Genetic Analysis of a Cold-sensitive Chromosome Segregation Mutant of *Escherichia coli* K12

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The cell division process of bacteria mainly consists of DNA replication, chromosome segregation and septation. Among them, the chromosome segregation process is almost unknown. Only two temperature-sensitive chromosome segregation mutants were isolated from *E. coli*.^{1,2)} Therefore, we isolated a cold-sensitive (*cs*) chromosome segregation mutant from *E. coli* K12 JE1011 and analyzed it physiologically.³⁾ In this note the genetic analysis of the chromosome segregation mutant, *cs*2-68, will be presented. Based on the results below, the *cs* gene of strain *cs*2-68 has now been mapped on the chromosome at approximately 81 min in accordance with the designation by B. J. Bachmann, K. B. Low and A. L. Taylor.⁴⁾

Our previous results of the conjugation experiments revealed that the *cs* gene of strain *cs*2-68 was located between approximately 79 min and 90 min on *E. coli* genetic map.^{3,4)}

To further examine the precise position, we tried to test the co-transduction by phage Plvir. The transduction was performed by the usual basic procedures.⁵⁾ The cold-sensitive chromosome segregation mutant, *cs*2-68, was used as the Pl-donor strain and the strains which had markers located in that region were used as recipients. Table I lists the strains used. Cold-sensitive or cold-resistant (*cr*) transductants were determined by observation of cell shape after incubation at 20°C. As shown in Table II, the *cs* gene of strain *cs*2-68 was co-transducible with *pyrE* at a frequency of 80 per cent but not with *xyl*, *ilv*, *metE*, *rha* or *argE*. We therefore concluded that the *cs* gene of strain *cs*2-68 was located near *pyrE*.

As described above, Hirota already reported the isolation and the genetic analysis of two temperature-sensitive chromosome segregation mutants, *parA* and *parB*. The *parA* gene was located near *purA* and the *parB* gene was located between *serA* and *metC* (Fig. 1).

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TABLE I. BACTERIAL STRAINS

Strain	Properties	Source
JE1011	F ⁻ <i>thr leu trp his thy</i> <i>thi ara lac gal xyl mtl</i> <i>str-r</i>	H. Matsuzawa
<i>cs</i> 2-68	<i>cs</i> mutant derivative of JE1011 <i>thr leu trp his pro</i> ^{a)} <i>thl</i> <i>thi ara lac gal xyl mtl</i> <i>str-r pcsA</i>	This paper
AB2277 ^{sus} -	F ⁻ <i>ilv metE his trp pro</i> <i>mtl mal ara lac gal rha</i> <i>thi Tl-r str-r</i>	M. Yamasaki
AB1157	F ⁻ <i>argE-3 his-4 thr-1</i> <i>leu-6 proA-2 ara-14</i> <i>galK-2 lacY-1 xyl-5 mtl-1</i> <i>thi-1 tsx-33 strA-31</i> <i>sup-37</i>	N. Otsuji
AT2243	Hfr C <i>pyrE met</i>	S. Shinomiya

^{a)} During mutagenesis *cs*2-68 acquired the auxotrophic marker *pro*.

TABLE II. TRANSDUCTION FREQUENCIES

Donor	Recipient	Selected marker	cs-transductants
			Total-transductants
<i>cs</i> 2-68	AB1157	<i>xyl</i>	0/52
<i>cs</i> 2-68	AT2243	<i>pyrE</i>	23/28
<i>cs</i> 2-68	AT2243	<i>pyrE</i>	24/30 ^{a)}
<i>cs</i> 2-68	AB2277 ^{sus} -	<i>ilv</i>	0/93
<i>cs</i> 2-68	AB2277 ^{sus} -	<i>metE</i>	0/39
<i>cs</i> 2-68	AB2277 ^{sus} -	<i>rha</i>	0/28
<i>cs</i> 2-68	AB1157	<i>argE</i>	0/58

Plvir phage was used.

*cs*2-68; *cs*. AT2243, AB1157, AB2277^{sus}-; *cr*.

^{a)} This result was obtained from another experiment.

FIG. 1. Linkage Map of *Escherichia coli* K12.

As indicated by the results of genetic analysis of strain cs2-68, the *cs* gene is distinct from them and is located near *pyrE*. Therefore the mutated gene in this strain is designated *pcsA* (partition *cs*).

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