Maintenance of Transcription Factor DataBase TFDB by *TFDB Maintenance System*

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1 Introduction

TFD [1]–[4] was a very useful and required database for molecular biologists analyzing transcription mechanisms and gene expressions, which was maintained by David Ghosh at NCBI until 1993. We took over his work as TFDB (which is based upon the *'sites'* table of the TFD [6, 7]), and we established *TFDB Maintenance System* described in [5] which gathers transcription factor data from articles, to update TFDB systematically.

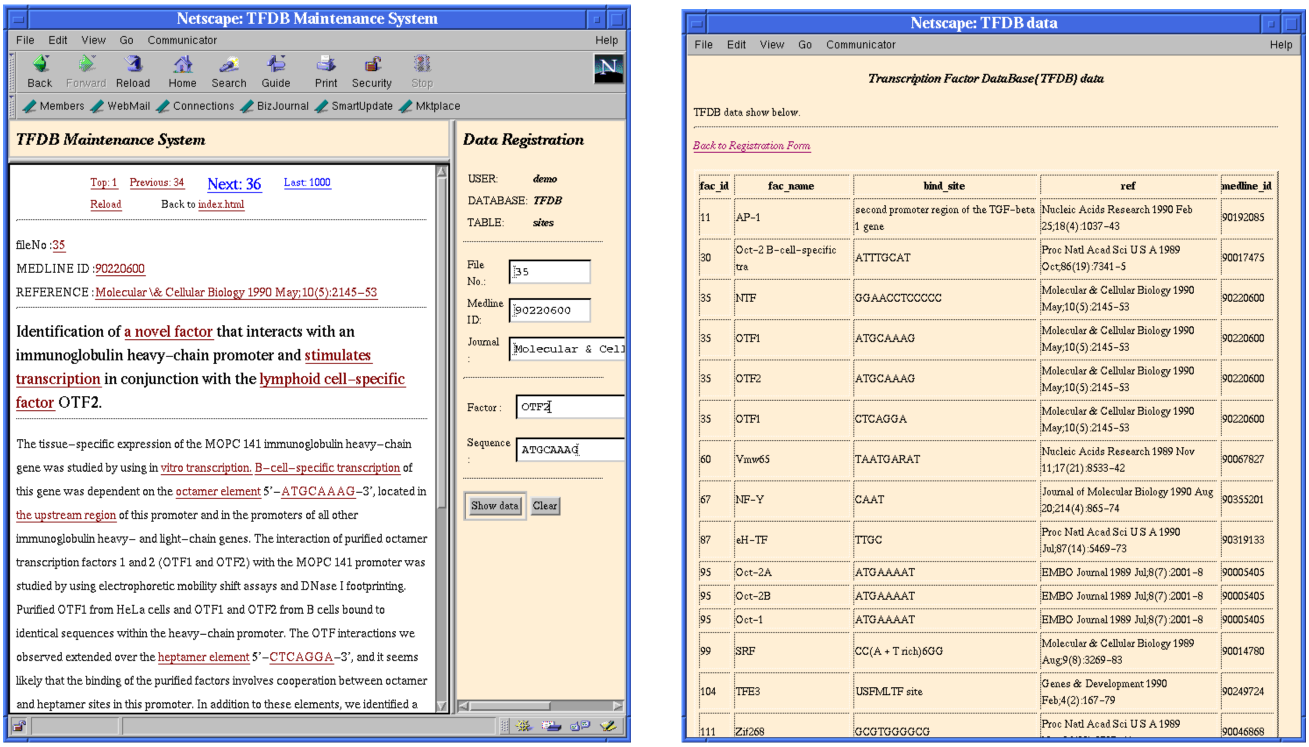
We started the maintenance of TFDB with this *TFDB Maintenance System* using many journals which we can obtain from MEDLINE database. In this paper, we describe how we maintain the TFDB using this system.

2 System

TFDB Maintenance System contains the following subsystems: (1) *Information Retrieval Subsystem* based on retrieval engine described in [8] which collects references related to transcription factor from MEDLINE correctly and efficiently, (2) *Information Extraction Subsystem* described in [5, 8] which extracts candidates of 'transcription factors' and 'target(transcription factor binding) sequences' from the result of *Information Retrieval Subsystem*, and (3) *Data Registration Subsystem* [5] which enables to register new data easily and interactively on WWW (the interface of *Data Registration Subsystem*, see Fig. 1).

3 Method

We are maintaining TFDB by the following method. (1) Collecting abstracts of the various fields, published in 1990 – 1998 from MEDLINE database as a text data format. (2) Scoring abstracts related to the transcriptional regulation using *Information Retrieval Subsystem.* (3) The words related to



TFDB Maintenance System

fileNo :35

MEDLINE ID :90220600

REFERENCE :Molecular \& Cellular Biology 1990 May;10(5):2145–53

Identification of a novel factor that interacts with an immunoglobulin heavy–chain promoter and stimulates transcription in conjunction with the lymphoid cell–specific factor OTF2.

The tissue–specific expression of the MOPC 141 immunoglobulin heavy–chain gene was studied by using in vitro transcription. B–cell–specific transcription of this gene was dependent on the octamer element 5'–ATGCAAAG–3', located in the upstream region of this promoter and in the promoters of all other immunoglobulin heavy– and light–chain genes. The interaction of purified octamer transcription factors 1 and 2 (OTF1 and OTF2) with the MOPC 141 promoter was studied by using electrophoretic mobility shift assays and DNase I footprinting. Purified OTF1 from HeLa cells and OTF1 and OTF2 from B cells bound to identical sequences within the heavy–chain promoter. The OTF interactions we observed extended over the heptamer element 5'–CTCAGGA–3', and it seems likely that the binding of the purified factors involves cooperation between octamer and heptamer sites in this promoter. In addition to these elements, we identified a

Data Registration

USER: *demo*
DATABASE: *TFDB*
TABLE: *sites*

File No.: 35
Medline ID: 90220600
Journal : Molecular & Cell

Factor : OTF2
Sequence : ATGCAAAG

Transcription Factor DataBase(TFDB) data

TFDB data show below.

fac_id	fac_name	bind_site	ref	medline_id
11	AP–1	second promoter region of the TGF–beta 1 gene	Nucleic Acids Research 1990 Feb 25;18(4):1037–43	90192085
30	Oct–2 B–cell–specific tra	ATTTGCAT	Proc Natl Acad Sci U S A 1989 Oct;86(19):7341–5	90017475
35	NTF	GGAACCTCCCCC	Molecular & Cellular Biology 1990 May;10(5):2145–53	90220600
35	OTF1	ATGCAAAG	Molecular & Cellular Biology 1990 May;10(5):2145–53	90220600
35	OTF2	ATGCAAAG	Molecular & Cellular Biology 1990 May;10(5):2145–53	90220600
35	OTF1	CTCAGGA	Molecular & Cellular Biology 1990 May;10(5):2145–53	90220600
60	Vmw65	TAATGARAT	Nucleic Acids Research 1989 Nov 11;17(21):8533–42	90067827
67	NF–Y	CAAT	Journal of Molecular Biology 1990 Aug 20;214(4):865–74	90355201
87	eH–TF	TTGC	Proc Natl Acad Sci U S A 1990 Jul;87(14):5469–73	90319133
95	Oct–2A	ATGAAAAT	EMBO Journal 1989 Jul;8(7):2001–8	90005405
95	Oct–2B	ATGAAAAT	EMBO Journal 1989 Jul;8(7):2001–8	90005405
95	Oct–1	ATGAAAAT	EMBO Journal 1989 Jul;8(7):2001–8	90005405
99	SRF	CC(A + T rich)6GG	Molecular & Cellular Biology 1989 Aug;9(8):3269–83	90014780
104	TFE3	USFMLTF site	Genes & Development 1990 Feb;4(2):167–79	90249724
111	Zif268	GCGTGGGCG	Proc Natl Acad Sci U S A 1989	90046868

Figure 1: TFDB Data Registration interface and new data of TFDB.

transcription factors and its *binding sequences* are automatically extracted from (2) with *Information Extraction Subsystem*. (4) Specialist authorizes the validity of (3) and register with *Data Registration Subsystem*.

4 Results and Discussion

We used 265,249 abstracts for the purpose of trying the performance of the *TFDB Maintenance System*. We chose the top 150 abstracts from the output result of *Information Retrieval Subsystem*.

All of the 150 abstracts related to transcriptional regulatory mechanisms. About 7 candidates of binding factor and about 1.6 candidates of binding sequence appeared per abstract in average. Analysis of experts selection resulted that 10% of the top 150 abstracts contains new TFDB data with Binding Sequences.

We can collect data related to transcription factors efficiently with *Information Retrieval subsystem* and extract candidate of 'Binding Factors', 'Binding Sequences' very easily with *Information Extraction subsystem*. We are now continually authorizing the extracted data with *Data Registration Subsystem*.

This system is also suitable for maintaining databases in other fields.

Acknowledgements

We thank Dr. Sarai (The Institute of Physical and Chemical Research, GENE BANK) for giving us advices about this system. This work was supported in part by a Grant-in-Aid for Scientific Research on Priority Areas, 'Genome Science', from the Ministry of Education,Science, Sports and Culture in Japan.

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