JOURNAL OF BACTERIOLOGY, Sept. 1991, p. 5252
0021-9193/91/175252-01$02.00/0

Vol. 173, No. 17

Physical Map Locations of the Genes That Encode Small Stable RNAs in *Escherichia coli*

YURIKO KOMINE AND HACHIRO INOKUCHI*

Department of Biophysics, Faculty of Science, Kyoto University, Sakyo-ku, Kyoto 606, Japan

To date, five small stable RNAs (spot 42 RNA, 4.5S RNA, 6S RNA, M1 RNA, and 10Sa RNA) in addition to tRNAs have been identified in *Escherichia coli*. Recently, we made an exhaustive survey of tRNA genes in *E. coli* by analyzing the tRNAs produced upon infection by each lambda clone in Kohara's library (7, 8). In addition to the tRNAs, we were able to detect various small stable RNAs, including all the RNAs mentioned above, and to determine the physical map locations of the genes that encode them. This information is summarized in Table 1.

An RNA transcribed from phage clones 149 and 150 was judged to be 4.5S RNA (115 nucleotides [nt], encoded by *ffs* at 10 min [2, 4]) from its mobility during electrophoresis on a 10% polyacrylamide gel and the chromosomal location. Moreover, since the restriction map around *ffs* reported by Hsu et al. (4) agrees well with the restriction map of the corresponding region determined by Kohara et al. (7), we were able to determine the exact location and orientation of the *ffs* gene. In the same way, RNAs transcribed from phage clones 470 and 471 and from phage clones 547 and 548 were revealed to be 6S RNA and spot 42 RNA, respectively.

In the case of M1 RNA, we found that five functional copies of *rnpB*, which encodes M1 RNA, are present on phage clones 479, 480, 501, and 502 (at 64 min, three copies) and on phage clones 514, 515, and 516 (at 68 min, two copies) as determined by complementation assays and DNA sequence analysis (9), even though *rnpB* has been reported to be located at 70 min (1).

In the case of a relatively large RNA transcribed from phage clones 438, 439, and 440, our nucleotide sequence analysis of the DNA from the appropriate region and of the RNA itself revealed that it corresponded to 10Sa RNA (10). Chauhan and Apirion have also determined the nucleotide sequence of the gene that encodes 10Sa RNA, and they named the gene *ssrA* (3).

From our analysis of the RNAs transcribed from each clone of Kohara's library (8), it appears that the five RNAs described here represent all of the small stable RNAs, other than tRNAs, that are recognized as distinct bands after gel electrophoresis. However, a few RNAs which seemed to be inefficiently transcribed and/or less stable remain to be identified.

TABLE 1. Physical map locations of the genes that encode small stable RNAs

Gene	Encoded RNA	Length (nt)	Genetic map location (min)[a]	Phages[b]	Physical map location(s) (kb)[c]	Reference(s)
ffs	4.5S	118	10	149, 150	488 (+)	2, 4
ssrA	10Sa	362	—[d]	438–440	2761 (+)	3, 10
ssr	6S	184	63	470, 471	3069 (+)	5, 11
rnpB	M1	377	70	479–502	3153, 3267, 3280 (−)	9, 12
				514–516	3323, 3337 (−)	
spf	spot 42	109	86	547, 548	3655 (−)	6

[a] From reference 1.
[b] Phage clones that encode the indicated RNAs in Kohara's library (miniset) (7). The reference numbers of these phages, as used by Kohara et al. (7), are as follows: 7E2(149), 19B7(150), 1B2(438), 12F2(439), 25D2(440), 10B4(470), 1A2(471), 21H2(479), 3B2(480), 8A5(501), 2F9(502), 8F8(514), 6B5(515), 20F4(516), 8D2(547), 10H11(548).
[c] Locations on the physical map determined by Kohara et al. (7) are indicated. The symbol + or − in parentheses indicates the orientation of each gene (clockwise or counterclockwise, respectively).
[d] —, not listed in reference 1.

* Corresponding author.

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