Complementation Between Different Mutations in the *ilvA* Gene of *Escherichia coli* K-12

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Received for publication 15 April 1974

An *ilvA* mutation carried by a $\phi 80i^{\circ}dilv$ transducing phage complemented some *ilvA* mutations and did not complement others. Complementation was accompanied by appearance of threenine deaminase activity in vivo. These results divided the *ilvA* mutations into two sets which formerly appeared to define two cistrons.

In Escherichia coli K-12 the isoleucine and valine biosynthesis is accomplished by five enzymatic steps which are specified by a cluster of five *ilv* genes designated A through E (16). A complex system of multivalent control allows these enzymes to exhibit derepression in response to limitations of isoleucine, of valine, or of leucine (5). Recent evidence implicates threonine deaminase [L-threonine hydrolyase (deaminating) EC 4.2.1.16], the product of the *ilvA* gene, in the regulation of both the *ilv* gene cluster and the branched-chain aminoacyl transfer ribonucleic acid synthetases, in addition to its catalytic role in isoleucine biosynthesis (3, 8, 11, 14, 19).

Mutations of the *ilvA* gene resulting in the loss of catalytic activity of threonine deaminase confers an Ile⁻ phenotype to strains bearing such lesions, although the phenotype of strains containing an ilvC, D, or E mutation is Ilv^- . We prepared a specialized defective transducing phage containing the *ilv* gene cluster of E. coli K-12 to facilitate studies on the mechanism of multivalent control (1). We then mutagenized strain MI199 (see Table 1 for the genotype of the strains used) with N-methyl-N-nitrosoguanidine as described elsewhere (6) and obtained a derivative with a mutation of the *ilvA* gene contained in the defective phage. The resulting Ile- strain (MI199d) was induced to produce transducing phage. Such purified phage lysates were used to transduce strain AB3590 (containing the *ilvDAC115* multisite mutation) and Val⁺Ile⁻ transductants were obtained at a frequency comparable to that of Ilv⁺ transductants obtained in similar crosses using a parental $\phi 80i^{dilv^{+}}$ phage lysate.

We performed crosses between various *ilv* mutant strains and a lysate of $\phi 80i^{\lambda} dilvA602$

phage. Table 2 shows that Ilv⁺ transductants are obtained with strains containing ilv E12, D538, C485, A201, A537, A601, and A2003 mutations, but not with strains bearing ilvA451. A454, A483, A529, A534, A550, A2001, and A2001 mutations. For each of MI2, CU2, CU26, CU97, CU105 and CU255, we purified a single Ilv⁺ transductant and induced and prepared a lysate. Each of these lysates contained the original $\phi 80i^{\lambda} dilvA602$ phage as indicated by transduction of AB3590. In all cases, Val+ Iletransductants appeared, but in no case were Ilv⁺ transductants observed. In addition, Ile⁺ transductants were obtained with a strain isogenic to strain AB3590, strain MI166i, which contains the *ilvA601* mutation of strain MI2. To determine whether the Ile⁺ clones were recombinants, a transductant of strain M12 and two transductants of strain MI166i were purified and induced, and lysates were made. These lysates contained $\phi 80i^{+}dilv$, ilvA602 phage as indicated by transduction of strain AB3590 to yield Val⁺, Ile⁻ transductants and by transduction of strain MI166i to yield Ile+ transductants. Furthermore, P1 phage grown on one of the Ile+ transductants of strain MI166i was used to determine if the two ilvA mutations had recombined. Strain AB3590 was transduced with this P1 lysate and Val+transductants were selected on plates containing isoleucine. All the transductants tested (20/20) were Ile-, which shows that $ilvA^+$ recombinants were absent. These results insure that the Ilv⁺ transductants reported in Table 2 are the result of complementation and not recombination in the *ilv* region of the chromosome.

Table 3 shows the enzymatic activity of threonine deaminase in different strains. Threonine deaminase is undetectable in strains

NOTES

Strain	Genotypes	Source
AB1255	thi-1 ilvA201 argH1 metB1 his-1 xyl-7 malA1 tsx-5 str-8,9, or 17 sup48 λ ^r	E. Adelberg (13)
AB1412	thi-1 ilvA44 argH1 metB1 his-1 xyl-7 malA1 gal-6 lac Y1 str8,9 or 17 mtl-2 \text{\text{y}}	E. Adelberg (13)
AB3590	thi, mtl, malA str his trpC tsx lacZ ilvDAC115	E. Adelberg (10)
CU2	ilvE453	H.E.Umbarger (18)
CU8	ilvA451	H. E. Umbarger (18)
CU24	ilvA483 metE200 rbs-215 gal	Pledger (14)
CU26	ilvC485	Pledger (14)
CU96	ilvA529 gal	Levinthal
CU97	ilvD530 gal	Levinthal
CU102	ilvA534 gal	Levinthal
CU105	ilvA537 gal	Levinthal
CU140	ilvA550 gal	Levinthal
CU253	ilvA2001 gal	Pledger
CU254	ilvA2002 gal	Pledger
CU255	ilvA2003 gal	Pledger
CU1008	ilvA451	McGilvray
M 12	argH trpA23 ilvA601	Iaccarino (9)
MI166b	thi mtl malA str his trpC tsx lacZ llv ⁺ trans- ductant of AB3590	Iaccarino
MI199	AB3590 lysogenic for \$\phi80i^ CI857 t68dilv^+ \$\phi80i^ CI857t68\$	Iaccarino (1)
MI199d	AB3590 lysogenic for \$\$\phi80i^ CI857 t68dilvA602\$ \$\$\phi80i^ CI857 t68\$	Iaccarino

TABLE 1. Escherichia coli strains: genotype and source

 TABLE 2. Transduction of ilv mutations with

 \$\oteq 80i^\dilvA602^a\$

 TABLE 3. Intracellular concentration of threonine deaminase in different strains

Recipients		Frequency
Strain no.	ilv allele no.	$\times 10^{-3}$ of <i>ilv</i> ⁺ transductants ^o
CU2	ilvE12	15.1
CU26	ilvC485	13.6
CU97	ilvD530	12.6
CU8	ilvA451	< 0.001
CU1008	ilvA454	< 0.001
CU24	ilvA483	< 0.001
CU96	ilvA529	< 0.001
CU102	ilvA534	< 0.001
CU140	ilvA550	< 0.001
CU253	ilvA2001	< 0.001
CU254	ilvA2002	< 0.001
AB1412	ilvA44	2.0
AB1255	ilvA201	0.2
CU105	ilvA537	20.8
M12	ilvA601	0.9
CU255	ilvA2003	2.3

^a Transductions were performed as described by Press et al. (15). Ilv⁺ transductants were selected by plating the transduction mixture on appropriately supplemented minimal agar plates.

 \dots The frequency of Ilv^+ transductants is computed as the number of transductant colonies divided by the titer of plaque-forming units.

AB3590 and MI2 and in a Val⁺ Ile⁻ transductant of strain AB3590. Strain MI166b contains a normal level of threonine deaminase. The Ilv⁺ transductant derived from strain MI2 shows

Strain	Threonine deaminase (sp act) ^a
MI166b	28
MI2 (<i>ilvA601</i> , Ile ⁻)	< 0.2
AB3590	< 0.3
Ile ⁺ transductant of MI2 ^b	5
Val ⁺ , Ile ⁻ transductant of AB3590	< 0.3

^a Threonine deaminase was assayed as described in by Guardiola and Iaccarino (6). Specific activity is expressed as nanomoles of product formed per minute per milligram of protein.

^bTransduction was performed with the $\phi 80i^{dilv}$, *ilvA602* phage described in this note.

some threonine deaminase activity (18% of strain MI166b). We conclude that the *ilvA* mutation carried by the transducing phage can complement some *ilvA* mutations and this complementation is accompanied by the appearance of detectable levels of intracellular threonine deaminase activity.

Our results indicate that the *ilvA* gene can be divided into two cistrons with respect to catalytic function. We assign *ilvA451*, 454, 483, 529, 534, 550, 602, 2001 and 2002 to the *ilvAa* cistron and *ilvA44*, 201, 537, 601, and 2003 to the *ilvAb* cistron.

Evidence was reported (4) that threonine

deaminase is a tetramer composed of four identical subunits as indicated by ultracentrifugation and acrylamide gel electrophoresis. However, the definition of a cistron (2) does not specify any relationship between the number of complementation groups and the number of polypeptide chains (identical or non-identical) in the protein specified by the gene. Indeed, the hisD gene of Salmonella typhimurium contains two complementation groups (7) while the enzyme it specifies, histidinol dehydrogenase, is composed of two identical polypeptide chains (12). This situation can be contrasted with the hisC gene which contains one cistron (7) and specifies the enzyme imidazole acetol phosphate transaminase, an enzyme also composed of two identical polypeptide chains (17).

In conclusion, our discovery of two complementation groups in the *ilvA* gene might indicate the occurrence in threonine deaminase of two non-identical polypeptide chains or noncovalent interactions between identical polypeptide chains. Work is in progress in one of our laboratories which will discriminate between these two possibilities.

We thank Maxine Levinthal, Bruno Esposito, and Alessandro Lamberti for skillful technical assistance. This work was supported by Public Health Service research grant GM12522 from the National Institute of General Medical Science.

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