Table 3.4

TABLE 3.4 Some *E. coli* nonsense suppressor tRNAs

Suppressor name	tRNA	Anticodon change	Suppressor type
supE	$tRNA^{Gln}$	CUG-CUA	Amber
supF	$tRNA^{Tyr}$	GUA-CUA	Amber
supB	$tRNA^{Gln}$	UUG-UUA	Ochre/amber
supL	$tRNA^{Lys}$	UUU-UUA	Ochre/amber

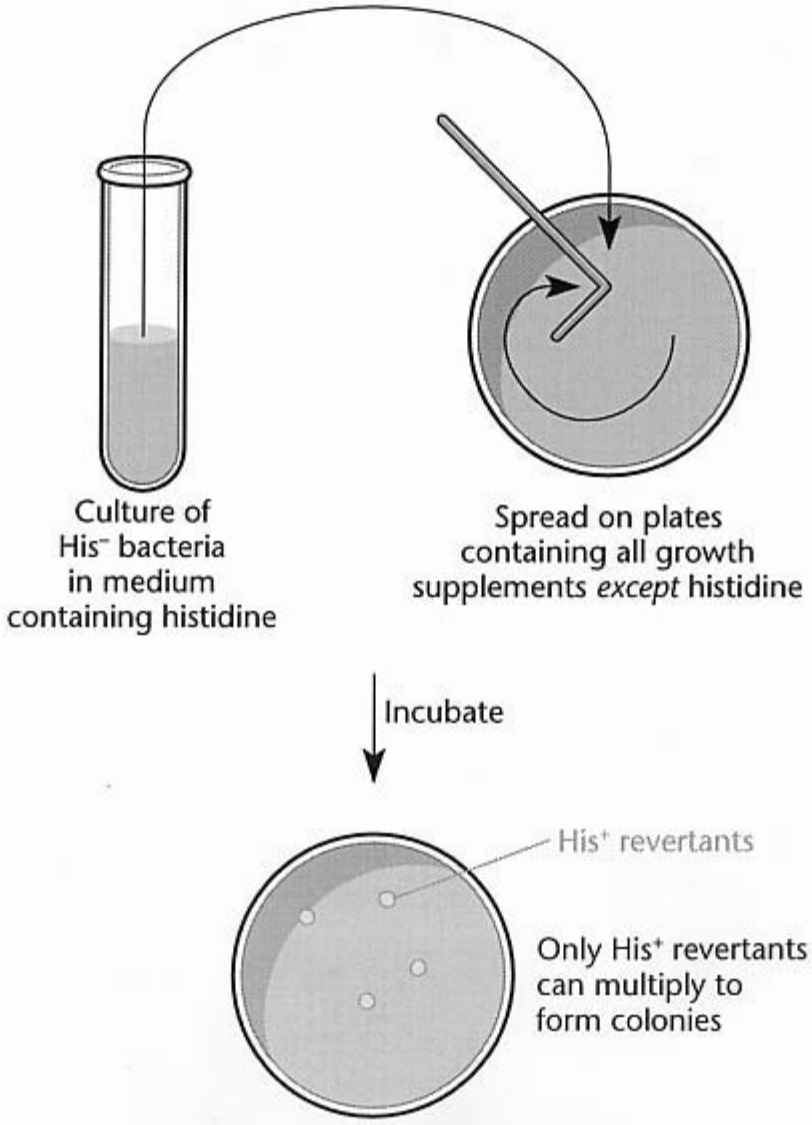
1. genotype — phenotype
   supE+ — Su−
   supE — Su+

2. nonsense ⟶ sense
   or ⟶ missense ⟶ functional
   or ⟶ non-functional

3. Major & minor isoaccepting tRNAs

Figure 3.21

POSITIVE SELECTION



Forward, Reverse & Suppressor mutations

Mutant Hunt (Isolating Mutants)

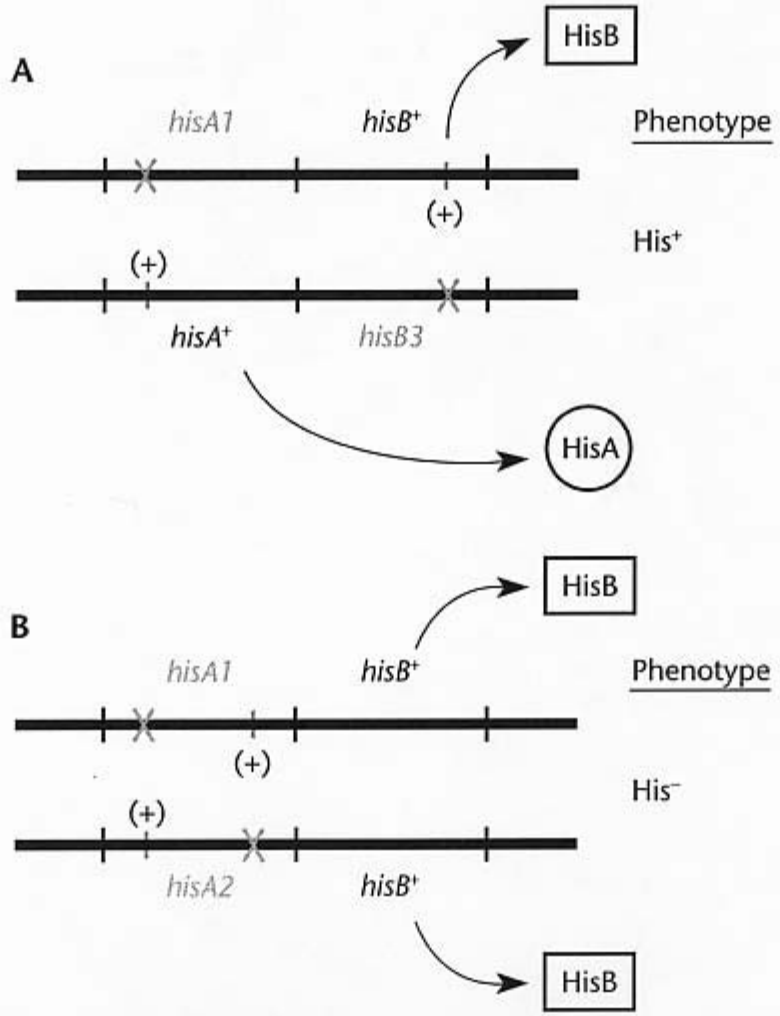
1. Mutagenesis
   spontaneous / mutagen
   If mutagen, which one

2. Intermediate cultivation
   increase absolute no. of mutants
   phenotypic lag
   eliminate some unwanted mutants
3. Selection (negative)
   Use agent (antibiotic) that is
   bactericidal for growing bacteric

4. Screen (replica plate)

Ex. - His^- (auxotroph)
ts (conditionally-lethal in essential genes
His^{ts} -

Figure 3.23



COMPLEMENTATION - how many genes (complementation groups) are represented among mutants with similar phenotypes?

TABLE 3.5 Interpretation of complementation tests

Test result	Possible explanations
x and y complement	Mutations are in different genes Intragenic complementation has occurred[a]
x and y do not complement	Mutations are in the same gene One of the mutations is dominant One of the mutations affects a regulatory site or is polar

[a]See the text for an explanation of intragenic complementation. This is a less likely explanation than the mutations being in different genes.