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Current Linkage Map of *Escherichia coli*

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INTRODUCTION

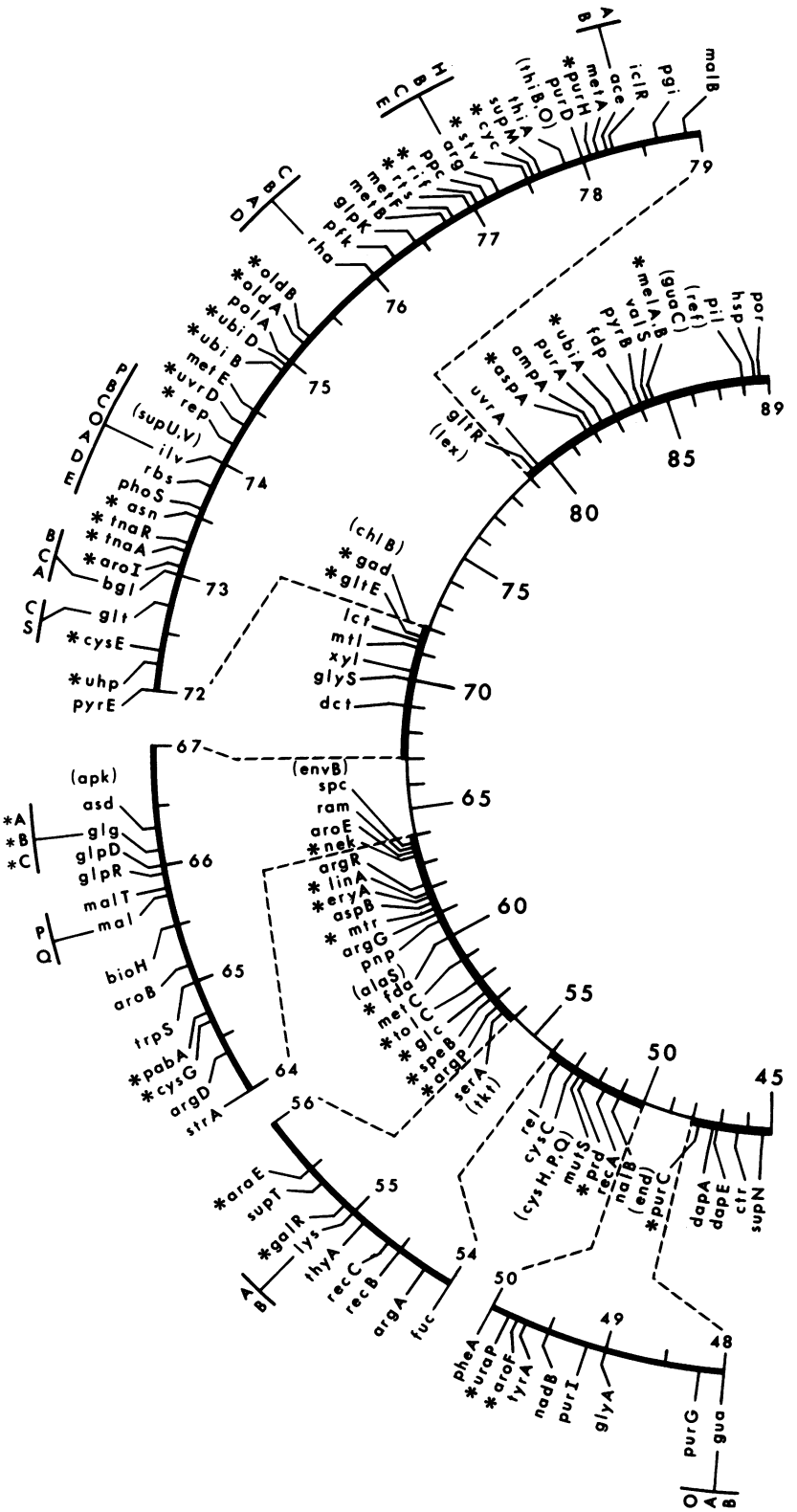
A survey of recent literature has shown that the sexually fertile strain K-12 of *Escherichia coli* continues to be a favorite subject for intensive genetic and biochemical investigation. Compared to the 220 genes which were identified and mapped only 2.5 years ago (215), there are now approximately 310 genes described in *E. coli*. Moreover, several of the older genes which were listed in the previous article (215) have now been mapped with much greater precision. This review consists of a comprehensive, updated report on the linkage map of *E. coli*. A similar review of known gene loci in the related species, *Salmonella typhimurium*, appears in a companion report by Sanderson (189).

The linkage map of *E. coli*, as of March 1970, is shown in Fig. 1. Although the large size of the map necessitated dividing the figure into right and left halves, it must be kept in mind that the haploid genome of *E. coli* is both genetically and physically a closed, continuous linkage group (31, 118). Accordingly, Fig. 1 should be viewed as an intact circle and not as two separate linkage groups. The functions, insofar as they are known, of all the genes depicted in Fig. 1 are listed in Table 1, together with references to both published and unpublished sources of information. The map scale is marked off in time units, in the manner originated by Jacob and Wollman (118). The overall map length of 90 min represents the sum of individual map segments measured by interrupted mating experiments with several different Hfr strains of *E. coli* (214). Precision of the 90-min figure is estimated to be around ± 3%, and it is in good agreement with the results of Fulton (80) who found that a single Hfr donor can transfer a complete chromosome in 90 min.

GENETIC NOMENCLATURE

The genetic nomenclature employed in this review conforms to the recommendations of Demerec et al. (52) in which gene loci are identified by italicized three-letter symbols, followed by capital letters A through Z to distinguish loci of similar or related function. Occasionally, two or more conventional symbols will crop up in the literature to denote the same gene locus or to identify different allelic states of the same gene. Rather than overcrowd the map with these extra symbols, only the original symbols are shown in Fig. 1 and the alternate symbols are given as cross-referenced entries in Table 1. There are also occasions when an old symbol becomes either misleading or inappropriate and there is good reason to change it altogether. One example is the symbol *nic* which has been used to specify genes determining nicotinic acid requirement. A recent study points out that the *nic* genes do not govern the synthesis of nicotinic acid per se, but

FIG. 1. *Scale drawing of the linkage map of E. coli adapted from Taylor and Trotter (215). The inner circle, which bears the time scale from 0 through 90 min, depicts the intact circular linkage map. The map is graduated in 1-min intervals beginning arbitrarily with zero at the thrA locus. Selected portions of the map (e.g., the 10- to 12-min segment) are displayed on arcs of the outer circle with a 4.5× expanded time scale to accommodate all of the markers in crowded regions. Gene symbols are explained in Table 1. Markers in parentheses are only approximately mapped at the positions shown. A gene identified by an asterisk has been mapped more precisely than the markers in parentheses, but its orientation relative to adjacent markers is not yet known.*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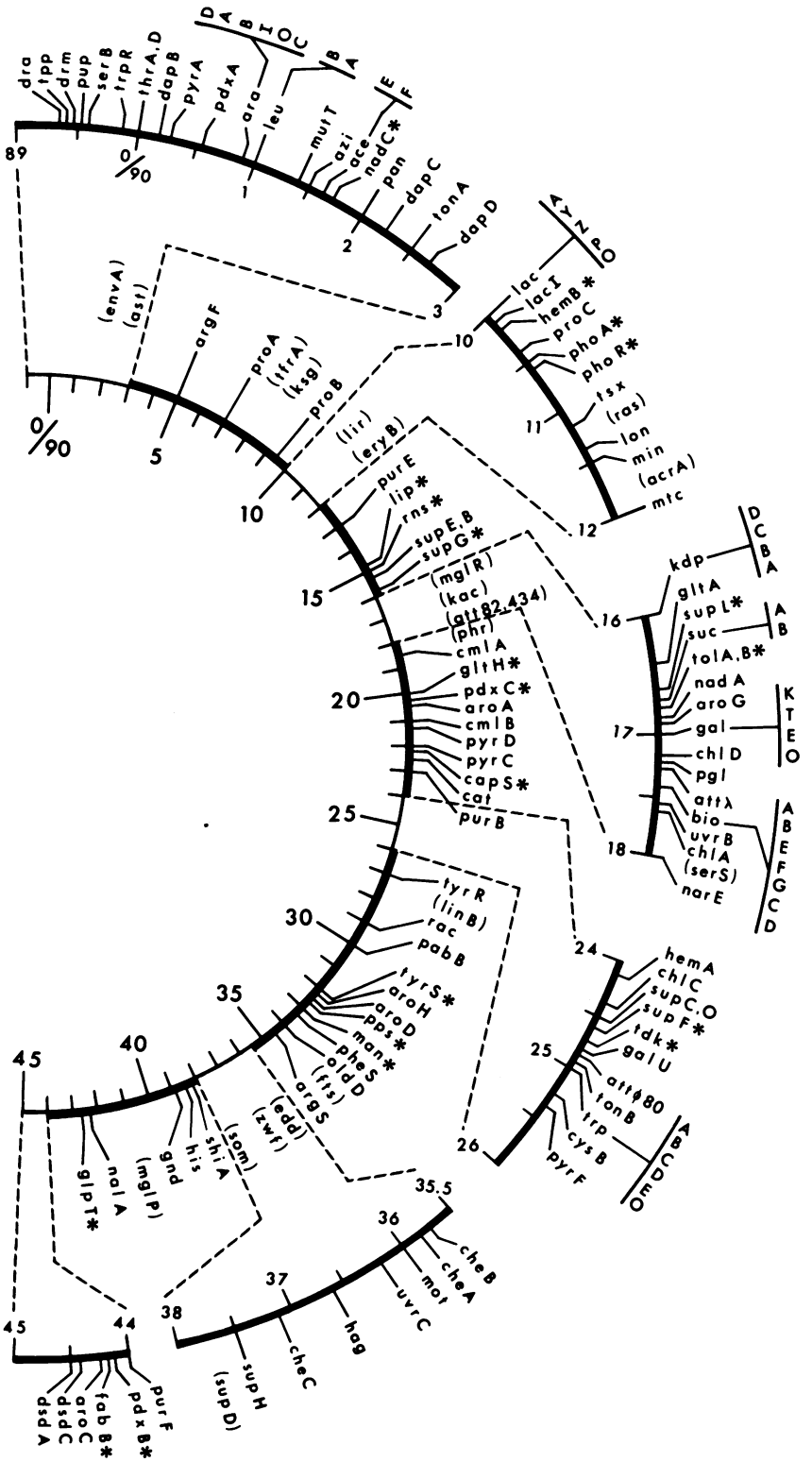
55
56
pgi
iclR
ace
melA
*purH
purD
(thiB,O)
thiA
supM
*cyc
*stv
arg
*rif
*rts
metF
metB
glpK
pfk
rho
*oldB
*oldA
polA
*ubiD
*ubiB
metE
*uvrD
*rep
(supU,V)
ilv
rbs
phoS
*asn
*tnaR
*tnaA
*aroI
bgl
glt
*cysE
*uhp
pyrE
(chlB)
*gad
*gltE
lct
mtl
xyl
glyS
dct
(envB)
spc
ram
aroE
*nek
argR
*linA
*eryA
aspB
*mtr
argG
pnp
(alaS)
*fda
metC
*tolC
*glc
*speB
*argP
serA
(lkr)
(apk)
asd
glg
glpD
glpR
malT
mal
bioH
aroB
trpS
*pabA
*cysG
argD
strA
*araE
supT
*galR
lys
thyA
recC
recB
argA
fuc
rel
cysC
(cysH,P,Q)
*mutS
*prd
recA
nalB
(end)
*purC
dapA
dapE
ctr
supN
pheA
*uraP
*aroF
tyrA
nadB
purI
glyA
purG
gua
*ubiA
purA
ampA
*aspA
uvrA
gltR
(lex)
*melA,B
pyrB
tdp
valS
(guaC)
(ref)
pil
hsp
por
maiB


dra
tpp
drm
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serB
trpR
thrA,D
dapB
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aro
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D A B H O C
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mutT
azi
ace
nadC*
pan
dapC
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E F
89
0/90
1
2
3
(envA)
(ast)
argF
proA
(tfrA)
(ksg)
proB
0/90
5
10
15
(lir)
(eryB)
purE
lip*
rns*
supE,B
supG*
(mglR)
(kac)
(gut82,434)
(phr)
cmlA
gltH*
pdxC*
aroA
cmlB
pyrD
pyrC
capS*
cat
purB
20
25
tyrR
(linB)
rac
pabB
30
tyrS*
aroH
aroD
pps*
man*
pheS
oldD
(ffs)
argS
(zwf)
(edd)
35
40
45
glpT*
nalA
(mglP)
gnd
his
shiA
(som)
45
44
dsdA
dsdC
aroC
fabB*
pdxB*
purF
38
(supD)
cheC
37
hag
36
uvrC
mot
cheA
cheB
35.5
10
lac
lacI
hemB*
proC
phoA*
phoR*
11
tsx
(ras)
lon
min
(acrA)
mtc
12
A Y N R O
16
kdp
gltA
supL*
suc
tolA,B*
D C B A
A B
17
nadA
aroG
gal
chlD
pgl
attλ
bio
uvrB
chlA
(serS)
narE
18
K T E O
A B E F G C D
24
hemA
chlC
supC,O
supF*
tdk*
galU
25
attφ80
tonB
trp
cysB
pyrF
26
A B U D O

rather the synthesis of nicotinamide adenine dinucleotide (218). Hence, the *nic* genes are now identified by the more appropriate symbol *nad* (218).

SUMMARY OF CURRENT MODIFICATIONS AND ADDITIONS TO THE LINKAGE MAP OF E. COLI

Two principal techniques of genetic mapping will be mentioned in the following discussion. The first method is mapping by "time of entry," in which genetic markers are positioned on the chromosome by determining the time when each marker first enters a recipient cell during the course of chromosome transfer from an Hfr donor strain. The method is described in detail by Jacob and Wollman (118), and references to more recent technical refinements are given in (215). Additional information pertaining to specific Hfr strains mentioned below is also available (215). The second, and generally more accurate, mapping technique relies on transduction crosses mediated by bacteriophage P1 of *E. coli*, as described by Lennox (130). Two-factor transduction crosses provide estimates of the distance between pairs of markers separated by not more than 1.5 to 2 min by making use of the empirical "minutes-to-per cent frequency of cotransduction" correlations summarized in Table 9 of reference 215. Multifactor transduction crosses involving three or more cotransducible markers permit precise determinations of the sequence of markers with respect to each other and to the linkage map as a whole. Groups of closely linked markers for which the gene sequence relative to the whole map is known are referred to in this review as having a known orientation.

In the following survey, which will be confined largely to new data appearing since 1967, the discussion begins with markers located in the 0- to 15-min map segment and then proceeds in a clockwise direction through successive 15-min increments of the map.

Region from 0 to 15 min. The locus *dapB*, which is placed at minute 0 between *thr* and *pyrA* by three-point transduction crosses, is one of five genes for α-ϵ-diaminopimelic acid biosynthesis recently mapped in this laboratory (A. I. Bukhari and A. L. Taylor, *in preparation*). We have assigned the suffix *B* to this *dap* locus since it determines the second enzyme of the biosynthetic pathway (Table 1). A new locus corresponding to an operator region (*araO*) has been added to the arabinose operon at minute 1 (125). This report (125) also indicates the orientation of the *leuA* and *leuB* genes of the leucine operon. The specific transversion-inducing mutator gene, *mutT*, is now accurately mapped at minute 1.5 (41, 97). A second mutator allele, *ast*, also maps in this general region, but a recent comparative study (245) shows that *ast* strains are phenotypically quite distinct from *mutT* stocks. The *azi* locus, originally described as determining resistance to sodium azide (117, 134), is now known to be associated with additional phenotypic alterations involving resistance to phenethyl alcohol and defective septum formation (242). It seems likely, as suggested by Yura and Wada (242), that the entire *mutT-azi-ace E, F* region may turn out to be a gene complex that specifies part of the structure and function of the cell membrane. The *nadC* locus, one of three known genes which determine nicotinic acid requirement, maps between *azi* and *pan* (85), but its exact position with respect to other nearby markers is not known. The *dapD* and *dapC* loci have been mapped by transduction at points immediately clockwise and anticlockwise, respectively, to *tonA*. The genes probably control the third and fourth steps in diaminopimelic acid biosynthesis, but this has not been confirmed by direct enzyme assays. It appears that certain mutations resulting in defective synthesis of cell wall peptidoglycan also map in the general vicinity of these *dap* genes (143). R. Curtiss (*personal communication*) informs us that the pleiotropic phage resistance gene *tfrA* was incorrectly placed at min 10 in the previous map (215) and that it actually lies somewhere between minutes 7 and 9. The *ksg* (210), *lir*, and *eryB* (9) genes are all concerned with the level of resistance to various antibiotics, and all three map roughly in the region between *leu* and *lac*. The preliminary indication seems to be that they represent at least two new regions, besides the one at minutes 63–64, which code for ribosomal proteins. Positions of the *tsx* and *purE* genes, previously placed at minutes 12.5 and 15, respectively (215), have been changed slightly in accord with new transduction data reported by Donch and Greenberg (56). Several laboratories have described mutants at minutes 11–12 which manifest altered sensitivities to mitomycin C, ultraviolet light, acridines, methylene blue, phenethyl alcohol, triphenyl tetrazolium chloride, or sodium dodecyl sulfate (110, 149, 161, 213). Mutants having defects in septum formation or alterations in radiation sensitivity also map in this region (*see lon*, *min*, and *ras*) and it therefore appears that the 11- to 12-min segment may contain a second gene complex concerned with membrane structure and function. Several mutants defective in lipoic acid biosynthesis have been mapped at the *lip* locus at minute 15 (100); the orientation of *lip* with respect to *rns*, also at minute 15 (181), is not known.

TABLE 1. *List of genetic markers of E. coli*

Gene symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected	References[b]
aceA	Acetate	78	*icl*; utilization of acetate: isocitrate lyase	26, 223
aceB	Acetate	78	*mas*; utilization of acetate: malate synthetase A	223
aceE	Acetate	2	*aceE1*; acetate requirement; pyruvate dehydrogenase (decarboxylase component)	98, 99
aceF	Acetate	2	*aceE2*; acetate requirement; pyruvate dehydrogenase (lipoic reductase-transacetylase component)	98, 99
acrA	Acridine	(11)	Sensitivity to acriflavine, phenethyl alcohol, Na dodecyl sulfate	149
alaS	Alanine	(60)	*ala-act*; alanyl-tRNA synthetase	150
ampA	Ampicillin	82	Resistance or sensitivity to penicillin	70
apk		(66)	Lysine-sensitive aspartokinase	164
araA	Arabinose	1	L-Arabinose isomerase	129
araB	Arabinose	1	L-Ribulokinase	129
araC	Arabinose	1	Regulatory gene	200, 201
araD	Arabinose	1	L-Ribulose 5-phosphate 4-epimerase	129
araE	Arabinose	56	L-Arabinose permease	67, 156, A
araI	Arabinose	1	Initiator locus	200, 201
araO	Arabinose	1	Operator locus	125
argA	Arginine	54	*argB*, *ArgI*, Arg_2; *N*-acetylglutamate synthetase	90, 111, 215, 226
argB	Arginine	77	*argC*; α-*N*-acetyl-L-glutamate-5-phosphotransferase	87, 88, 133, 226
argC	Arginine	77	*argH*, *arg2*; *N*-acetylglutamic-γ-semialdehyde dehydrogenase	87, 88, 133, 226
argD	Arginine	64	*argG*, Arg_1; acetylornithine-δ-transaminase	112, 226, B
argE	Arginine	77	*argA*, *Arg4*; L-ornithine-*N*-acetylornithine lyase	87, 88, 133, 226
argF	Arginine	5	*argD*, *Arg5*; ornithine transcarbamylase	90, 133, 226
argG	Arginine	61	*argE*, *Arg6*; argininosuccinic acid synthetase	133, 214, 215, 226
argH	Arginine	77	*argF*, *Arg7*; L-argininosuccinate arginine lyase	87, 88, 133, 226
argP	Arginine	57	Arginine permease	132, C
argR	Arginine	62	*Rarg*; regulatory gene	90, 119, 133, 226
argS	Arginine	35	Arginyl-tRNA synthetase	40
aroA	Aromatic	21	3-Enolpyruvylshikimate-5-phosphate synthetase	170, 178, 214
aroB	Aromatic	65	Dehydroquinate synthetase	109, 170, 232
aroC	Aromatic	44	Chorismic acid synthetase	170, 214
aroD	Aromatic	32	Dehydroquinase	170, 214
aroE	Aromatic	64	Dehydroshikimate reductase	170, 215, 232
aroF	Aromatic	50	3-Deoxy-D-arabinoheptulosonic acid-7-phosphate (DHAP) synthetase (tyrosine-repressible isoenzyme)	228

[a] Numbers refer to the time scale shown in Fig. 1. Parentheses indicate approximate map locations.

[b] Numbers refer to the Literature Cited section; letters refer to the following: (A) E. Englesberg, *personal communication*; (B) A. L. Taylor, *unpublished data* mentioned in this paper; (C) W. K. Maas and P. Popkins, *personal communication*; (D) R. Curtiss, III, *personal communication*; (E) A. I. Bukhari and A. L. Taylor, *in preparation*; (F) H. Yamaguchi, C. Fetterolf, and J. G. Flaks, *personal communication*; (G) E. J. Murgola, *personal communication*; (H) H. I. Adler, *personal communication*; (I) G. J. Tritz and R. K. Gholson, *personal communication*; (J) T. T. Wu and E. C. C. Lin, *personal communication*; (K) B. Low, *personal communication*; (L) W. F. Doolittle, *personal communication*; (M) W. K. Maas, *personal communication*; (N) E. Whitney, *personal communication*.

TABLE 1.—*Continued*

Gene symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected	References[b]
aroG	Aromatic	17	DHAP synthetase (phenylalanine-repressible isoenzyme)	1, 27, 228
aroH	Aromatic	32	DHAP synthetase (tryptophan-repressible isoenzyme)	228
aroI	Aromatic	73	Function unknown	86
asd	—	66	*dap* + *hom*; aspartic semialdehyde dehydrogenase	38, 95, 196
asn	—	73	Asparagine synthetase	34
aspA	—	82	Aspartase	138
aspB	Aspartate	62	*asp*; aspartate requirement	118, 180
ast	Astasia	(4)	Generalized high mutability	244, 245
attλ	Attachment	17	Integration site for prophage λ	118, 184
attφ80	Attachment	25	Integration site for prophage φ80	204
att82	Attachment	(17)	Integration site for prophage 82	118, 184
att434	Attachment	(17)	Integration site for prophage 434	118, 184
azi	Azide	2	*pea*, *fts*; resistance or sensitivity to Na azide or phenethyl alcohol; filament formation at 42C	117, 134, 221, 242
bglA	β-Glucoside	73	*β-glA*; aryl β-glucosidase	192
bglB	β-Glucoside	73	*β-glB*; β-glucoside permease	192
bglC	β-Glucoside	73	*β-glC*; regulatory gene	192
bioA	Biotin	17	Group II; 7-oxo-8-aminopelargonic acid (7KAP) → 7,8-diaminopelargonic acid (DAPA)	1, 51, 65, 182
bioB	Biotin	17	Conversion of dethiobiotin to biotin	1, 51, 65, 182
bioC	Biotin	17	Unknown block prior to 7KAP synthetase	1, 51, 65, 182
bioD	Biotin	17	Dethiobiotin synthetase	1, 51, 64, 65, 182
bioE	Biotin	17	Unknown block prior to 7KAP synthetase	1, 51, 65, 182
bioF,G	Biotin	17	7KAP synthetase	1, 51, 65, 182
bioH	Biotin	66	*bioB*; early block prior to 7KAP synthetase	95, 182, 196
capS	Capsule	22	Regulatory gene for capsular polysaccharide synthesis	139
cat	—	23	*CR*; catabolite repression	219
cheA	Chemotaxis	36	*motA*; chemotactic motility	11, 12
cheB	Chemotaxis	36	*motB*; chemotactic motility	11, 12
cheC	Chemotaxis	37	Chemotactic motility	12
chlA	Chlorate	18	*narA*; pleiotropic mutations affecting nitrate-chlorate reductase and hydrogen lyase activity	1, 174, 175, 224
chlB	Chlorate	(71)	*narB*; pleiotropic mutations affecting nitrate-chlorate reductase and hydrogen lyase activity	174
chlC	Chlorate	25	*narC*; structural gene for nitrate reductase	93, 174, 187
chlD	Chlorate	17	*narD*, *narF*; nitrate-chlorate reductase	1, 224
cmlA	Chloramphenicol	19	Resistance or sensitivity to chloramphenicol	178
cmlB	Chloramphenicol	21	Resistance or sensitivity to chloramphenicol	178
ctr	—	46	Mutations affecting the uptake of diverse carbohydrates	231
cyc	Cycloserine	78	Resistance or sensitivity to D-cycloserine	47, D
cysB	Cysteine	25	Pleiotropic mutations affecting cysteine biosynthesis	120, 205, 239
cysC	Cysteine	53	Adenosine 5′-sulfatophosphate kinase	120, 144, 215

TABLE 1.—*Continued*

Gene symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected	References[b]
cysE	Cysteine	72	Apparently pleiotropic	120
cysG	Cysteine	65	Sulfite reductase	215
cysH	Cysteine	(53)	Adenosine 3′-phosphate 5′-sulfato-phosphate reductase	120
cysP	Cysteine	(53)	Sulfate permease and sulfite reductase	120
cysQ	Cysteine	(53)	Sulfite reductase	120
dapA	Diaminopimelate	47	Dihydrodipicolinic acid synthetase	38, E
dapB	Diaminopimelate	0	Dihydrodipicolinic acid reductase	73, E
dapC	Diaminopimelate	2	Tetrahydrodipicolinic acid → N-succinyl-diaminopimelate	E
dapD	Diaminopimelate	3	Tetrahydrodipicolinic acid → N-succinyl diaminopimelate	E
dapE	Diaminopimelate	47	*dapB*; N-succinyl-diaminopimelic acid deacylase	38, E
darA	—	—	*See uvrD*	222
dct	—	69	Uptake of C_4-dicarboxylic acids	124
deo	Deoxythymidine	—	*See dra, drm, pup* and *tpp*	131
dra	—	89	*deoC, thyR*; deoxyriboaldolase	4, 131, 159
drm	—	89	*deoB, thyR*; deoxyribomutase	4, 131, 159
dsdA	D-Serine	45	D-Serine deaminase	144
dsdC	D-Serine	45	Regulatory gene	144
edd	—	(35)	Entner-Doudoroff dehydrase (gluconate-6-phosphate dehydrase)	167
end	—	(50)	*endoI*; endonuclease I	59
envA	Envelope	(3)	Anomalous cell division involving chain formation	155
envB	Envelope	(65)	Anomalous spheroid cell formation	154
eryA	Erythromycin	62	Resistance or sensitivity to erythromycin	F
eryB	Erythromycin	(11)	High level resistance to erythromycin	9
exr	—	—	*See lex*	
fabB	—	44	Fatty acid biosynthesis	69
fda	—	60	*ald*; fructose-1, 6-diphosphate aldolase	20
fdp	—	84	Fructose diphosphatase	77, 78, 240
ftsA	—	—	*See azi*	221
fts	—	(35)	*fts-9*; filamentous growth and inhibition of nucleic acid synthesis at 42 C	221
fuc	Fucose	54	Utilization of L-fucose	71, 215
gad	—	72	Glutamic acid decarboxylase	135, 137
galE	Galactose	17	*galD*; uridinediphosphogalactose 4-epimerase	3, 29
galK	Galactose	17	*galA*; galactokinase	3, 29
galO	Galactose	17	*galC*; operator locus	29, 30
galT	Galactose	17	*galB*; galactose 1-phosphate uridyl transferase	3
galR	Galactose	55	*Rgal*; regulatory gene	30, 188
galU	Galactose	25	*UPDG*; uridine diphosphoglucose pyrophosphorylase	198, 93
glc	Glycolate	58	Utilization of glycolate; malate synthetase G	223
glgA	Glycogen	66	Glycogen synthetase	33, 203
glgB	Glycogen	66	α-1,4-Glucan: α-1,4-glucan 6-glucosyltransferase	33, 203
glgC	Glycogen	66	Adenosine diphosphate glucose pyrophosphorylase	33, 203
glpD	Glycerol phosphate	66	*glyD*; L-α-glycerophosphate dehydrogenase	44, 196
glpK	Glycerol phosphate	76	Glycerol kinase	45

TABLE 1.—*Continued*

Gene symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected	References[b]
glpT	Glycerol phosphate	43	L-α-Glycerophosphate transport system	44
glpR	Glycerol phosphate	66	Regulatory gene	44
gltA	Glutamate	16	*glut*; requirement for glutamate; citrate synthase	13, 68, 100
gltC	Glutamate	73	Operator locus	135,136
gltE	Glutamate	72	Glutamyl-tRNA synthetase	G
gltH	Glutamate	20	Requirement	135
gltR	Glutamate	79	Regulatory gene for glutamate permease	136
gltS	Glutamate	73	Glutamate permease	136
glyA	Glycine	49	Serine hydroxymethyl transferase[c]	48, 215
glyS	Glycine	70	*gly-act*; glycyl-tRNA synthetase	21
gnd	—	39	Gluconate-6-phosphate dehydrogenase	167
guaA	Guanine	48	gua_b; xanthosine-5′-monophosphate aminase	151, 211, 215
guaB	Guanine	48	gua_a; inosine-5′-monophosphate dehydrogenase	151, 211
guaC	Guanine	(88)	Guanosine-5′-monophosphate reductase	151
guaO	Guanine	48	Operator locus	151, 152
hag	H antigen	37	*H*; flagellar antigens (flagellin)	12
hemA	Hemin	24	Synthesis of δ-aminolevulinic acid	93, 190, 191
hemB	Hemin	10	*ncf*; synthesis of catalase and cytochromes	191
his	Histidine	39	Requirement	214
hsp	Host specificity	89	*hs*, *rm*; host restriction and modification of DNA	23, 39, 128, 235
icl	—	—	*See aceA*	26
iclR	—	78	Regulation of the glyoxylate cycle	26
ilvA	Isoleucine-valine	74	*ile*; threonine deminase	169, 177
ilvB	Isoleucine-valine	74	Condensing enzyme (pyruvate + α-ketobutyrate)	169, 177
ilvC	Isoleucine-valine	74	*ilvA*; α-hydroxy-β-keto acid reductoisomerase	169, 177
ilvD	Isoleucine-valine	74	*ilvB*; dehydrase	169, 177
ilvE	Isoleucine-valine	74	*ilvC*; transminase B	169, 177
ilvO	Isoleucine-valine	74	Operator locus for genes *ilvA*, *D*, *E*	176, 177
ilvP	Isoleucine-valine	74	Operator locus for gene *ilvB*	176, 177
kac	K-accumulation	17	Defect in potassium ion uptake	28
kdpA-D	K-dependent	16	Requirement for a high concentration of potassium	68
ksg	Kasugamycin	(8)	Resistance or sensitivity to kasugamycin (30*S* ribosomal subunit)	210
lacA	Lactose	10	*a*, *lacAc*; thiogalactoside transacetylase	18, 145, 243
lacI	Lactose	10	*i*; regulator gene	49, 145
lacO	Lactose	10	*o*; operator locus	49, 145
lacP	Lactose	10	*p*; promoter locus	49, 116, 145
lacY	Lactose	10	*y*; galactoside permease (M protein)	76, 117, 145
lacZ	Lactose	10	*z*; β-galactosidase	117, 134, 145
lct	Lactate	71	L-Lactate dehydrogenase	163
leuA	Leucine	1	α-Isopropylmalate synthetase	117, 125, 134
leuB	Leucine	1	β-Isopropylmalate dehydrogenase	125
lex	—	(79)	Resistance or sensitivity to X rays and UV light	106
linA	Lincomycin	62	Resistance or sensitivity to lincomycin	F
linB	Lincomycin	(28)	High-level resistance to lincomycin	9
lip	Lipoic acid	15	Requirement	100, 225
lir	—	(11)	Increased sensitivity to lincomycin or erythromycin, or both	9

[c] Enzymatic defect is inferred from studies on the homologous mutant in *S. typhimurium*. Refer to Sanderson (189) for additional references.

TABLE 1.—*Continued*

Gene symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected	References[b]
lon	Long form	11	*capR, dir, muc*; filamentous growth, radiation sensitivity, and regulation of capsular polysaccharide synthesis	2, 56, 108, 140, 221
lysA	Lysine	55	Diaminopimelic acid decarboxylase	118, 214, E
lysB	Lysine	55	Lysine or pyridoxine requirement	E
malB	Maltose	79	*mal-5*; maltose permease and phage λ receptor site	196, 197
malP	Maltose	66	*malA*; maltodextrin phosphorylase	95, 96, 118, 196
malQ	Maltose	66	*malA*; amylomaltase	95, 96, 118, 196
malT	Maltose	66	*malA*; probably a positive regulatory gene	95, 96, 118, 196
man	Mannose	33	Phosphomannose isomerase	141, 215
melA	Melibiose	84	*mel-7*; α-galactosidase	195
melB	Melibiose	84	*mel-4*; thiomethylgalactoside permease II	173, 195
metA	Methionine	78	met_3; homoserine *O*-transsuccinylase	107, 118, 186, 196
metB	Methionine	77	*met-1*, met_1; cystathionine synthetase	87, 118, 186, 214
metC	Methionine	59	Cystathionase	186, 215
metE	Methionine	75	*met-*B_{12}; N^5-methyltetrahydropteroyl triglutamate-homocysteine methylase[c]	63, 207, 214
metF	Methionine	77	*met-2*, met_2; N^5, N^{10}-methyltetrahydrofolate reductase[c]	87, 88, 118, 207
mglP	Methyl-galactoside	(40)	*P-MG*; methyl-galactoside permease	82, 185
mglR	Methyl-galactoside	(17)	*R-MG*; regulatory gene	82
min	Minicell	11	Formation of minute cells containing no DNA	36, H
mot	Motility	36	Flagellar paralysis	12
mtc	Mitomycin C	12	*Mb, mbl*; sensitivity to acridines, methylene blue and mitomycin C	110, 161, 213
mtl	Mannitol	71	Utilization of D-mannitol	214
mtr	Methyl tryptophan	61	Resistance to 5-methyltryptophan	103
mutS	Mutator	53	Generalized high mutability	202
mutT	Mutator	1	Generalized high mutability; specifically induces AT → CG transversions	41, 97, 202, 206
nadA	Nicotinamide adenine dinucleotide	17	*nicA*; nicotinic acid requirement	1, 215
nadB	Nicotinamide adenine dinucleotide	49	*nicB*; nicotinic acid requirement	118, 218
nadC	Nicotinamide adenine dinucleotide	2	Quinolinate phosphoribosyl transferase	85, I
nalA	Nalidixic acid	42	Resistance or sensitivity to nalidixic acid	94
nalB	Nalidixic acid	51	Resistance or sensitivity to nalidixic acid	94
nar	Nitrate reductase	—	*See chl*	
narE	—	18	Nitrate reductase (*see* also *chl*)	175, 224
nek	—	63	Resistance to neomycin and kanamycin (30*S* ribosomal protein)	10
nic	—	—	*See nad*	
oldA	Oleate degradation	75	*old-30*; thiolase	162
oldB	Oleate degradation	75	*old-64*; hydroxyacyl-coenzyme A dehydrogenase	162
oldD	Oleate degradation	34	*old-88*; acyl-coenzyme A synthetase	162
pabA	*p*-Aminobenzoate	65	Requirement	109, 232
pabB	*p*-Aminobenzoate	30	Requirement	109
pan	Pantothenic acid	2	Requirement	53

TABLE 1.—*Continued*

Gene symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected	References[b]
pdxA	Pyridoxine	1	Requirement	215
pdxB	Pyridoxine	44	Requirement	54
pdxC	Pyridoxine	20	Requirement	B, D
pfk	—	76	Structural or regulatory gene for fructose 6-phosphate kinase	146
pgi	—	79	Phosphoglucoisomerase	77
pgl	—	17	6-Phosphogluconolactonase	127
pheA	Phenylalanine	50	Prephenic acid dehydratase	170, 214, 215
pheS	Phenylalanine	33	*phe-act*; phenylalanyl tRNA synthetase	22
phoA	Phosphatase	11	*P*; alkaline phosphatase	60, D
phoR	Phosphatase	11	*R1 pho*, *R1*; regulatory gene	60, D
phoS	Phosphatase	74	*R2 pho*, *R2*; regulatory gene	8, 60
phr	Photoreactivation	(17)	Photoreactivation of UV-damaged DNA (K12-B hybrids)	222
pil	Pili	88	*fim*; presence or absence of pili (fimbriae)	134
pnp	—	61	Polynucleotide phosphorylase	180
polA	Polymerase	75	DNA polymerase	50, 92
por	P1 restriction	89	Restriction of phage P1 DNA	236
ppc	—	77	*glu*, *asp*; succinate, aspartate, or glutamate requirement; phosphoenolpyruvate carboxylase	87, 88, 118
pps		33	Utilization of pyruvate or lactate; phosphopyruvate synthetase	25
prd	Propanediol	53	1,2-Propanediol dehydrogenase	237, J
proA	Proline	7	pro_1; block prior to L-glutamate semialdehyde	46, 214
proB	Proline	9	pro_2; block prior to L-glutamate semialdehyde	46, 214
proC	Proline	10	pro_3; *Pro2*; probably Δ-pyrroline-5-carboxylate reductase	46
pup	—	89	Purine nucleoside phosphorylase	4
purA	Purine	82	ade_k, Ad_4; adenylosuccinic acid synthetase	70, 118
purB	Purine	23	ade_h, adenylosuccinase	205, 211, 214
purC	Purine	48	ade_g; phosphoribosyl-aminoimidazole-succinocarboxamide synthetase	151, 211
purD	Purine	78	$adth_a$; phosphoribosylglycineamide synthetase[c]	211, 214
purE	Purine	13	ade_3; ade_f; Pur_2; phosphoribosyl-aminoimidazole carboxylase	56, 211
purF	Purine	44	*purC*, $ade_{u,b}$; phosphoribosyl-pyrophosphate amidotransferase[c]	211, 214, 215
purG	Purine	48	$adth_b$; phosphoribosylformylglycineamidine synthetase[c]	211, 218
purH	Purine	78	ade_i; phosphoribosyl-aminoimidazole-carboxamide formyltransferase	211
purI	Purine	49	Aminoimidazole ribotide synthetase[c]	217, 218
pyrA	Pyrimidine	0	*cap*, *arg* + *ura*; glutamino-carbamoyl-phosphate synthetase	17, 214, 215
pyrB	Pyrimidine	84	Aspartate transcarbamylase	17, 214
pyrC	Pyrimidine	22	Dihydroorotase	17, 205
pyrD	Pyrimidine	21	Dihydroorotic acid dehydrogenase	17, 205
pyrE	Pyrimidine	72	Orotidylic acid pyrophosphorylase	192, 214
pyrF	Pyrimidine	25	Orotidylic acid decarboxylase	205
rac	Recombination activation	29	Suppressor of *recB* and *recC* mutant phenotype	K
ram	Ribosomal ambiguity	64	Nonspecific suppression of all nonsense codons	183

TABLE 1.—*Continued*

Gene symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected	References[b]
ras	Radiation sensitivity	(11)	Sensitivity to UV and X-ray irradiation	227
rbs	Ribose	74	Utilization of D-ribose	215
recA	Recombination	52	Ultraviolet sensitivity and competence for genetic recombination	233
recB	Recombination	55	Ultraviolet sensitivity and competence for genetic recombination	66, 106, 233, 234
recC	Recombination	55	Ultraviolet sensitivity and competence for genetic recombination	66, 234
ref	Refractory	(88)	*refII*; specific tolerance to colicin E2	105
rel	Relaxed	54	*RC*; regulation of RNA synthesis	5, 74
rep	Replication	74	Inhibition of lytic replication of temperate phages	32
rhaA	Rhamnose	76	L-Rhamnose isomerase	88, 172
rhaB	Rhamnose	76	L-Rhamnulokinase	88, 172
rhaC	Rhamnose	76	Regulatory gene	88, 172
rhaD	Rhamnose	76	L-Rhamnulose-1-phosphate aldolase	88, 172
rif	Rifampicin	77	DNA-dependent RNA polymerase sensitivity to rifampicin	16, 55, L
rns	Ribonuclease	15	Ribonuclease I	181
rts	—	77	*ts-9*; altered electrophoretic mobility of 50*S* ribosomal subunit	75
serA	Serine	57	3-Phosphoglyceric acid dehydrogenase	214, 215, 220
serB	Serine	89	Phosphoserine phosphatase	215, 220
serS	Serine	(18)	Seryl-tRNA synthetase	104
shiA	Shikimic acid	38	Shikimate and dehydroshikimate permease	171
som	Somatic	(37)	*O*; somatic (O) antigens	160
spc	Spectinomycin	64	Resistance or sensitivity to spectinomycin	7, 10, 75, 232
speB	Spermidine	57	Putrescine (or spermidine) requirement; agmatine ureohydrolase	M
strA	Streptomycin	64	Resistance, dependence, or sensitivity; "K-character" of the 30*S* ribosomal subunit	75, 118, 183, 196
stv	Streptovaricin	77	DNA-dependent RNA polymerase sensitivity to streptovaricin	241
sucA	Succinate	17	*suc*, *lys* + *met*; succinate requirement; α-ketoglutarate dehydrogenase (decarboxylase component)	100, 101, 215
sucB	Succinate	17	*suc*, *lys* + *met*; succinate requirement; α-ketoglutarate dehydrogenase (dihydrolipoyltranssuccinylase component)	100, 101
supB	Suppressor	16	su_B; suppressor of *ochre* mutation (not identical to *supL*)	24
supC	Suppressor	25	su_C; suppressor of *ochre* mutation (possibly identical to *supO*)	24, 81, 205, 212
supD	Suppressor	(38)	su_I, *Su-1*; suppressor of *amber* mutations	205, 212
supE	Suppressor	16	su_{II}; suppressor of *amber* mutations	68, 205
supF	Suppressor	25	su_{III}, *Su-3*; suppressor of *amber* mutations	83, 212
supG	Suppressor	16	*Su-5*; suppressor of *ochre* mutations	81
supH	Suppressor	38		61, 63
supL	Suppressor	17	Suppressor of *ochre* mutations	62, 63
supM	Suppressor	78	Suppressor of *ochre* mutations	62, 63
supN	Suppressor	45	Suppressor of *ochre* mutations	62, 63, 144
supO	Suppressor	25	Suppressor of *ochre* mutations (possibly identical to *supC*)	62, 63
supT	Suppressor	55		63
supU	Suppressor	74	*su7*; suppressor of *amber* mutations	208
supV	Suppressor	74	*su8*; suppressor of *ochre* mutations	208

TABLE 1.—*Continued*

Gene symbol	Mnemonic	Map position (min)[a]	Alternate gene symbols; phenotypic trait affected	References[b]
tdk	—	25	Deoxythymidine kinase	102
tfrA	T-four	(8)	ϕ^r; resistance or sensitivity to phages T4, T3, T7, and λ	46, D
thiA	Thiamine	78	*thi*; synthesis of thiazole	122, 211
thiB	Thiamine	(78)	Thiamine phosphate pyrophosphorylase	122
thiO	Thiamine	(78)	Probable operator locus for *thiA* and *thiB* genes	123
thrA	Threonine	0	Block between homoserine and threonine	117, 134
thrD	Threonine	0	*HS*; aspartokinase I-homoserine dehydrogenase I complex	89, 165, 166
thyA	Thymine	55	Thymidylate synthetase	6, 111, 215
tkt	—	(55)	Transketolase	121
tnaA	—	73	*ind*; tryptophanase	84, 168
tnaR	—	73	R_{tna}; regulatory gene	84
tolA	Tolerance	17	*cim*; *tol-2*; tolerance to colicins E2, E3, A, and K	147, 148, 153, 179
tolB	Tolerance	17	*tol-3*; tolerance to colicins E1, E2, E3, A, and K	147, 148, 153, 179
tolC	Tolerance	58	*colE1-i*, *tol-8*, *refI*; specific tolerance to colicin E1	35, 105, 148, N
tonA	T-one	2	*T1*, *T5 rec*; resistance or sensitivity to phages T1 and T5	46, 53, 134, E
tonB	T-one	25	*T1 rec*; resistance to phages T1, ø80 and colicins B, I, V; active transport of Fe	91, 204, 230, 239
tpp	—	89	*deoA*, *TP*; thymidine phosphorylase	4, 72, 131
trpA	Tryptophan	25	*tryp-2*; tryptophan synthetase, A protein	113, 238, 239
trpB	Tryptophan	25	*tryp-1*; tryptophan synthetase, B protein	113, 238, 239
trpC	Tryptophan	25	*tryp-3*; indole-3-glycerol phosphate synthetase	113, 238, 239
trpD	Tryptophan	25	*tryE*; phosphoribosyl anthranilate transferase	58, 113, 142, 238
trpE	Tryptophan	25	*tryD*, *anth*, *tryp-4*; anthranilate synthetase	113, 142, 238, 239
trpO	Tryptophan	25	Operator locus	142, 209, 238
trpR	Tryptophan	90	*Rtry*; regulatory gene	37, 114, B
trpS	Tryptophan	65	Tryptophanyl-tRNA synthetase	57, 115
tsx	T-six	11	*T6 rec*; resistance or sensitivity to phage T6 and colicin K	46, 56, 79, 134
tyrA	Tyrosine	50	Prephenic acid dehydrogenase	170, 214, 215
tyrR	Tyrosine	27	Regulatory gene for *tyrA* and *aroF* genes	229
tyrS	Tyrosine	32	Tyrosyl-tRNA synthetase	194
ubiA	Ubiquinone	83	4-Hydroxybenzoate → 3-octaprenyl 4-hydroxybenzoate (OPHB)	42
ubiB	Ubiquinone	75	2-Octaprenylphenol → ubiquinone	42, 43
ubiD	Ubiquinone	75	OPHB decarboxylase	43
uhp	—	72	Uptake of hexose phosphates	126
uraP	Uracil	50	Uracil permease	K
uvrA	Ultraviolet	80	*dar-3*; repair of ultraviolet radiation damage to DNA	107, 222
uvrB	Ultraviolet	18	*dar-1,6*; repair of ultraviolet radiation damage to DNA	1, 107, 222
uvrC	Ultraviolet	37	*dar-4,5*; repair of ultraviolet radiation damage to DNA	12, 107, 222
uvrD	Ultraviolet	74	*dar-2*, *rad*; repair of UV radiation damage to DNA	14, 157, 222
valS	Valine	84	*val-act*; valyl-tRNA synthetase	19, 216
xyl	Xylose	70	Utilization of D-xylose	118, 214
zwf	Zwischenferment	(35)	Glucose-6-phosphate dehydrogenase	167

Region from 15 to 30 min. The *kdp* loci at minute 16 represent four contiguous complementation groups of mutants that are defective in unknown functions affecting the utilization of potassium ion (68). Mutants of *E. coli* strain B that are specifically deficient in potassium accumulation (*kac* mutants) have also been mapped in the vicinity of minute 16 (28). The correct order of the genes *supE*, *kdpA-D*, *gltA*, *suc*, and *gal* is now known from transduction data presented in references 68 and 100. The *suc* locus for α-ketoglutarate dehydrogenase has been resolved into two cistrons, *sucA* and *B*, which are functionally analogous to the *aceE* and *F* loci for pyruvate dehydrogenase at minute 2 (101). A new transfer ribonucleic acid (tRNA) synthetase gene, *serS*, has been mapped approximately between minutes 17 and 19 (104). A deletion analysis of the region near *gal* at minute 17 (1) has shown that certain deletions can generate *gal-aroG* multisite mutants that have no requirement for nicotinic acid. Accordingly, the *nadA* (formerly *nicA*) locus has been shifted from its previous position between *gal* and *aroG* (215) to a point slightly anticlockwise to *aroG*. This report (1), together with a follow-up study by Puig et al. (175), also shows that the correct position of the *chlA* gene is now just slightly clockwise from *uvrB* at minute 17.5. Two additional sites of pleiotropic mutations affecting nitrate-chlorate reductase activity, *chlD* [also known as *narF* (1, 224)] and *narE* (175, 224), also map in the 17- to 18-min segment. In vitro complementation tests (15) suggest that the various pleiotropic *chl* genes may code for different structural "subassemblies" which can unite to form a complex endowed with several catalytic functions. A new gene, *pgl*, has been mapped between *attλ* and *chlD* by means of overlapping deletion analysis (127). The old *bioA* locus at minute 17.5 is now recognized to contain at least six contiguous genes concerned with biotin synthesis (1, 51, 65, 182). Moreover, these *bio* genes appear to comprise an operon since at least some of the enzymes are regulated in coordinate fashion (64). Current nomenclature, which assigns the symbol *bioB* to one of the genes in this operon, requires us to change the designation of the unlinked *bio* locus at minute 65 from *bioB* to *bioH*.

Two new genes, *cmlA* and *cmlB*, that determine resistance to chloramphenicol are located at minutes 18.5 and 21, respectively (178). The *pdxC* locus at minute 20 represents a third and hitherto unmapped gene for pyridoxine requirement. The Pdx⁻ allele was present in strain X961, kindly given to us by R. Curtiss. Preliminary results (A. L. Taylor, *unpublished data*) indicate that *pdxC* is very close to *aroA* (95 to 97% cotransduction of these two markers). It is not known, however, whether *pdxC* lies clockwise or anticlockwise to *aroA*. Other additions to the 22- to 25-min segment of the map include *capS* (139), *cat* (219), and *hemA* (190, 191). The *chlC* locus, (174), also known as *narC* (93), has now been mapped with greater precision at a point between *hemA* and *supC* (93). A new regulatory gene, *tyrR*, that controls expression of the structural genes *aroF* and *tyrA*, has been mapped at minute 27 by time of entry with Hfr Hayes (229). The *tyrR* locus appears to be quite distinct from the tyrosyl-tRNA synthetase gene, *tyrS*, which maps 5 min away at minute 32 (194). The *rac* gene at minute 29 has the curious effect of suppressing the recombination-deficient phenotype of mutants at the *recB* and *recC* loci (B. Low, *personal communication*).

Region from 30 to 45 min. The symbol *oldD* is proposed here to identify the locus of the *old-88* allele which was recently mapped at minute 34 by time-of-entry experiments (162). Two genes for chemotactic motility, which had been previously designated *motA* and *B* (215), are now renamed *cheA* and *cheB* in accord with the nomenclature of Armstrong and Adler (12). The symbol *mot* at minute 36 now serves to identify flagellar paralysis mutants (12). This latter report also describes a third chemotaxis gene, *cheC*, at minute 37 and it further proposes that the symbol *fla* be reserved to denote unmapped genes that control the formation of flagella. The *nalA* locus at minute 42 is one of two new genes which determine resistance to nalidixic acid; the second gene, *nalB*, maps at minute 51 (94). The *pdxB* locus has been mapped by three-point transduction crosses at minute 44, between *purF* and *aroC* (54). A mutation affecting unsaturated fatty acid biosynthesis (*fabB*) has also been mapped in the short interval between *aroC* and *purF*, but the relative order of *fabB* and *pdxB* is not known (69).

Region from 45 to 60 min. The position and orientation of *dapA* and *dapE* at minute 47 are based on the results of three-point transduction crosses performed in this laboratory (A. I. Bukhari and A. L. Taylor, *in preparation*). The locus previously designated as *dapB* (215) is renamed *dapE*, as it codes for the fifth enzyme of the diaminopimelic acid pathway (38). Nijkamp and Oskamp (152) recently presented further evidence that the two genes for guanine biosynthesis at minute 48 comprise a true operon. The *nicB* locus, now renamed *nadB* as recommended by Tritz et al. (218), has been moved from its former incorrect location at minute 46 (215) to minute 49.5. In addition to mapping *nadB*,

Tritz et al. (217, 218) identified and mapped a new purine locus of *E. coli*, *purI*, at a point between *glyA* and *nadB*. Three new cysteine genes, *cysH*, *P*, and *Q*, have been mapped near *cysC* at minute 53 (120). Although fine-structure genetics of the region remains to be done, it seems likely that all four of these *cys* loci will make up a contiguous gene cluster analogous to the *cysCDHIJ* cluster in *S. typhimurium* (189). Three genes that affect genetic recombination have been accurately mapped. The *recA* locus is placed at minute 51.5, slightly closer to *cysC* than to *pheA* on the basis of transduction data reported by Willetts et al. (233). The position and orientation of the closely linked *recB* and *recC* loci at minute 54.5 were determined by means of multifactor transduction crosses (66, 234). A recent study by Oishi (158) indicates that mutations in the *recB* and *recC* genes are associated with the loss of a specific deoxyribonuclease activity. The structural gene for diaminopimelic acid decarboxylase at minute 55 has been divided into two regions, *lysA* and *lysB*, to identify two phenotypically distinct classes of mutants which will be described in detail elsewhere (A. I. Bukhari and A. L. Taylor, *in preparation*). A new structural (or regulatory) gene for agmatine ureohydrolase, which catalyzes the second step in spermidine synthesis from arginine, has been named *speB* and mapped near *serA* at minute 56.5; its orientation with respect to *serA* and *argP* is not yet known (W. K. Maas, *personal communication*). The *tolC* locus, also known as *refI* (105), has been mapped with good precision at minute 58 both by time-of-entry and by transduction methods (E. Whitney, *personal communication*).

Region from 60 to 75 min. Mutants resistant to the antimetabolite 5-methyl tryptophan have been mapped very close to *argG* at minute 61, but the orientation of *mtr* was not determined (103). The *mtr* mutants are phenotypically distinct from resistant strains resulting from mutations in the *trpR* or *trpO* genes (103). The region from minutes 63 to 64 contains at least four genes that specify components of the 30*S* ribosome: these are *nek* (10), *ram* (183), *spc* (10, 75), and *strA* (75). The orientation of *ram*, *spc*, and *strA* with respect to each other and to *aroE* is based on recombination and transduction data presented in several recent reports (7, 10, 183, 232). The *nek* locus appears to be closely linked and anticlockwise to *spc*, but its orientation relative to *aroE* is not known (10).

The *argD* locus, previously mapped near the *strA* region (226), is now precisely located at minute 64.5 by transduction analyses done in this laboratory (A. L. Taylor and S. Paigen, *unpublished data*). Following the lead of Itikawa et al. (112), we obtained a number of *argD* mutants of *E. coli* among proline-independent "revertants" of a proline auxotroph blocked at a step prior to glutamic γ-semialdehyde. One of these double mutants (strain AT 3141, *proA*$^-$ *argD*$^-$) was used in multifactor transduction crosses with strains carrying mutant alleles at several loci close to *strA*. The results, in summary form, of one cross showed that *aroE* was cotransduced with *strA* and *argD* at frequencies at 64 and 14%, respectively; the gene order indicated was *aroE-strA-argD*. In a second cross, *cysG* was cotransduced at a frequency of 41% with *argD*, 22% with *strA*, and 13% with *malP*, and the indicated gene order was *strA-argD-cysG-malP*.

The structural gene for a tryptophanyl-tRNA synthetase lies about midway between *strA* and *malP*, as shown by transduction studies (57, 115). The locus formerly designated as *malA* at minute 66 (215) has been shown to contain two structural genes, *malQ* and *malP*, and a regulatory gene, *malT* (95). Present evidence suggests that *malQ* and *malP* form an operon, and that *malT* probably does not belong to this operon, even though it maps immediately adjacent to *malP* (95). As explained earlier in this survey, the *bioB* gene at minute 65.5 is renamed *bioH*. Three closely linked genes that affect the formation of glycogen have been mapped at minute 66 between *glpD* and *asd* (33, 203); orientation of the *glgA*, *B*, and *C* genes has not yet been determined and it is not known whether the three genes represent an operon (33). The *dct* locus, which controls the transport of several four-carbon dicarboxylic acids, maps at minute 69 by time-of-entry determination (124). A new structural (or regulatory) gene for lactate dehydrogenase has been named *lct* and mapped at minute 71.5 by transduction (163). Other new genes in the 71- to 72-min region include *gad* (137) and the locus for a glutamyl-tRNA synthetase (*gltE*) with unknown orientation with respect to *lct* (E. J. Murgola, *personal communcation*). The *uhp* (126) and *cysE* (120) loci both map near *pyrE* at minute 72, but their orientation with respect to each other and to *pyrE* is uncertain. The *gltC* locus is now placed at a corrected position between *pyrE* and *tna* (136). A new gene, *asn*, maps at minute 73.5 midway between *bgl* and *ilv* and appears to be the earliest marker known to be transferred by Hfr strain AB313 (34). Two unusual nonsense suppressor alleles, *su7* and *su8* (symbolized here as *supU* and *supV*, respectively), have been mapped recently at a point close to the *ilv* operon at minute 74 (208). There have been at least four separate reports on mutations that map near *metE* at minute 74.5

and which cause altered sensitivity to ultraviolet or X-irradiation. The genes involved in these various mutations have been called *rad* (14), *dar*-2 (222), *uvrD* (157), and most recently *rep* (32). It may be that some or even all of these mutations will turn out to be different alleles of a single locus, but current data are too fragmentary to permit such an interpretation at this time. A fifth gene (*polA*) that also maps near *metE* and which also affects sensitivity to ultraviolet light has been identified as the probable structural gene for DNA polymerase (50, 92). These workers conclude that *polA* and *uvrD* are likely to be separate genes because of phenotypic differences between the two types of mutants. It is also clear that *polA* and *rep* must be separate genes because the former locus maps clockwise to *metE* (92), whereas the latter maps anticlockwise to *metE* (32). Two genes concerned with ubiquinone biosynthesis, *ubiB* and *ubiD*, have been mapped within 0.5 min of the clockwise side of *metE* (43). The *old-30* and *old-64* alleles described by Overath et al. (162) are designated here as *oldA* and *oldB*, respectively; both genes are located between *metE* and *rha*, but their orientation relative to other nearby markers is not known.

Region from 75 to 90 min. Morrissey and Fraenkel (146) showed that *pfk* maps between *rha* and *glpK* at minute 76 in a detailed report that lists the cotransduction frequencies of several other standard markers in the 76- to 78-min region. Recent studies on antibiotic-resistant mutants of *E. coli* that possess altered deoxyribonucleic acid (DNA)-dependent RNA polymerases seem to indicate that mutations affecting this enzyme can occur in two distinct regions. On the one hand, rifampicin-resistant mutants, designated *rif*, cotransduce with the *argH* locus at high frequencies of 65 to 77%, and preliminary evidence favors placing *rif* at minute 77 between *argH* and *metB* (16, 55; W. F. Doolittle, *personal communication*). On the other hand, streptovaricin-resistant mutants, designated *stv* (241), and streptolydigin-resistant mutants (193) cotransduce with *argH* at lower frequencies of 20 to 35%, and the first indication is that *stv* maps clockwise to *argH*, away from *rif* (241). The *ace* operon, together with a closely linked regulatory gene for the operon (*iclR*, also known as *aceD*), is placed near minute 78 between *metA* and *pgi* on the basis of transduction data (26, 223). The structural gene for aspartase, *aspA*, has been mapped near minute 82 by time of entry, but its position relative to other nearby markers is not known (138). Both the position and orientation of the *ampA* and *purA* genes near minute 82 have now been corrected with the aid of new transduction data reported by Eriksson-Grennberg (70). A third gene concerned with ubiquinone formation, *ubiA*, maps near minute 83 by time-of-entry determinations, but its exact position relative to standard markers such as *purA* or *fdp* is not known (42). The *mel-7* and *mel-4* alleles described by Schmitt (195) are symbolized here as *melA* and *melB*, respectively; time-of-entry experiments indicate that both genes map near minute 84, but precise ordering of the *mel* loci with respect to other nearby markers has not been done (195). The *melB* locus is of particular interest, as it specifies the hitherto unmapped second thiomethylgalactoside permease described by Prestidge and Pardee (173). Preliminary genetic studies of Holland and Threlfall (105) showed that certain pleiotropic mutations (*ref*), which result in both increased sensitivity to ultraviolet irradiation and specific tolerance to colicin E2, map in the general vicinity of minutes 88 to 89. A gene responsible for specific host restriction of phage P1 (*por*) has been mapped at minute 89 (236), very close to the site of other restriction markers (23, 39, 128, 235) which are collectively identified here by the tentative symbol *hsp*.

Lomax and Greenberg (131) proposed the term *deo* operon to denote a cluster of three closely linked genes that code for enzymes involved in deoxyribonucleoside catabolism. The genes were mapped with the following orientation at a point about 0.5 min anticlockwise to *thr* at minute 90/0: *deoA*-(*deoB*)-*deoC*-*thr* (131). Subsequently, Ahmad and Pritchard (4) presented a more detailed genetic analysis of the region in which these three genes plus a fourth related gene, *pup*, were sequenced with respect to each other and also in relation to the nearest known outside markers, *hsp* and *serB*. The *deoA*, *B*, and *C* loci were termed *tpp*, *drm*, and *dra*, respectively, and the order deduced from many crosses was *hsp*-*dra*-*tpp*-*drm*-*pup*-*serB*-*thr*. Both reports (4, 131) concur that *dra*(*deoC*) and *tpp*(*deoA*) probably belong to a common operon; it is not certain, however, that *drm*(*deoB*) and *pup* also belong to this operon and there is some evidence to support a two-operon model (4). In view of these uncertainties, the relatively noncommittal gene symbols of Ahmad and Pritchard (4) have been adopted here in preference to the earlier *deo* convention (131). As the final entry in this survey, it should be noted that unpublished data from this laboratory show that the position of the *trpR* locus (37, 114) is anticlockwise to *thr* at minute 90/0.

CONCLUDING REMARKS

The circular genome of *E. coli* has a contour length of about 1,000 μm (31), which is equivalent

to about 3 × 10^6 nucleotide pairs per chromosome or approximately 3,000 genes, assuming the average gene contains 1,000 nucleotide pairs. If one ascribes an informational role to all of the DNA in the bacterial genome, it follows that the 310 genes identified thus far account for roughly 10% of the potential information content of *E. coli*.

As Fig. 1 shows, the distribution of genes on the map is now fairly uniform so that few genetically silent regions remain. The most conspicuous quiet region is the segment from minutes 3 to 9, and there are smaller silent areas at minutes 27–31, 39–42, and 85–88. For the most part, attempts to locate new markers in these regions will have to rely upon the time of entry approach to mapping. The rest of the map, however, now seems to contain a sufficient number of markers per minute of map length to assure the feasibility of mapping most new markers by transduction methods.

Although the present genetic map must inevitably contain some errors and imperfections, it is nevertheless substantially more accurate than previous maps. Much of the high precision of gene placement in Fig. 1 can be attributed to the widespread use of multifactor transduction crosses and overlapping deletion analyses in current genetic investigations. Continuing efforts along these lines will unquestionably lead to further clarification of the overall genetic structure of *E coli*.

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