of Actinosynnema mirum type strain (101). *Stand Genomic Sci* **1**, 46-53
16. Ichikawa, N., Oguchi, A., Ikeda, H., Ishikawa, J., Kitani, S., Watanabe, Y., Nakamura, S., Katano, Y., Kishi, E., Sasagawa, M., Ankai, A., Fukui, S., Hashimoto, Y., Kamata, S., Otoguro, M., Tanikawa, S., Nihira, T., Horinouchi, S., Ohnishi, Y., Hayakawa, M., Kuzuyama, T., Arisawa, A., Nomoto, F., Miura, H., Takahashi, Y., and Fujita, N. (2010) Genome sequence of Kitasatospora setae NBRC 14216T: an evolutionary snapshot of the family Streptomycetaceae. *DNA Res* **17**, 393-406
17. Zhao, W., Zhong, Y., Yuan, H., Wang, J., Zheng, H., Wang, Y., Cen, X., Xu, F., Bai, J., Han, X., Lu, G., Zhu, Y., Shao, Z., Yan, H., Li, C., Peng, N., Zhang, Z., Zhang, Y., Lin, W., Fan, Y., Qin, Z., Hu, Y., Zhu, B., Wang, S., Ding, X., and Zhao, G. P. (2010) Complete genome sequence of the rifamycin SV-producing Amycolatopsis mediterranei U32 revealed its genetic characteristics in phylogeny and metabolism. *Cell Res* **20**, 1096-1108
18. Silby, M. W., Winstanley, C., Godfrey, S. A., Levy, S. B., and Jackson, R. W. (2011) Pseudomonas genomes: diverse and adaptable. *FEMS Microbiol Rev* **35**, 652-680
19. Goldman, B. S., Nierman, W. C., Kaiser, D., Slater, S. C., Durkin, A. S., Eisen, J. A., Eisen, J., Ronning, C. M., Barbazuk, W. B., Blanchard, M., Field, C., Halling, C., Hinkle, G., Iartchuk, O., Kim, H. S., Mackenzie, C., Madupu, R., Miller, N., Shvartsbeyn, A., Sullivan, S. A., Vaudin, M., Wiegand, R., and Kaplan, H. B. (2006) Evolution of sensory complexity recorded in a myxobacterial genome. *Proc Natl Acad Sci U S A* **103**, 15200-15205
20. Cervantes, M., and Murillo, F. J. (2002) Role for vitamin B(12) in light induction of gene expression in the bacterium Myxococcus xanthus. *J Bacteriol* **184**, 2215-2224

Publication of Award Lecture

The Society for Actinomycetes Japan Hamada Award 2011,
Dr. Motoki Takagi
Japan Biological Informatics Consortium (JBIC), Tokyo, Japan
"Construction of a natural product library containingsecondary metabolites produced by actinomycetes"
Motoki Takagi and Kazuo Shin-ya, **The Journal of Antibiotics (2012) 65, 443–447**

The Society for Actinomycetes Japan Hamada Award 2012,
Dr. Hideaki Takano
Life Science Research Center, College of Bioresource Sciences, Nihon University
"Regulatory mechanisms of light-inducible transcription in non-phototrophic bacteria"
Hideaki Takano, **Actinomycetlogica (2012) 17, S3-S8**

The 2012 Annual Meeting of the Society for Actinomycetes Japan (SAJ2012)

Chairperson: Masahiro Natsume (Tokyo University of Agriculture and Technology)

General Information

Dates: September 6 (Thu) – 7 (Fri), 2012

Venue: Fuchu-no-mori Art Theater

1-12 Sengen-Cho, Fuchu 183-0001, Japan

TEL: +81-42-335-6211 http://www.fuchu-cpf.or.jp/theater/

Scientific Program

September 6 (Thursday)

9:40 Opening Remarks

9:45 Contributed Papers

O-1 Diversity in genome structure among closely related *Frankia* strains

○Kucho, K.[1], Sasakawa, H.[2], Yamanaka, T.[3] and Uchiumi, T.[1]

([1]Grad. Sch. Sci. Eng., Kagoshima Univ., [2]Facl. Agric., Okayama Univ., [3]Forestry Forest Prod. Res. Inst.)

O-2 Insight into the relation of antibiotic-production and phylogenetic-classification of *Rhodococcus erythropolis*

○Kitagawa, W.[1,2] and Tamura, T.[1,2]

([1]Bioproduction Res. Inst., AIST, [2]Grad. Sch. Agric., Hokkaido Univ.)

O-3 Studies on the isolation and classification of actinomycetes belonging to the family *Demequinaceae* from marine sediments

○Hamada, M.[1,2], Tamura, T.[1], Yamamura, H.[2], Hayakawa, M.[2] and Suzuki, K.[1]

([1]Biological Resource Center, NITE (NBRC), [2] Div. Appl. Biol. Sci., Univ. Yamanashi)

O-4 Various properties of actinomycetes distributed in Ogasawara Island, oceanic islands

○Harunari, E.[1], Imada, C.[1], Horikoshi, K.[2], Suzuki, H.[2], Sasaki, T.[2], Terahara, T.[1], Kobayashi, T.[1]

([1]Grad. Sch. Marine Sci. Technol., Tokyo Univ. Marine Sci. Technol., [2]Inst. BONINOLOGY)

O-5 Structures and biosynthesis of a-and g-pyrones from a marine-derived *Nocardiopsis*

○Kim, Y., Ogura, H. and Igarashi, Y.

(Toyama Pref. Univ. Eng.)

10:45 Break

10:55 The SAJ Plenary Meeting

11:25 **Awarding Ceremony**

SAJ Award

Chemotaxonomic study of actinomycetes and Biological Resource Center

Dr. Ken-ichiro Suzuki

(NBRC, National Institute of Technology and Evaluation)

Hamada Award

Studies on Regulatory Mechanisms of Stress Responses in *Streptomyces*

Dr. Hideaki Takano (College of Bioresource Sciences, Nihon University)

Hamada Award

Physiological and molecular characterization of drug resistance mutations that develop the potential of actinomycetes to produce secondary metabolites and its application to antibiotic discovery

Dr. Takeshi Hosaka (Department of Bioscience and Biotechnology, Faculty of Agriculture, Shinsyu University)

11:45 **Awardee's Lectures**

Hamada Award

Dr. Hideaki Takano

Hamada Award

Dr. Takeshi Hosaka

12:35 Lunch

13:45 **Short Presentations for Poster Session (odd numbers)**

15:15 **Poster Session (odd numbers)**

16:15 **Invited Lectures**

Molecular interaction and coevolution of tomato and tomato wilt fungus, *Fusarium oxysporum* f. sp. *lycopersici*

Dr. Tsutomu Arie

(Institute of Agriculture, Tokyo University of Agriculture and Technology)

Insect pathogens as biological control agents: Current developments and future perspectives

Dr. Yasuhisa Kunimi

(Institute of Agriculture, Tokyo University of Agriculture and Technology)

17:45 Break

18:00 Reception

September 7 (Friday)

9:30 Contributed Papers

O-6 Identification and characteristic analysis of a novel erythromycin resistance mutation that develops the potential to produce antibiotics in *Streptomyces* strains

○Imai, Y.[1], Watanabe, K.[2], Ayaki, K.[3], Ochi, K.[4] and Hosaka, T.[3]

([1]Interdisc. Grad. Sch. Sci. Technol., Shinshu Univ., [2]Grad. Sch. Agric. Shinshu Univ., [3]Fac. Agric. Shinshu Univ., [4]Fac. Life Sci. Hiroshima Inst. Technol.)

O-7 Analysis of phosphorylation sites on AfsR which activates secondary metabolism in *Streptomyces coelicolor* A3(2)

○Shin, T., Tanaka, A., Horinouchi, S. and Ohnishi, Y.

(Dept.Biotechnol., Grad. Sch. Agric. Life Sci., Univ. Tokyo)

O-8 Disruption of terminal respiratory chain causes unusual accumulation of ATP and suppression of differentiation

○Fujimoto, M., Takano, H. and Ueda, K.

(College of Bioresource Sci., Nihon Univ.)

O-9 An acetyltransferase involved in aerial mycelium formation in *Streptomyces griseus*

○Katsumata, N., Takano, H. and Ueda, K.

(College of Bioresource Sci., Nihon Univ.)

10:20 **Short Presentations for Poster Session (even numbers)**

11:30 **Poster Session (even numbers)**

12:30 Lunch

13:30 **Awardee's Lectures**

SAJ Award

Dr. Ken-ichiro Suzuki

14:00 Contributed Papers

O-10 Succinylation of tertiary alcohol in reveromycin biosynthesis

○Takahashi, S., Miyazawa, T., Kumano, T., Oowada, E., Takagi, H., Uramoto, M., Shimizu, T. and Osada, H.

(Chem. Biol., Dept., RIKEN ASI)

O-11 Identification of small molecules inducing reveromycin production

○Panthee, S., Takahashi, S., Hayashi, T., Shimizu, T., Muroi, M., Nogawa, T., Futamura, Y. and Osada, H.

(Chem. Biol., Dept., RIKEN ASI)

O-12 Molecular mechanism for the *O*-ureido-L-serine synthesizing activity of an enzyme found in the D-cycloserine biosynthetic pathway

○Uda, N., Matoba, Y., Oda, K., Noda, M., Kumagai, T. and Sugiyama, M.

(Grad. Sch. Biomed. Health Sci., Hiroshima Univ.)

O-13 Crystallographic study to provide the substrate specificity of an L-serine acetylating enzyme found in the D-cycloserine biosynthetic pathway
○Oda, K., Matoba, Y., Kumagai, T., Noda, M. and Sugiyama, M.
(Grad. Sch. Biomed. Health Sci., Hiroshima Univ.)

14:50 Break

15:00 Contributed Papers

O-14 Genome mining in *Actinomycetales* strains: Discovery of genes involving biosynthesis of mycosporine-like amino acids
○Miyamoto, K. T., Komatsu, M., and Ikeda, H.
(Kitasato Inst. for Life Sci., Kitasato Univ.)

O-15 Functional characterization by swapping labdan-type diterpene synthase genes
○Yamada, Y., Nishide, T., Miyano, K. and Ikeda, H.
(Kitasato Inst. for Life Sci., Kitasato Univ.)

O-16 Analysis of the benzastatin biosynthetic enzymes
○Hayashi, T.[1], Takagi, M.[2] , Kazuo Shin-ya, K.[3] and Yasuo Ohnishi, Y.[1]
([1]Univ. Tokyo, [2]JBIC, [3]AIST)

O-17 Chemoenzymatic synthesis of the ST derivative compounds using the ST biosynthetic enzymes
○Maruyama C.[1], Toyoda J.[1], Katano H.[1], Kato Y.[2], Izumikawa M.[3], Takagi M.[3], Shin-ya K.[4], Utagawa T.[1] and Hamano Y.[1]
([1]Fukui Pref. Univ., [2]Toyama Pref. Univ., [3]JBIC, [4]AIST)

O-18 Function analysis of the streptomycin exporter StrVW in *Streptomyces griseus*
Nanamiya, H., ○Mouri, Y. and Ohnishi, Y.
(Dept. Biotechnol., Grad. Sch. Agric. Life Sci., Univ. Tokyo)

16:00 Awarding Ceremony (Poster Award)
Closing Remarks

Poster Session

P-1 Isolation of new species belonging to genera *Friedmanniella* and *Microlunatus* from spider samples and characteristics of their membrane lipid constituents
○Iwai, K., Iwamoto, S., Katahira, R., Onodera, H. and Suzuki, M.
(Res. Div., Kyowa Hakko Kirin Co., Ltd)

P-2 Isolation of actinomycetes from deep-sea core samples
Ulanova, D.
(Sci. Res. Center, Kochi Univ.)

P-3 Taxonomic study of a novel actinomycete strain isolated from plant roots
○Kawaguchi, Y.[1], Matsumoto, A.[2], Ōmura, S.[2] and Takahashi, Y.[1,2]
([1]Grad. Sch. Infection Control Sci., [2]Kitasato Inst. Life Sci., Kitasato Univ.)

P-4 Taxonomic study of endophytic actinomyces isolated from vegetables
○Matsumura, N., Ishihara, M. and Tokuyama, S.
(Fac. Agric., Shizuoka Univ.)

P-5 Taxonomic studies of *Streptomyces* sp. OM-6519 producing lactacystin and *Streptomyces* sp. K04-0144 producing cyslabdan
○Také, A.[1], Matsumoto, A.[2], Ōmura, S.[2] and Takahashi, Y.[1,2]
([1]Grad. Sch. Infection Control Sci., [2]Kitasato Inst. Life Sci., Kitasato Univ.)

P-6 A Taxonomic study of the genus *Actinoplanes* using a genotyping method
○Shimizu, A.[1], Yamamura, H.[1], Nakagawa, Y.[1], Hamada, M.[2], Otoguro, M.[2], Tamura, T.[2] and Hayakawa, M.[1]
([1]Div. Appl. Biol. Sci. , Univ. Yamanashi, [2]NITE Biol. Res. Center (NBRC))

P-7 Diversity and phylogenetic evaluation of flagellin genes in motile actinomycetes
○Ueda, M.[1], Yamamura, H.[1], Hanawa, K.[1], Shimizu, A.[1], Nakagawa, Y.[1], Hamada, M.[2], Otoguro, M.[2], Tamura, T.[2] and Hayakawa, M.[1]
([1]Div. Appl. Biol. Sci. , Univ. Yamanashi, [2]NITE Biol. Res. Center (NBRC))

P-8 Phytotoxins produced by *Streptomyces turgidiscabies* strains
○Okaniwa, N.[1], Nagagata, A.[1], Valkonen, J. P. Y.[2], Kawaide, H.[1] and Natsume, M.[1]

([1]Grad. Sch. Agric. , Tokyo Univ. Agric. Technol, [2]Univ. Helsinki)

P-9 Stereochemistry of actinomycetal cytotoxin rakicidin A
○Matoba, S., Oku, N., Miyanaga, K., Shimasaki, R. and Igarashi, Y.
(Biotechnol. Res. Center, Toyama Pref. Univ.)

P-10 Isolation and identification of berninamycin E from *Streptomyces atroolivaceus*
○Ninomiya, A.[1] and Kodani, S.[1,2]
([1]Grad. Sch. Agric., Shizuoka Univ., [2]Grad. Sch. Sci. Tech., Shizuoka Univ.).

P-11 Isolation and structural determination of new anti-yeast compound from the newly isolated *Streptomyces* sp. MK-30
○Hidaki, M.[1], Murao, A.[2], Sato, K.[1], Ogawa, N.[2] and Kodani, S.[1,3]
([1]Grad. Sch. Agric., Shizuoka Univ., [2]Fac. Agric., Shizuoka Univ., [3]Grad. Sch. Sci. Tech., Shizuoka Univ.)

P-12 Bioconversion of FR901459, a novel derivative of cyclosporin A, by *Lentzea* sp. No.7887
○Sasamura S.[1] Kobayashi M.[1] Muramatsu H.[2] Takase S.[1] Shibata T.[1] and Hashimoto M.[2]
([1]Astellas Pharma Inc., [2]Astellas Res. Technol. Co., Ltd.)

P-13 The structures and activities of new anti-invasive compounds from *Streptomyces* sp.
○Yu L.[1], Trujillo, M. E.[2], Miyanaga, S.[3], Ikuo Saiki, I.[3] and Igarashi, Y.[1]
([1]Toyama Pref. Univ., [2]Mahidol Univ., [3]Univ. Toyama)

P-14 Studies on isolation, structure determination and biosynthesis of a new naphthoquinone compound, JBIR-85
○Izumikawa M.[1], Motohashi K.[1], Satou R.[2], Nagai A.[3], Ohnishi Y.[2], Takagi M.[1] and Shin-ya K.[4]
([1]JBIC, [2]Univ. Tokyo, [3]Technol. Res. Association for Next generation natural products chemistry, [4]AIST)

P-15 Various properties of a hyaluronidase inhibitor produced by marine streptomycete
○Harunari, E.[1], Imada, C.[1], Terahara, T.[1], Kobayashi, T.[1] and Igarashi, Y.[2]
([1]Grad. Sch. Marine Sci. Technol., Tokyo Univ. Marine Sci. Technol., [2]Toyama Pref. Univ.)

P-16 Screening of Quorum sensing inhibitor derived from *Streptomyces* spp.
○Ooka, K., Fukumoto, A., Sugi, S., Shimada, K., Yamanaka, C., Ishihara, R., Anzai, Y. and Kato, F.
(Fac. Pharmaceutical Sci., Toho Univ.)

P-17 Genomic information-directed analysis of secondary metabolites in the genus *Gordonia*
○Fukuda T.[1], Komaki H.[2], Suzuki K.[2] and Igarashi Y.[1]
([1]BRC, Toyama pref. Univ., [2]NBRC, NITE)

P-18 Temperature-dependent metabolic change and exhaustive metabolite analysis in Thai endophytic *Microbispora*
○Akiyama, H.[1], Oku, N.[1], Indanada, C.[2], Thamchaipenet, A.[2] and Igarashi, Y.[1]
([1]Toyama Pref. Univ., [2]Kasetsart Univ.)

P-19 Secondary metabolites of *Thermosporothrix hazakensis*, a thermophilic spore-forming bacterium of the phylum *Chloroflexi*
○Yamamoto, K., Oku, N. and Igarashi, Y.
(Toyama Pref. Univ.)

P-20 Search for novel microbial products from actinomycete strains in plants by chemical screening
○Okuyama, R.[1], Nakashima, T.[2], Matsumoto, A.[3], Ōmura, S.[3], Takahashi, Y.[1, 3]
([1]Grad. Sch. Infect. Cont. Sci., [2]Res. Organi. Infect. Cont. Sci., [3]Kitasato Inst. Life Sci., Kitasato Univ.)

P-21 Large-scale and wide-range library construction of biosynthesis gene cluster from actinomycetes
○Kozone, I.[1], Sakai, N.[2], Suzuki, M.[2], Nishida, M.[2], Nagai, A.[2], Shiraishi, K.[2], Hashimoto, J.[1], Takagi, M.[1] and Shin-ya, K.[3]
([1]JBIC, [2] Technol. Res. Association for Next generation natural products chemistry, [3]AIST)

P-22 Mode of action study of a new broad spectrum antibiotic, Amycolamicin
○Ishizaki, Y., Hashizume, H., Hayashi, C., Igarashi, M., Adachi, H., Nishimura, Y. and Nomoto, A.
(Inst. Microb. Chem.)

P-23 Molecular mechanism for the copper transportation to tyrosinase assisted by a metallochaperone, caddie
○Matoba, Y., Bando, N., Oda, K., Noda, M., Higashikawa, F., Kumagai, T. and Sugiyama, M.

(Grad. Sch. Biomed. Health Sci., Hiroshima Univ.)

P-24 Structural elucidation of an *in vitro* reaction product of the *Rhodospillirum centenum* type III PKS

○Sugai, Y., Awakawa, T., Katsuyama, Y. and Ohnishi, Y.
(Dept. Biotechnol., Grad. Sch. Agric. Life Sci., Univ. Tokyo)

P-25 Analysis of 2-alkylmalonyl-CoA biosynthetic pathway

○Miyazawa, T.[1], Takahashi, S.[2], Takagi, H.[2], Uramoto, M.[2] and Osada, H.[1,2]
([1]Dept. Biochem. Mol. Biol., Grad. Sch. Sci. Eng., Saitama Univ., [2]Chem. Biol., RIKEN ASI)

P-26 Production of mycinosyl-izenamicin by the engineered *Micromonospora* sp. TPMA0041

○Sakai, A.[1], Mitsumori, A.[1], Aida, K.[1], Kinoshita, K.[2], Anzai, Y.[1] and Kato, F.[1]
([1]Fac. Pharmaceutical Sci. Toho Univ., [2]Sch. Pharmaceutical Sci., Mukogawa Women's Univ.)

P-27 Isolation and the biosynthesis gene cluster of antifungal pentamycin from the *Streptomyces rochei* mutant

○Kataoka, Y.[1], Yoshida, R.[1], Cao, Z.[1], Ishikawa, J.[2], Kinashi, H.[1] and Arakawa, K.[1]
([1]Dept. Mol. Biotechnol., Grad. Sch. AdSM, Hiroshima Univ., [2]NIID)

P-28 Functional studies of two-component flavin-dependent monooxygenases involved in the benzo-isochromanequinone biosyntheses

Odaki, H.[1], Shinozaki, M.[1], Taguchi, T.[1], Okamoto, S.[1,2] and ○Ichinose, K.[1]
([1]Musashino University, [2] Natl. Food Res. Inst.)

P-29 *In vitro* conversion of rosamicin biosynthetic intermediates by cytochrome P450 proteins RosC and RosD

○Iizaka, Y., Ichikawa, Y., Takeda, M., Higashi, N., Anzai, Y. and Kato, F.
(Fac. Pharmaceutical Sci. Toho Univ.)

P-30 Identification of the actinorhodin monomer and its related compound from a deletion mutant of the *act*VA-ORF4 gene of *Streptomyces coelicolor* A3(2)

○Taguchi, T.[1], Ebihara, T.[1], Hurukawa, A.[1], Okamoto, S.[1,2] and Ichinose, K.[1]
([1]Musashino University, [2] Natl. Food Res. Inst.)

P-31 Biosynthetic pathway of the signaling molecules SRBs that induce antibiotics production in *Streptomyces rochei*

○Tsuda N., Xie L., Kawahara H., Kinashi H. and Arakawa K.
(Dept. Mol. Biotechnol., Grad. Sch. AdSM, Hiroshima Univ.)

P-32 Colorimetric assay for NRPS adenylation-domain by the formation of molybdopyrophosphate

○Hamano, Y., Maruyama, C. and Katano, H.
(Dept. Biosci., Fukui Pref. Univ.)

P-33 Characterization of DcsA essential in the biosynthesis of D-cycloserine

○Kumagai, T., Takagi, K., Matoba, Y., Noda, M. and Sugiyama, M.
(Grad. Sch. Biomed. & Health Sci., Hiroshima Univ.)

P-34 Functional analysis of *orf*7, a NRPS gene, for the biosynthesis of virginiamycin M

○Hendriyanto, M.R., Kitani S., Ningsih, F. and Nihira, T.
(Int. Center for Biotechnol., Osaka Univ.)

P-35 Lactazole A, a novel ribosome-synthesized thiopeptide and the biosynthetic gene cluster isolated from *Streptomyces lactacystinaeus* OM-6519

○Hayashi, S.[1], Ikeda, H.[2], Ōmura, S.[2], Oku, N.[1], Igarashi, Y.[1] and Onaka H.[1]
([1]Biotech. Res. Center, Toyama Pref. Univ., [2]Kitasato Inst. Life Sci., Kitasato Univ.)

P-36 Production of lantibiotic by using lantibiotic synthetase derived from *Streptomyces* sp. TP-A0584

○Ebata K., Fuhshuku K., Asano Y., Oku N., Igarashi Y. and Onaka H.
(Toyama Pref. Univ.)

P-37 Investigation in biosynthetic pathway of antimycin and production of its novel analogs

○Awakawa, T.[1], Zhang, L.[1], Yan, Y.[3], Ito, T.[2], Asakawa, Y.[2], Liu, W.[3] and Abe, I.[1]
([1]Grad. Sch. Pharmaceutical Sci., Univ. of Tokyo, [2]Fac. Pharmaceutical Sci., Tokushima Bunri Univ., [3]Shanghai Inst.Org. Chem., Chinese Acad. Soc.)

P-38 Studies on the futalosine pathway, a new menaquinone biosynthetic pathway and screening for a specific inhibitor of the pathway

○Ikeda, S.[1], Ikeda, A.[1], Sato, Y.[1], Noike, M.[1], Seto, H.[2] and Dairi, T.[1]

([1]Grad. Sch. Eng., Hokkaido Univ., [2]Appl. Bio-Sci., Tokyo Univ. of Agric.)

P-39 Functional analysis of afsR homologue regulatory gene in Streptomyces acidiscabies producing thaxtomin A

○Son, D.H., Kim, M.J., Park, J.Y., Choi, S.U., and Hwang, Y.I.

(Dept. Food Sci. Biotechnol., Kyungnam Univ., Republic of Korea)

P-40 Comprehensive analysis of factors contributing to the enhanced translational activity during the stationary phase in an antibiotic-overproducing *rpsL*K88E mutant of *Streptomyces coelicolor* A3(2)

○Iwakawa, C.[1], Ochi, K.[2] and Hosaka, T.[3]

([1]Grad. Sch. Agric. Shinshu Univ., [2]Fac. Life Sci. Hiroshima Inst. Technol., [3]Fac. Agric. Shinshu Univ.)

P-41 Identification of a novel lincomycin resistance mutation that provokes antibiotic overproduction in *Streptomyces coelicolor* A3(2)

Wang, G.[1], Tanaka,Y.[2], Hosaka,T.[3], and ○Ochi, K.[2]

([1]Natl. Food Res. Inst., [2]Dept. Life Sci., Hiroshima Inst. Technol., [3]Fac. Agric. Shinshu Univ.)

P-42 Activation of the secondary metabolite-biosynthetic gene clusters by *rpoB* mutants of various actinomycetes

○Tanaka, Y.[1], Hirose, Y.[2], Kugimiya, R.[2], Kasahara , K.[2] and Ochi, K.[1]

([1]Hiroshima Inst. Technol., [2]Neo-Morgan Laboratory Inc.)

P-43 Biodegradation of chitin in soil by *Streptomyces coelicolor* A3(2)

○Nazari, B.[1], Kobayashi, M.[2] and Fujii, T.[1]

([1]Div. Environ. Biofunc., NIAES, [2]Life Environ. Sci., Univ. Tsukuba)

P-44 Analysis of a novel route of b-ketoadipate pathway in *Rhodococcus jostii* RHA1

○Yamanashi, T.[1], Ohishi, N.[1], Torii, H.[2], Hara, H.[2] and Funa, N.[1]

([1]Grad. Sch. Integr. Pharmaceutical and Nutrit. Sci.,Univ. Shizuoka, [2]Grad. Sch. Engineering, Okayama Univ. Sci.)

P-45 Fermentative degradation of hyaluronic acid by a strain of *Sinomonas atrocyanea*

○Nakamura, Y.[1] and Tsuchizaki, N.[2]

([1]JuJu Cosmetics, [2] Japan Microbiological Clinic)

P-46 Identification of *Streptomyces* sp. P4-Ro-7 and effect of plant growth promoting effect in hydroponic culture

○Sasaki, H.[1], Hayashi, Y.[1], Ashizawa, H.[1], Hamada, M.[2], Tamura, T.[2], Yamamura, H.[1] and Hayakawa, M.[1]

([1]Div. Appl. Biol. Sci., Univ. Yamanashi, [2]NITE Biological Resource Center (NBRC))

P-47 Site-directed mutagenesis for the novel type of isonitrile hydratase

○Hashimoto, Y., Sato, H. and Kobayashi, M.

(Grad. Sch. Life and Environ. Sci., Univ. Tsukuba)

P-48 Selective isolation of actinomycetes from marine environments and various properties of alginate lyase (A.L.)-producing strains

○Sakata, K., Imada, C., Kobayashi, T. and Terahara, T.

(Grad. Sch. Marine Sci. Technol., Tokyo Univ. Marine Sci. Technol.)

P-49 Gene cloning and analysis of cellulolytic enzymes in streptomycetes for antibiotic production from cellulosic biomass

○Tomotsune, K.[1], Tsuchida, M.[1], Kasuga, K.[1], Kobayashi, M.[1], Agematsu, H.[2], Ikeda, H.[3] and Kojima, I.[1]

([1]Dept. Biotechnol., Akita Pref. Univ., [2]Akita Natl. College Technol., [3]Kitasato Inst. Life Sci., Kitasato Univ.)

P-50 Construction of a new scheme for isolating useful actinomycetes using transglutaminase gene sequences as a marker

○Nishizawa, M.[1], Date, M.[2], Yokoyama, K.[2], Yamamura, H.[1], Hayakawa, M.[1]

([1]Div. Appl. Biol. Sci., Interdisc. Grad. Sch. Medicine and Engineering, Univ. Yamanashi, [2]Inst. for Innovation, Ajinomoto Co., Inc.)

P-51 High expression of transglutaminase gene derived from *Streptomyces platensis* YK-2 in *Streptomyces* strains

○Cheon, M.Y., Lee S.E., Kim, N.S., Choi, S.U., and Hwang, Y.I.,

(Dept. Food Sci. Biotechnol., Kyungnam Univ., Republic of Korea)

P-52 Introduction of gene cluster for secondary metabolism using liner plasmid SAP1
○Komatsu, M.[1], Kozone, I.[2], Shin-ya, K.[3], Kataoka, M.[4] and Ikeda, H.[1]
([1]Kitasato Univ., Kitasato Inst. Life Sci., [2]JBIC, [3]AIST, [4]Shinshu Univ.)

P-53 Evaluation of the genomic DNA transformation procedure as a general tool for strain construction in *Streptomyces*
○Okamoto, S.[1] and Ochi, K.[2]
([1]Natl. Food Res. Inst., [2]Dept. Life Sci., Hiroshima Inst. Technol.)

P-54 Construction of *Streptomyces* expression vectors that enable production of epitope-tagged proteins
○Yabe, M.,[1,2] Onaka, H.[3], Arai, T.[2] and Okamoto, S.[1]
([1]Natl. Food Res. Inst., [2]Dept. Appl. Biol. Sci., Grad. Sch. Sci. Technol., Tokyo Univ. Sci., [3]Toyama Pref. Univ.)

P-55 Construction of a novel constitutive expression vector for *Rhodococcus*
○Liu, R., Hashimoto, Y. and Kobayashi, M.
(Grad. Sch. Life and Environ. Sci., Univ. Tsukuba)

P-56 Analysis of the circularization of the *Streptomyces rochei* linear chromosome
○Nindita, Y.[1], Cao, Z.[1], Shiwa, Y.[2], Yoshikawa, H.[2], Arakawa, K.[1] and Kinashi, H.[1]
([1]Dept. Mol. Biotechnol., Grad. Sch. AdSM, Hiroshima Univ., [2]Dept. Biosci., Tokyo Univ. Agric.)

P-57 Transcriptional analysis of genes involved in submerged spore formation in *Kitasatospora* setae KM-6054^T
○Yagisawa, Y.[1], Miura, H.[2], Kato, Y.[1], Ōmura, S.[2] and Takahashi, Y.[1,2]
([1]Grad. Sch. Infection Control Sci., [1]Kitasato Inst. Life Sci., Kitasato Univ.)

52 th Regular Colloquim

Date: Nov. 16 (Fri.), 2012
Place: The Kitasato Institute

Program:

1. "Screening of actinomycete strains based on biosynthetic genes of secondary metabolites."
Hisayuki KOMAKI (NITE/NBRC)

2. "Identification and application of the bifidobacterial enzymes involving in the metabolism of human milk oligosaccharides."
Motomitsu KITAOKA (National Food Research Institute)

3. "Biosyntheses and metabolisms of triterpene hydrocarbons produced by a green microalga *Botryococcus braunii* that is promising as a source of biofuel."
Shigeru OKADA[1], Joe CHAPPELL[2]
([1]University of Tokyo, [2]University of Kentucky)

4. "The Microstructure of Soil Harboring Diverse Microbes."
Tsutomu HATTORI (Atic Lab.)

The 2013 Annual Meeting of the Society for Actinomycetes Japan

Chair person: Masanori Sugiyama (Hiroshima University)

The 2013 annual meeting of SAJ will be held in September 2013 in Hiroshima, Japan. We look forward to welcoming you to participate in the meeting and to submit papers. Updated information will be provided on the SAJ Home Page (http://www0.nih.go.jp/saj/index-e.html).

General Outline

Dates: September 5 (Thu)-6 (Fri), 2013
Venue: Mielparque Hiroshima (http://www.mielparque.jp/hiroshima/en/)
Address: Moto-machi 6-36, Naka-ku, Hiroshima, Japan, 730-0011
TEL: +81-82-222-8501

Registration fee including abstracts:

SAJ member	8,000 yen (6,000 yen until June 14, 2013)
Student	4,000 yen (3,000 yen until June 14, 2013)
Non-member	10,000 yen (8,000 yen until June 14, 2013)
Abstracts only	2,000 yen

Registration procedure may be acceptable through the following e-mail address (saj2013@ml.hiroshima-u.ac.jp), effective from March 1st, 2013.

Reception: September 5 (Thu), 2013 at Mielparque Hiroshima

Fee: SAJ member	10,000 yen (8,000 yen until June 14, 2013)
Student	7,000 yen (5,000 yen until June 14, 2013)
Non-member	10,000 yen (8,000 yen until June 14, 2013)

Scientific program:
An invited lecture, SAJ award lectures, and contributing paper sessions will be arranged.

Submission of abstracts:
Abstracts for contributing paper should be submitted via an exclusive e-mail address (saj2013@ml.hiroshima-u.ac.jp) as an attachment file written by using MS Word. Deadline for submission of abstracts is June 28, 2013.

For further information contact:

SAJ2013 congress secretariat
c/o Department of Molecular Microbiology & Biotechnology
Institute of Biomedical & Health Sciences, Hiroshima University
Kasumi 1-2-3, Minami-ku, Hiroshima, Japan 734-8553
Tel: +81-82-257-5280, FAX: +81-82-257-5284
E-mail: saj2013@ml.hiroshima-u.ac.jp

The 2013 annual meeting of SAJ will be held in September 2013 in Hiroshima, Japan. We look forward to welcoming you to participate in the meeting and to submit papers
Updated information will be provided on the SAJ Home Page: http://www.nih.go.jp/saj/index-e.html

Online access to The Journal of Antibiotics for SAJ members

Eligible members of SAJ can access to online issues of The Journal of Antibiotics (JA) by taking following steps;

1. Open the SAJ official website (URL: http://www.nih.go.jp/saj/index-e.html) and click the banner of JA.
2. To register, enter your Membership number (10-digit figures starting with 154), First name, Last name, and E-mail address to receive a password and click 'Send'. You can find your Membership number on the envelope from SAJ.
3. Then, you will receive your password from SAJ.
4. Open the SAJ official website (URL: http://www.nih.go.jp/saj/index-e.html) and click the banner of JA again. To access the JA website, enter Membership number and password and click 'Login'.
5. Upon recognition of Membership number and password, SAJ site relays the access to the journal's website on nature.com
6. In the journal's website on nature.com, contents are freely available. Members can find the article from current issue table of contents, or archive issues list. Click 'PDF' or 'HTML' link of each article to read full contents.

Please note;

Unique set of Membership number and password is issued and provided to each eligible members of SAJ. Members are not allowed to distribute this information to the third person or third parties.

Depending on the network environment there's a case where access to full contents is not permitted even though Membership number and password is correct. In such case please contact us by email for alternative access method. When contacting please provide your membership number and password, and specify name and version of your Internet browser.

RBA Helpdesk- The Journal of Antibiotics
E-mail : ja@natureasia.com