資料 4

Plant and plant-related bacteria genome projects @ Kazusa

species	Publication	gene №	Feature
Synechosystis PCC 6803	Kaneko *et al.*, 1996*	3672	cyanobacterium
Arabidopsis thaliana	Kaneko *et al.*, 2000	6124	model plant
Mesorhizobium loti	Kaneko *et al.*, 2000	7283	rhizobium
Anabaena PCC 7120	Kaneko *et al.*, 2001	6132	N-fixation cyanobacterium
Thermosynechococcus elongatus	Nakamura *et al.*, 2002	2477	thermophilic cyanobacterium
Bradyrhizobium japonicum	Kaneko *et al.*, 2002	8317	rhizobium
Gloeobacter violaceus	Nakamura *et al.*, 2003	4431	cyanobacterium
Microcystis aeruginosa	Kaneko *et al.*, 2007	6312	cyanobacterium
Lotus japonicus	Sato *et al.*, 2008	30799	model legume plant

*Re-annotated in 2002

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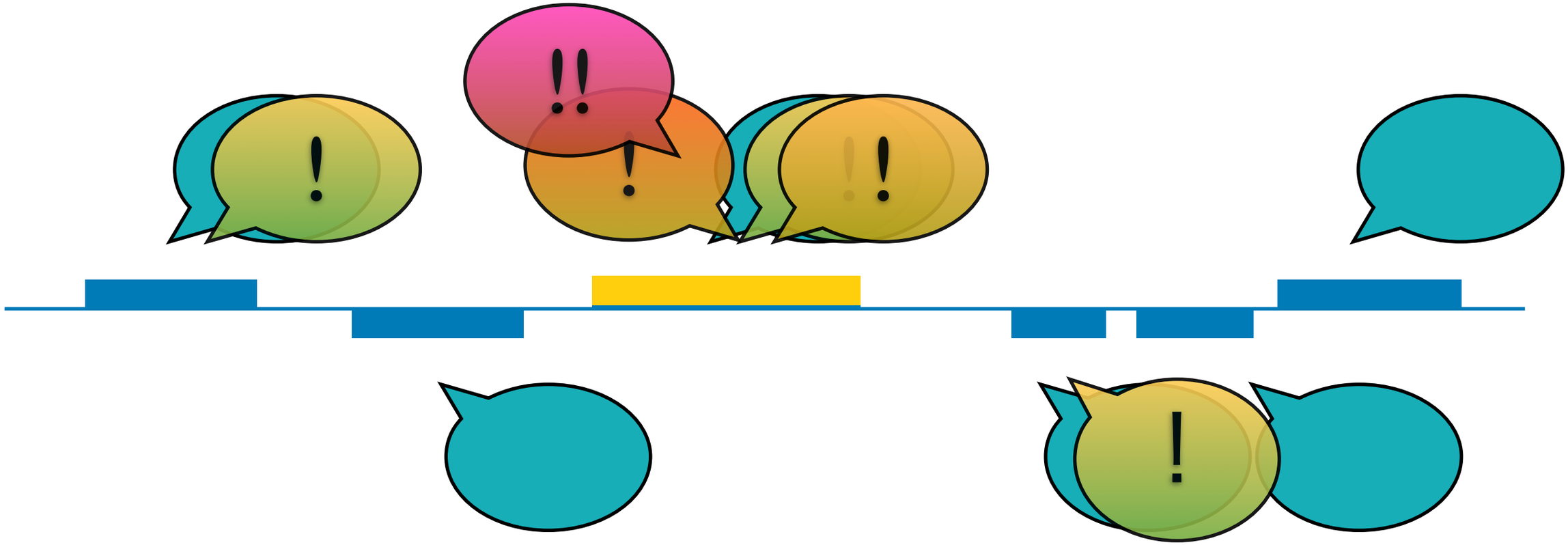
ソーシャルブックマークによるゲノムアノテーション

ユーザからのフィードバックを容易に、簡便に、速攻で反映



http://a.kazusa.or.jp

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現在までの成果

- 高度情報集積データベースの開発・運用
  - KazusaAnnotation: http://a.kazusa.or.jp/
  - KazusaNavigation: http://navi.kazusa.or.jp/
  - KazusaWiki: http://wiki.kazusa.or.jp/
- ゲノムアノテーション情報の蓄積・公開
  - 文献情報と実験情報をマニュアルで蓄積
  - 3,004報 95,152エントリの入力
- 情報を閲覧するためのビューワの開発

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Gene Indexing

JOURNAL OF BACTERIOLOGY, Apr. 2007, p. 2750–2758 Vol. 189, No. 7
0021-9193/07/$08.00+0 doi:10.1128/JB.01903-06

Coordinated High-Light Response of Genes Encoding Subunits of Photosystem I Is Achieved by AT-Rich Upstream Sequences in the Cyanobacterium *Synechocystis* sp. Strain PCC 6803▽

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Received 16 December 2006/Accepted 23 January 2007

Genes encoding subunits of photosystem I (PSI genes) in the cyanobacterium *Synechocystis* sp. strain PCC 6803 are actively transcribed under low-light conditions, whereas their transcription is coordinately and rapidly down-regulated upon the shift to high-light conditions. In order to identify the molecular mechanism of the coordinated high-light response, we searched for common light-responsive elements in the promoter region of PSI genes. First, the precise architecture of the *psaD* promoter was determined and compared with the previously identified structure of the *psaAB* promoter. One of two promoters of the *psaAB* genes (P1) and of the *psaD* gene (P2) possessed an AT-rich light-responsive element located just upstream of the basal promoter region. These sequences enhanced the basal promoter activity under low-light conditions, and their activity was transiently suppressed upon the shift to high-light conditions. Subsequent analysis of *psaC*, *psaE*, *psaK1*, and *psaLI* promoters revealed that their light response was also achieved by AT-rich sequences located at the −70 to −46 region. These results clearly show that AT-rich upstream elements are responsible for the coordinated high-light response of PSI genes dispersed throughout *Synechocystis* genome.

Photosynthetic organisms have ability to cope with the changes in light environment by modulating both the structure and the function of the photosynthetic machinery (31, 59). A typical example is the flexible control of the amounts of photosystem (PS) and light-harvesting antenna complexes depending on the availability of light energy (4, 27, 38). Under light-limiting conditions, the amount of these complexes is maintained at high level, because maximal capture of light energy is required to fulfill the energy demand of cells. Under light-saturating conditions, on the other hand, they are largely down-regulated since absorption of excess light energy tends to cause the generation of harmful reactive oxygen species (6).

The dynamics of reaction center complexes during the process of high-light (HL) acclimation have been well characterized in cyanobacteria. Amount of PSI is more strictly down-regulated than that of PSII upon the exposure to HL (28, 40). The analysis of the *pmgA* mutant deficient in down-regulation of PSI content revealed that the selective repression of PSI is essential for growth under continuous HL conditions (28, 54). Although the primary determinant of PSI content under HL conditions has not been identified, transcriptional regulation is likely to be one of the important factors. The cyanobacterial PSI complex is comprised of about 11 subunits, with some exceptions (23), and genes encoding these subunits (PSI genes) are dispersed throughout the genome. In *Synechocystis* sp. strain PCC 6803, PSI genes are actively transcribed under low-light (LL) conditions, whereas their transcription is coordinately and rapidly down-regulated upon the shift to HL conditions (26, 29, 30, 42, 57), except for the *psaK2* gene encoding an HL-inducible isoform of the PsaK subunit (19). PSI transcripts become barely detectable within 1 h of HL exposure and then gradually reaccumulate after 3 h. The change in promoter activities of PSI genes is well coincident with the change in transcript levels (42, 43), suggesting that the coordinated light response of PSI genes is achieved at the level of transcriptional regulation. In the course of HL acclimation, cells need to activate genes related to several processes such as CO_2 fixation, protection from photoinhibition, and general stress management (29). The down-regulation of high promoter activities of PSI genes upon the shift to HL conditions may be important not only for the repression of PSI content, but also for the recruitment of RNA polymerases to active transcription of such HL-inducible genes.

As the first step for the elucidation of the molecular mechanism of coordinated HL response of PSI genes in *Synechocystis* sp. strain PCC 6803, we recently dissected the promoter architecture of the *psaAB* genes encoding reaction center subunits (43). The *psaAB* genes have two promoters, P1 and P2, both of which are responsible for the photon flux density-dependent transcription. Deletion analysis of the upstream region of *psaAB* fused to bacterial luciferase reporter genes (*luxAB*) indicated that the light responses of P1 and P2 are achieved in different manners. The *cis* element required for the light response of P1, designated as PE1, was located just upstream of the −35 element of P1 and was comprised of AT-rich sequence. PE1 activated P1 under LL conditions, and the down-regulation of P1 was achieved by rapid inactivation of PE1 upon the shift to HL conditions. On the other hand, the *cis* element required for the light response of P2, designated as

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▽ Published ahead of print on 2 February 2007.

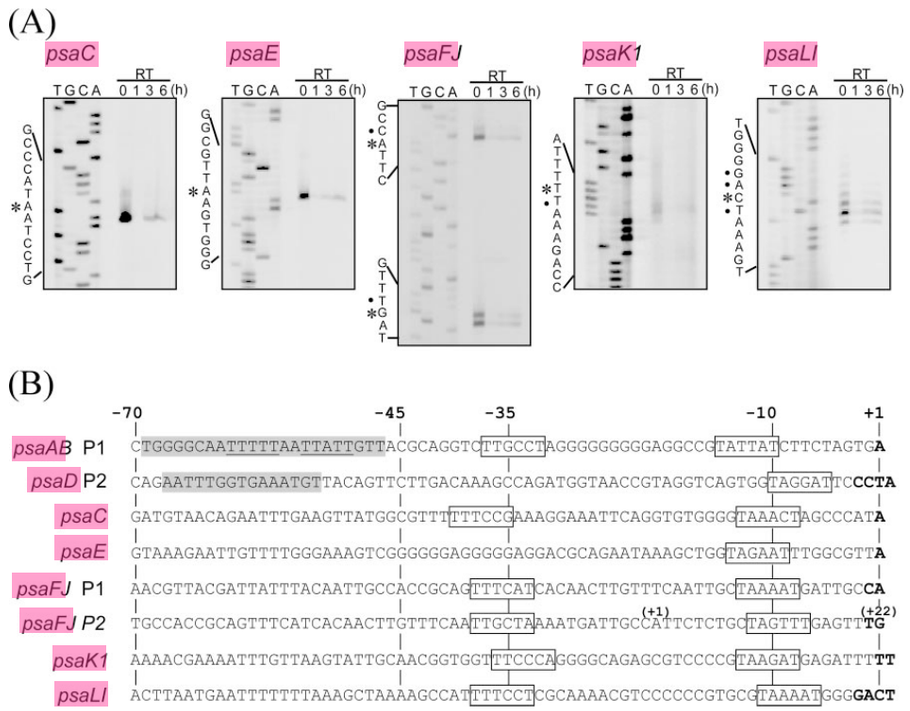


FIG. 3. Mapping of the 5′ ends of PSI transcripts. (A) Total RNA was isolated from the wild-type cells incubated under HL conditions for 0, 1, 3, and 6 h and used for primer extension analysis of *psaC*, *psaE*, *psaFJ*, *psaK1*, and *psaLI*. Detected 5′ ends of the major transcripts are indicated by asterisks, and those of minor ones are indicated by dots. (B) Nucleotide sequences of the core promoter and its upstream region of PSI promoters. Transcriptional start points are shown in boldface letters. The promoters are aligned according to the major transcriptional start point noted as +1. Putative −35 and −10 hexamers are boxed. Light-responsive positive elements identified in *psaAB* and *psaD* promoters are shaded in gray. The nucleotides shown to be critical for the light response of *psaAB* promoter (43) are underlined. The numbers in parentheses shown above the nucleotide sequence of the P2 promoter of *psaFJ* indicate the position according to the major transcriptional start point of the P1 promoter.

the analysis since the arrangement of regulatory elements for two overlapping promoter is difficult to predict without precise promoter analysis.

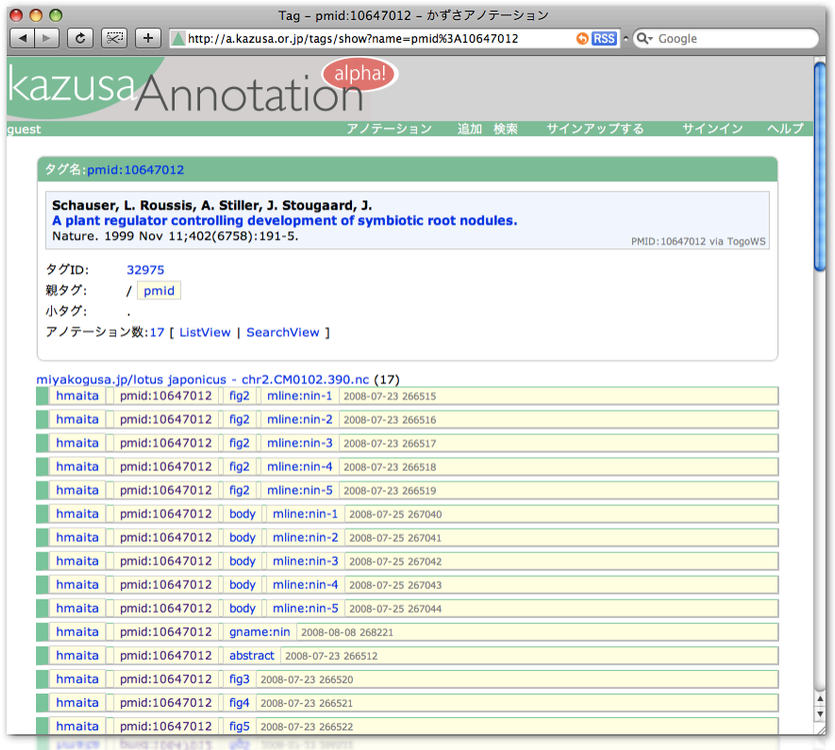
Effect of the −70 to −46 region on the promoter activity of PSI genes. Figure 4A shows the bioluminescence level of *Synechocystis* cells harboring PSI promoter-*luxAB* reporter genes with or without the upstream region under LL conditions. The reporter activities of the downstream promoter fragments alone were generally low, but there existed some differences among them. For example, the promoter activity of the downstream region was low in the case of *psaD* [$(8.2 \pm 0.2) \times 10^5$ relative units/OD_{730}] and *psaK1* [$(2.3 \pm 0.4) \times 10^5$ relative units/OD_{730}], whereas that of *psaLI* was significantly high [$(1.1 \pm 0.2) \times 10^7$ relative units/OD_{730}]. It is possible that the high activity of the *psaLI* promoter is brought about by a positive regulatory element located within the downstream region. When the AT-rich upstream region was added, each promoter displayed much higher activity compared with the corresponding derivative containing only the downstream region. This demonstrates that the −70 to −46 region can work as a positive regulatory element for every PSI gene examined here. The low activity of *psaD* and *psaK1* promoters was largely up-regulated in the presence of the upstream region by 40.1- and 99.9-fold, respectively. On the other hand, strong promoter activity of *psaLI* was not enhanced as much by the upstream region (5.1-fold). As a result, similar promoter activity (around 5.0×10^7 relative units/OD_{730}) was attained among PSI genes irrespective of the activity of the downstream promoter region.

Next, we transformed *E. coli* cells with the above mentioned reporter constructs and measured the level of bioluminescence to see whether the upstream region can work as a positive regulatory element in *E. coli* cells (Fig. 4B). In all strains harboring PSI promoter-*luxAB* constructs, the luminescence level was higher than that of the control cells having promoterless *luxAB* genes [$(1.4 \pm 0.5) \times 10^8$ relative units/OD_{600}], showing that PSI promoters can be recognized by RNA polymerase of *E. coli*. The rank orders of promoter strength are similar in both *Synechocystis* and *E. coli* cells. Namely, the activities of the downstream promoter fragments of *psaD* and *psaK1* were low [$(2.4 \pm 1.0) \times 10^8$ relative units/OD_{600} and

ソーシャルブックマーク(SBM)による
遺伝子＝URLへの文献情報蓄積

slr0473 Cph1, phytochrome

http://bacteria.kazusa.or.jp/cyanobase/Synechocystis/cgi-bin/orfinfo.cgi?title=Chr&name=slr0473



[pmid: 9278513] [introduction]
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[pmid: 9278513] [discussion]
[pmid: 9278513] [table1]
[pmid: 9278513] [fig3]

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プログレス

2008-1-25

Rhizobia

マイルストーン: [Rhizo] Bradyrhizobium japonicum USDA110
完了期限が設定されていません
12%
解決済みのチケット: 114　未解決のチケット: 819

114 papers

マイルストーン: [Rhizo] Mesorhizobium loti MAFF303099
完了期限が設定されていません
99%
解決済みのチケット: 177　未解決のチケット: 2

177 papers

マイルストーン: [Rhizo] Sinorhizobium meliloti strain 1021
完了期限が設定されていません
94%
解決済みのチケット: 113　未解決のチケット: 7

113 papers

Cyano-bacteria

マイルストーン: [cyano] Anabaena sp. PCC7120
完了期限が設定されていません
99%
解決済みのチケット: 518　未解決のチケット: 3

- 2008-7-25 Anabaenaの名前の表記ゆれにより検索対象から落ちていた文献を追加しました

518 papers

マイルストーン: [cyano] Synechococcus sp. PCC7942
完了期限が設定されていません
100%
解決済みのチケット: 438　未解決のチケット: 2

438 papers

マイルストーン: [cyano] Synechocystis sp. PCC6803
完了期限が設定されていません
99%
解決済みのチケット: 1342　未解決のチケット: 11

1342 papers

Legume

マイルストーン: [plant] Lotus japonicus
完了期限が設定されていません
98%
解決済みのチケット: 302　未解決のチケット: 5

302 papers

Total 95152 entries

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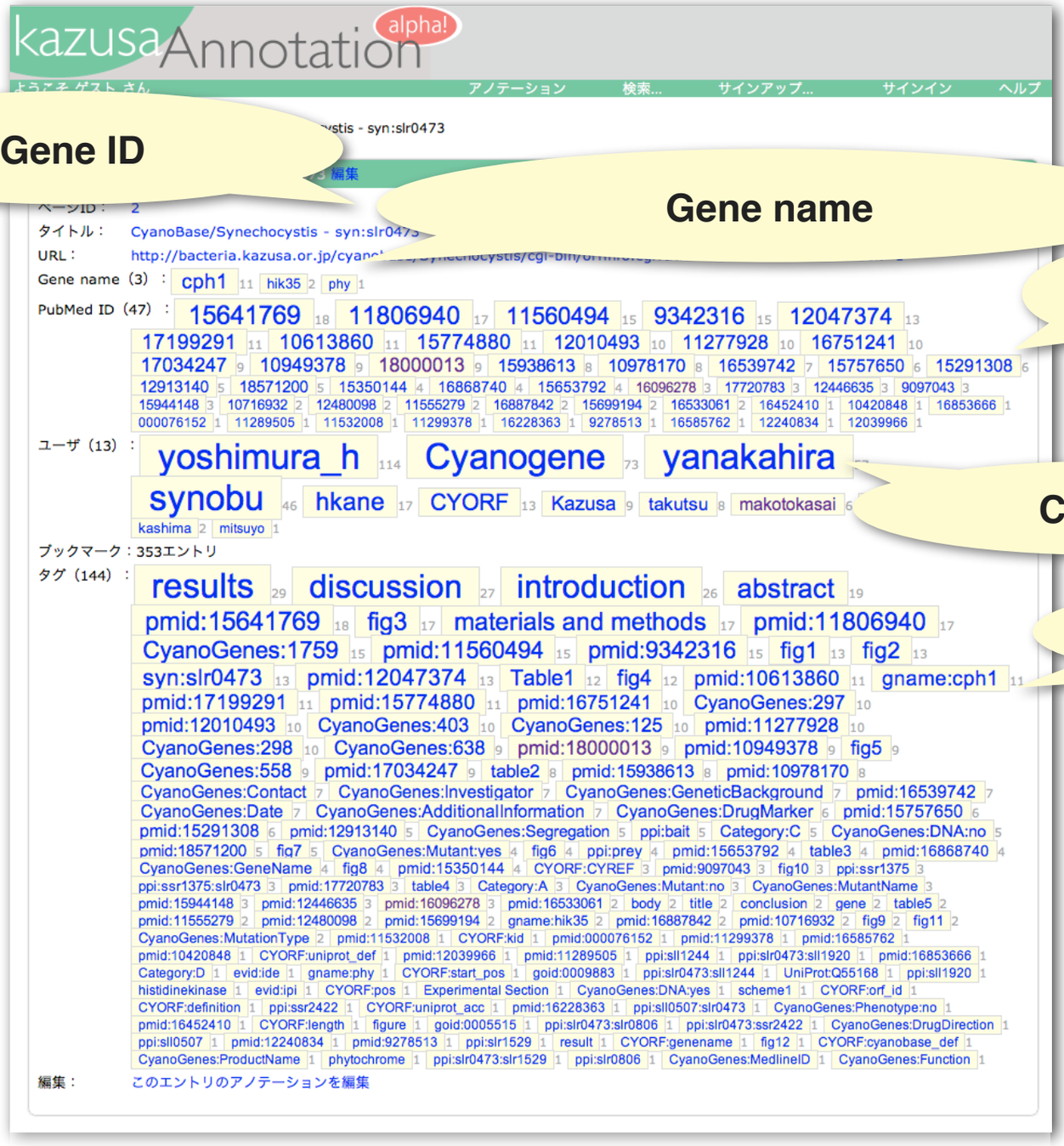
KazusaAnnotation: http://a.kazusa.or.jp/



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植物および植物関連微生物のゲノム情報データベース統合と高度化@かずさ
H21実施計画案

1. 高度情報集積データベースの運用と改良	分子データ上のポジションを統合のための基盤情報とし、<u>アノテーション・キュレーションの統合と高度化</u>を可能とするデータベース (KazusaAnnotation: http://a.kazusa.or.jp/) を植物および植物関連微生物のゲノム解析情報を対象として運用しつつ、ユーザの要望を汲みあげて改善を加え、さらなる利便性の向上を行う。 同時に以下の項目も実施する ・集積した情報から生物学的な意味を取り出すための情報表現技術 ・情報を閲覧するためのビューワ(genoDivePro, genoDiveEu)の改善と提供 ・データベース中の遺伝子名や遺伝子IDの食い違いを解決
2. ゲノムアノテーション情報の蓄積と高度化	かずさDNA研究所でゲノム塩基配列が決定されたモデル生物を中心に、より<u>広範な生物種の遺伝子情報について、引き続き論文記載情報および実験情報の蓄積業務を実施</u>し、ゲノムの位置情報と論文記載情報の統合を図る。 ・登録した情報は、KazusaAnnotationシステムなどから完全公開 ・効率的なアノテーションを行うための方法の開発 ・アノテーター・キュレーターの育成、技術向上のためにIT技術を利用したミーティング手法などを開発

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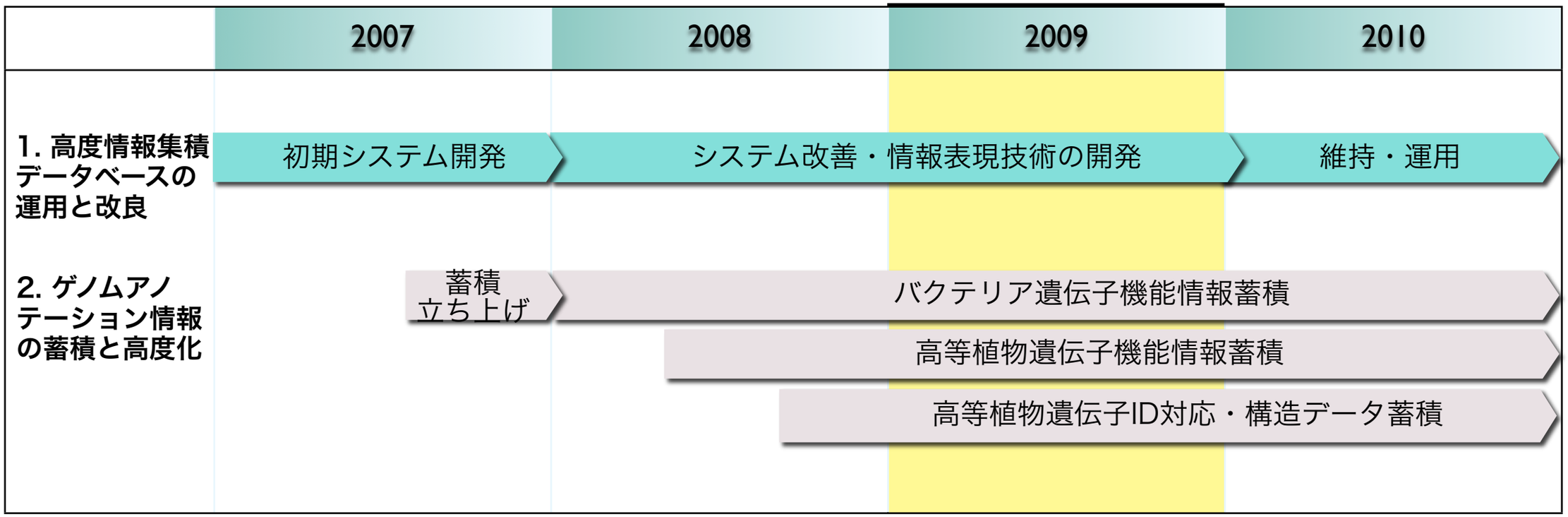
４年間の中でのH21 (2009)年度



- 更に1,500 報以上の文献情報蓄積
  - シアノバクテリア
  - 根粒菌
  - シロイヌナズナ (植物の統合)

- 集積した情報から生物学的な意味を取り出すための情報表現技術
- ビューワの改善と提供
- 食い違う遺伝子名やIDの統合
- アノテーション手法の改善

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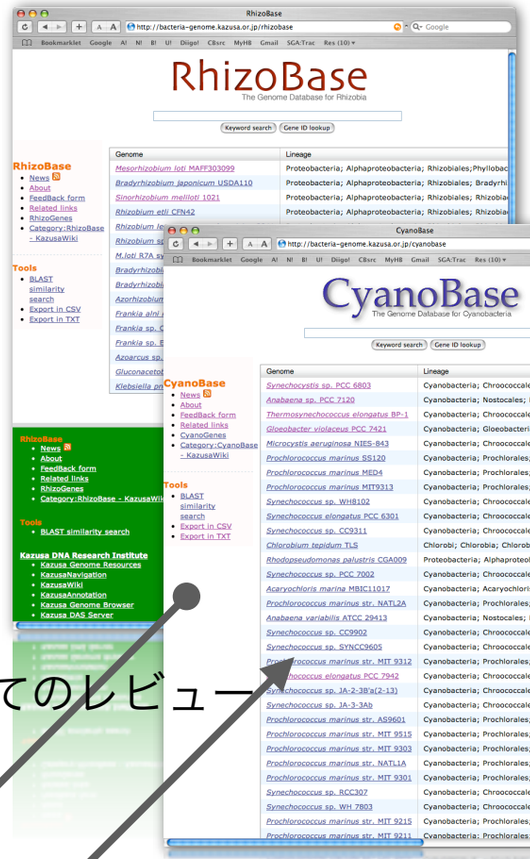
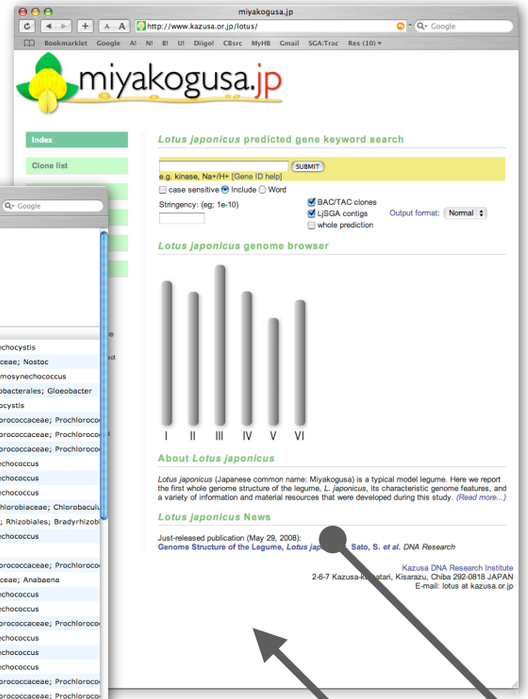
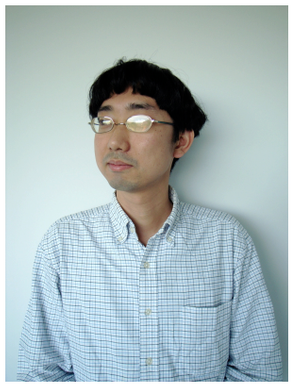
アノテーション体制の整備

KDRI DB Resources







Annotation作業を通じてのレビュー

Annotation情報の統合

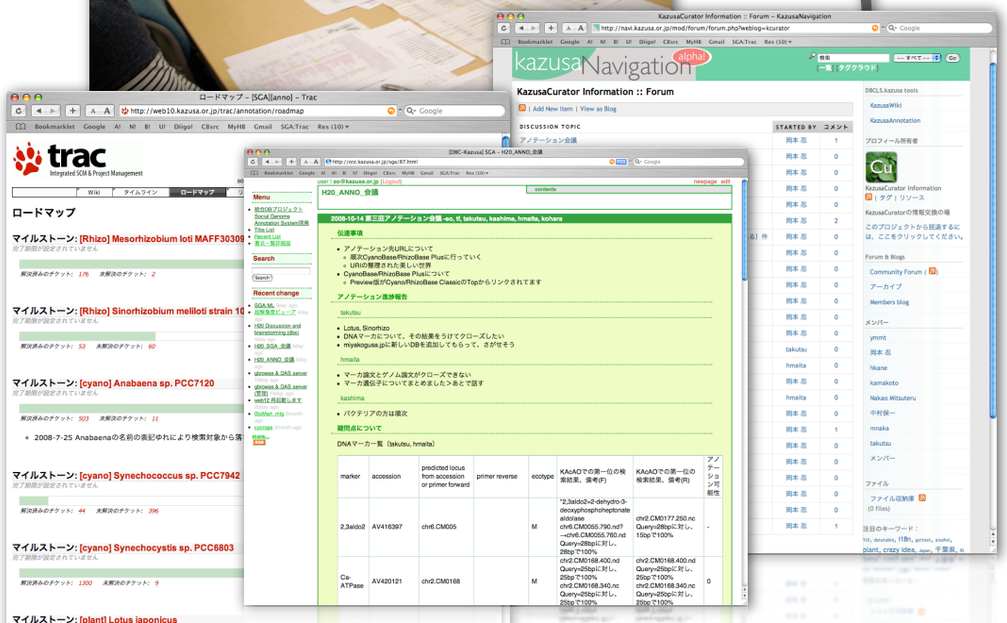
KazusaAnnotation

Annotation Meeting

物理的・仮想的

機能・内容改善

遠隔地Curator



Annotation, Curation

問題発見, 問題共有

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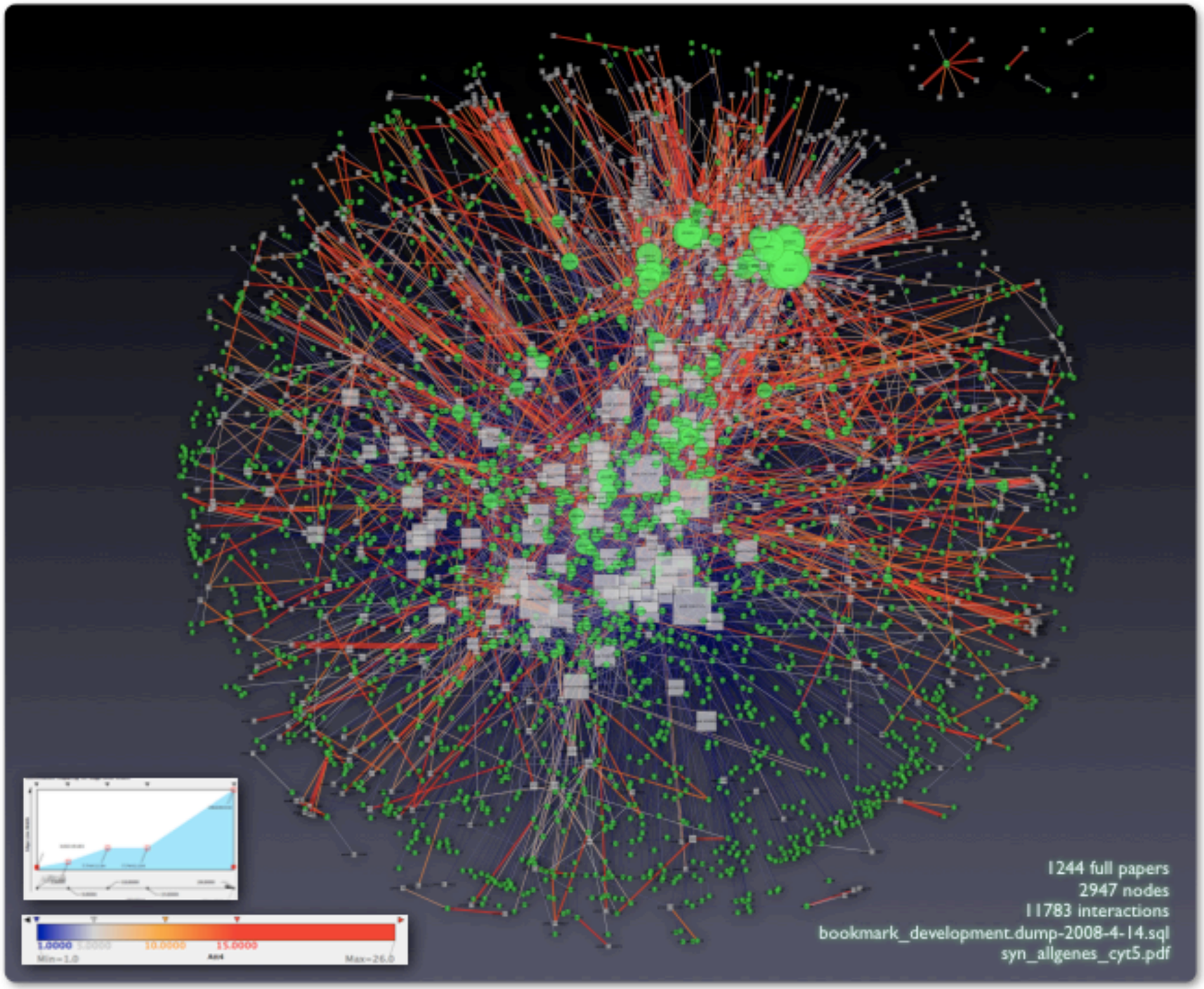
The bibliome of *Synechocystis* sp. PCC 6803



- 1,244 full-text papers
- 11,783 associations

between papers and genes

Green circle: gene
Gray square: paper

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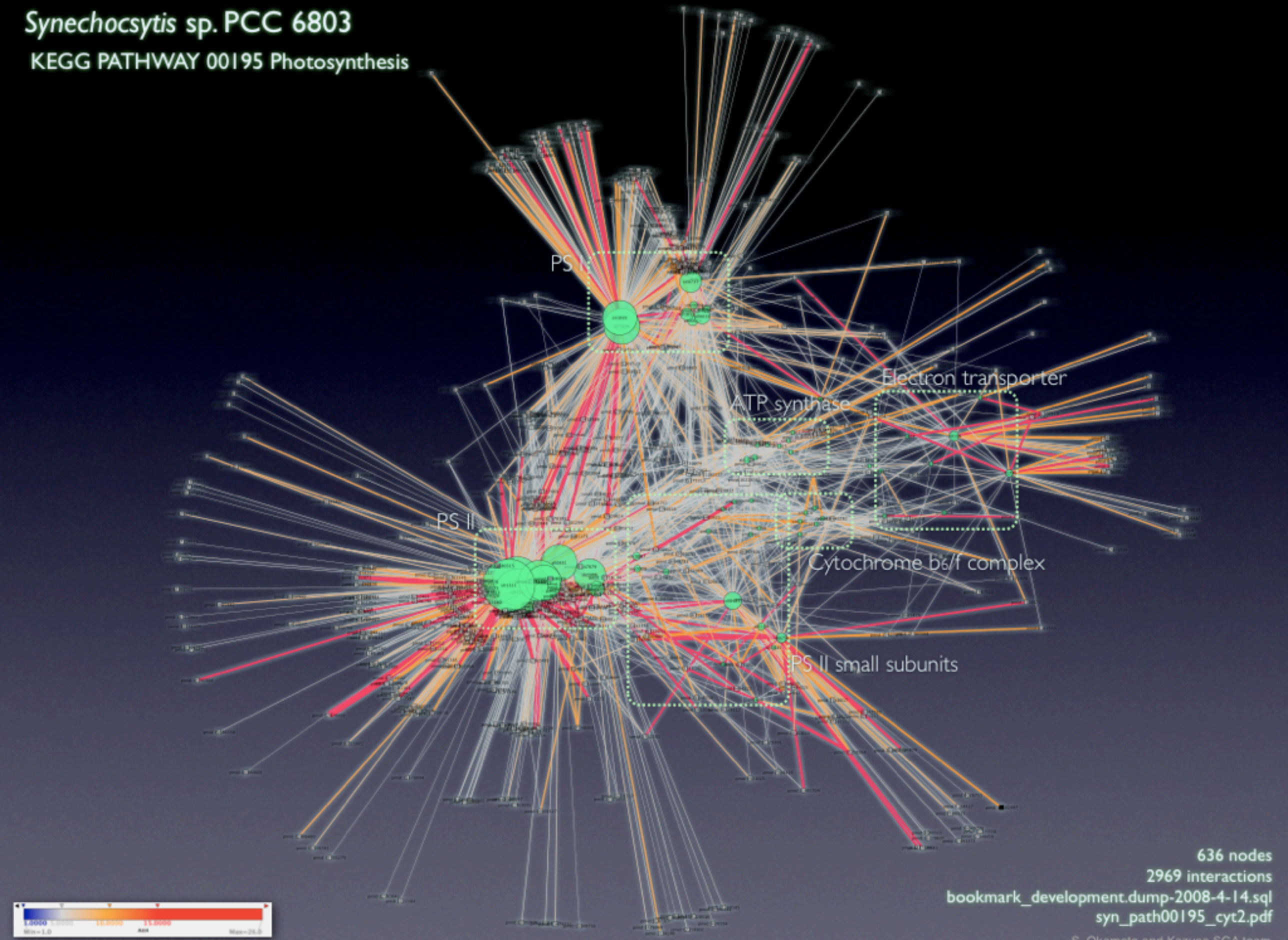
Synechocsytis sp. PCC 6803

KEGG PATHWAY 00195 Photosynthesis



636 nodes
2969 interactions
bookmark_development.dump-2008-4-14.sql
syn_path00195_cyt2.pdf

S. Okamoto and Kazusa SGA team