268–269 *Nucleic Acids Research, 2001, Vol. 29, No. 1*

REBASE—restriction enzymes and methylases

Richard J. Roberts* and Dana Macelis

New England BioLabs, 32 Tozer Road, Beverly, MA 01915, USA

Received October 31, 2000; Accepted November 1, 2000

ABSTRACT

REBASE contains comprehensive information about restriction enzymes, DNA methylases and related proteins such as nicking enzymes, specificity subunits and control proteins. It contains published and unpublished references, recognition and cleavage sites, isoschizomers, commercial availability, methylation sensitivity, crystal data and sequence data. Homing endonucleases are also included. Most recently, extensive information about the methylation sensitivity of restriction enzymes has been added and a new feature contains complete analyses of the putative restriction systems in the sequenced bacterial and archaeal genomes. The data is distributed via email, ftp (ftp.neb.com) and the Web (http://rebase.neb.com).

INTRODUCTION

REBASE has undergone considerable growth since the 2000 NAR Database Issue (1). In addition to restriction enzymes, methylases and homing endonucleases, REBASE also includes information about other types of related proteins: nicking enzymes, specificity subunits of the Type I enzymes, control proteins and methyl-directed restriction enzymes. With the explosion of bacterial and archaeal genome sequences that are appearing in GenBank we include the putative gene products predicted from these sequences. These potential DNA methylases and restriction enzymes are given names that resemble those of normal restriction enzymes [using the conventions employed by Smith and Nathans (2)], but with the suffix 'P' added to indicate their putative status. The REBASE web site (http://rebase.neb.com) provides details of whatever information is known about every restriction enzyme, such as commercial availability, sequence data, crystal structures, cleavage sites, recognition sequences, isoschizomers, growth temperatures and methylation sensitivity. One focus has been on the genes that encode restriction systems and we provide both schematic illustrations of the organization of these systems and their nearest neighbors. It is also possible to run BLAST searches against all known restriction enzyme and methylase genes from the home page.

There are currently 3392 restriction enzymes in REBASE; 238 well-characterized restriction enzymes have been added since the last review (1). These include three new Type II specificities shown in Table 1. Of the 3333 Type II restriction enzymes, 531 are commercially available (200 distinct specificities of the 228 total specificities known). In addition, 20 DNA methyltransferases and seven homing endonucleases are commercially available. We currently have 6059 references in REBASE (journal and book publications, patents and unpublished observations). These are complete with abstracts when available. References are provided for every enzyme.

Table 1. New Type II restriction enzyme specificities

Enzyme[a]	Recognition[b] Sequence	References
*Bsp*NCI	CCAGA	Nkenfou,C., Polisson,C., Nkenfou,J., Notedji,A. and Morgan,R. (unpublished)
*Oli*I	CACNN↓NNGTG	Maneliene,Z., Zakareviciene,L., Padegimiene,E., Petrusyte,M., Capskaja,L., Kiuduliene,L., Butkus,V. and Janulaitis,A. (unpublished)
*Uba*KI	RTGCGCAY	Kesmiene,A., Vitkute,J., Petrusyte,M., Capskaja,L. Kiuduliene,L., Butkus,V. and Janulaitis,A. (unpublished)

[a]The endonucleases are named in accordance with the proposal of Smith and Nathans (2).
[b]Cleavage sites are indicated as ↓ when cleavage is at the identical position on both strands. R = A or G; Y = C or T; N = any base.

REBASE has its own dedicated web server (http://rebase.neb.com) and can be searched extensively. From the REBASE Lists icon on the home page a number of tables of specialized information can be accessed. This includes crystal data, cloned/sequenced genes, enzymes listed by cleavage properties and other useful compilations. Suggestions for new lists are always welcomed. During the last year extensive effort has gone into checking and recompiling information about the sensitivity of restriction enzymes to methylation. A previous compilation (3) had numerous errors and each item listed there has been checked rigorously for its accuracy. In the case of unpublished observations from that earlier compilation, individual authors are being contacted to verify the observations. In addition, published literature is being scanned and much new information is now available. This data can be accessed both from an enzyme's home page as well as from a compilation and an example is shown in Figure 1. Importantly, the data is shown in double-strand format so that the effects of hemimethylation and double-strand methylation are clearly differentiated.

The REBASE Files icon brings up the growing list of currently available monthly data formats. Click on any of the numbered choices for their descriptions or to download these

*To whom correspondence should be addressed. Tel: +1 978 927 3382; Fax: +1 978 921 1527; Email: roberts@neb.com

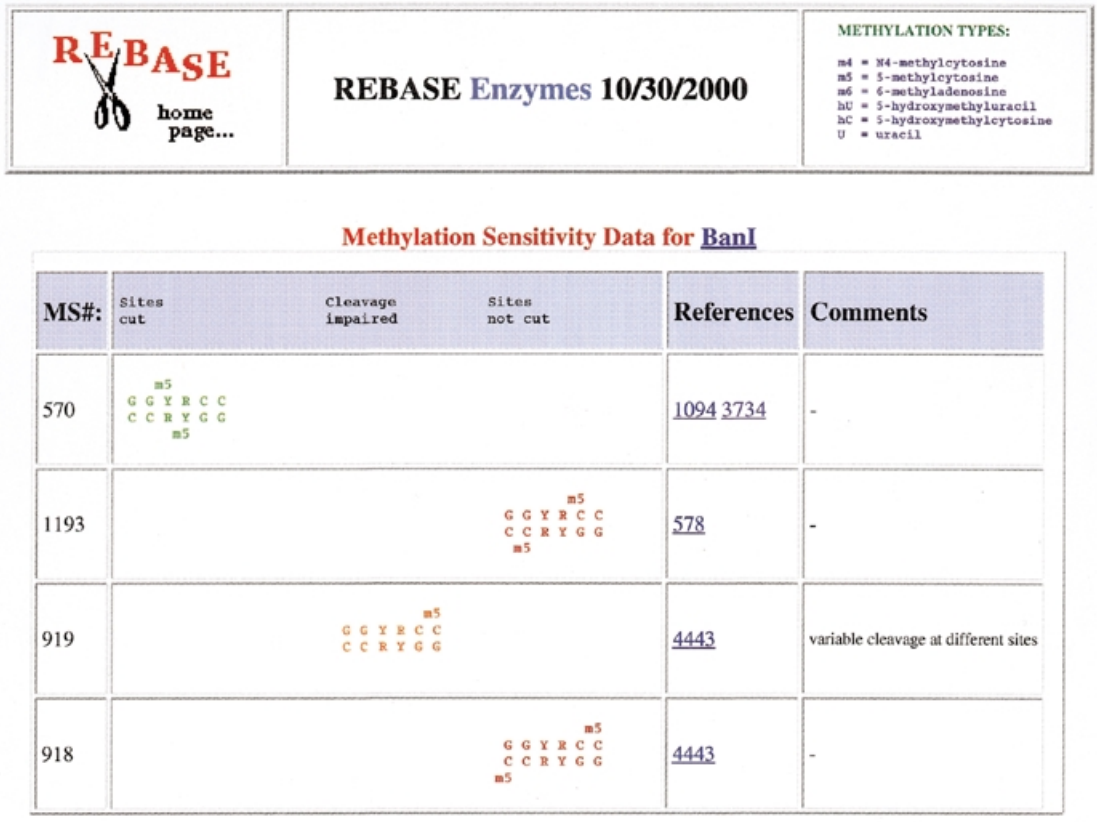

Figure 1. The page detailing the methylation sensitivity for the restriction enzyme, *Ban*I. The second column, labeled 'cleavage impaired', indicates that cleavage is slow when this modification is present. Sometimes this means that rates have been explicitly measured and shown to be much slower than usual, but more often it is inferred from an observation of incomplete digestion under conditions more than sufficient to give complete digestion. For each observation the paper(s) in which the result is documented is listed or, in the case of unpublished observations, the author(s) and contact information can be found from the link in the reference column.

files. Users who prefer retrieving REBASE data via anonymous ftp may continue to do so at ftp.neb.com (cd/pub/rebase). We also continue to maintain a monthly emailing list. Send a request to macelis@neb.com to join.

ACKNOWLEDGEMENTS

Special thanks are due to the many individuals who have so kindly contributed their unpublished results for inclusion in this compilation and to the REBASE users who continue to steer our efforts with their helpful comments. We are especially grateful to Janos Posfai and Tamas Vincze for developing the software that enables the display of the sequence organization of RM genes. This database is supported by the National Library of Medicine (LM04971).

REFERENCES

1. Roberts,R.J. and Macelis,D. (2000) REBASE—restriction enzymes and methylases. *Nucleic Acids Res.*, **28**, 306–307.
2. Smith,H.O. and Nathans,D.J. (1973) A suggested nomenclature for bacterial host modification and restriction systems and their enzymes. *J. Mol. Biol.*, **81**, 419–423.
3. Nelson,M., Raschke,E. and McClelland,M. (1993) Effect of site-specific methylation on restriction endonucleases and DNA modification methyltransferases. *Nucleic Acids Res.*, **21**, 3139–3154.