

Nucleotide and amino acid polymorphism in the gene for L-histidinol dehydrogenase of *Escherichia coli* K12

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The *hisD* gene of *E. coli* K12 codes for a bifunctional enzyme L-histidinol dehydrogenase, (EC 1.1.1.23) (1). Its nucleotide sequence and predicted amino acid sequence of the gene product, derived from an *E. coli* K12 W3110 strain, was recently determined (3). We report the sequence of the *hisD* gene from the other *E. coli* K12 W3110 strain (DY100 *thyA metE deoC polA1*) (4). Comparative analysis reveals remarkable difference between the two sequences including 14 single base-pair differences of no coding significance, and 5 single base-pair differences which change codons of 5 amino acids (Figure 1).

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1  ATG AGC TTT AAC ACA ATC ATT GAC TGG AAT AGC TGT ACT GCG GTG CAA CAA CGC CAG CTG TTA ATG CGC
2                                     GAG
3                                     Val→Glu
1  CCG GCG ATT TCC GCC TCT GAA AGC ATT ACC CGC ACT GTT AAC GAT ATT CTC GAT AAC GTG AAA GCA CGC
1  GGC GAT GAG GCC CTG CCG GAA TAC AGC GCG AAG TTT GAT AAA ACC ACG GTT ACC GCG CTG AAG GTG TCT

1  GCA GAG GAG ATC GCC GCC GCC AGC GAA CGC CTG AGC GAC GAG CTA AAA CAG GCG ATG GCG GTG GCA GTA
1  AAG AAT ATT GAA ACC TTC CAC ACT GCG CAA AAA CTG CCG CCG GTA GAT GTA GAA ACG CAG CCA GGC GTG
1  CGT TGC CAG CAG GTC ACG CGT CCG GTA GCT TCA GTT GGG TTG TAT ATT CCT GGC GGC TCC GCC CCG CTC
1  TTC TCA ACG GTA TTA ATG CTG GCG ACT CCG GCG CGT ATT GCG GGC TGT AAA AAA GTG GTG CTG TGC TCA
2                                     AGT
3                                     Arg→Ser
1  CCG CCG CCG ATT GCC GAT GAG ATC CTT TAT GCG GCG CAG CTG TGC GGT GTG CAG GAC GTG TTC AAC GTC
2                                     TTT
3                                     Phe
1  GGC GGC GCA CAG GCC ATT GCC GCA CTG GCG TTT GGT ACG GAA TCC GTG CCA AAA GTG GAC AAA ATC TTC
2                                     TCT
3                                     Ser
1  GGG CCG GGT AAC GCC TTT GTC ACC GAA GCG AAA CGT CAG GTG AGC CAG CGT CTG GAC GGT GCG GCG ATC
1  GAT ATG CCC GCA GGC CCG TCG GAA GTG CTG GTG ATT GCT GAC AGC GGC GCA ACG CCG GAT TTC GTG GCT
2                                     GCT
3                                     Ala
1  TCT GAT TTG CTC TCT CAG GCT GAA CAC GGC CCG GAC TCA CAG GTG ATT TTA CTG ACG CCC GCT GCT GAT
1  ATG GCG CGT CGC GTT GCC GAG GCC GTC GAA CGC CAA CTG GCG GAA CTG CCG CGT GCC GAA ACC GCC CGC
2                                     GCA
3                                     Ala
1  CAG GCA CTG AAC GCC AGC CGC CTG ATC GTG ACT AAA GAT TCA GCG CAG TGC GTG GAG ATC TCT AAT CAG
2                                     TTA
3                                     Ser→Leu
1  TAC GGC CCG GAG CAC CTG ATC ATT CAG ACC CGC AAC GCC CGT GAA CTG GTC GAT AGC ATC ACC AGC GCC
1  GGT TCG GTA TTT CTT GGT GAC TGG TCA CCG GAA TCG GCA GGT GAT TAC GCC TCC GGA ACC AAC CAC GTT
2                                     GGC
3                                     Gly
1  CTA CCG ACT TAC GGT TAC ACC GCC ACC TGT TCC AGC CTC GGG CTG GCA GAT TTC CAG AAG CGT ATG ACC
2                                     CGC
3                                     Arg
1  GTA CAG GAA CTG TCG AAA GAG GGG TTC TCC GCG GTG GCT TCA ACC ATA GAA ACA CTG GCC GCC GCC GAA
2                                     CTG
3                                     Val→Leu
1  CGT CTG ACC GCC CAT AAA AAT GCC GTT ACC TTG CCG GIT AAC GCC CTC AAG GAG CAA GCA TGA
2  CGC                                     CAC
3  Arg                                     His                                     Thr                                     Arg                                     Leu

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Figure 1. Row 1: *E. coli* K12 W3110 wild type (2,3); Row 2: *E. coli* K12 W3110 DY100 (4); Row 3: Relevant amino acids.