Codon-Based Mutagenesis Introduction

Directed molecular evolution and combinatorial methods are key strategies used for protein engineering research. These approaches commonly involve using partially randomized synthetic oligonucleotides to generate a partially randomized gene library, expressing it in an appropriate vector to generate the protein set encoded by the library, and then screening the expressed proteins for improved or modified characteristics. Examples of the latter include changes in protein-ligand binding affinity, enzyme selectivity, or protein stability. While a variety of site-directed mutagenesis methods can be employed to introduce randomization at specific base positions of a gene, such methods often introduce significant amounts of undesirable codon bias into the library, due to the mismatch between the base-by-base nature of classical oligonucleotide synthesis and the triplet nature of the codon (1). The problem of unwanted codon bias can be eliminated by synthesizing the random portion of the oligos codon-by-codon, with trimer phosphoramidites, instead of base-by-base. This codon-based mutagenesis system conveys the ability to effectively control codon bias in the system. The researcher can choose to completely randomize a particular amino acid position in the expressed protein, or flexibly tune the relative amounts of different amino acids at that position, as needs require (2). The combination of standard and custom Trimer Codon phosphoramidite mixes is a powerful research tool for anyone doing protein engineering research.

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<td>Trimer Codon Mix 2 Sense (Mix of 19 codons without Cys)</td>
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Codon-Based Mutagenesis Design Protocols

Codon-Directed Mutagenesis--Design Considerations

I. When are standard Trimer Codon Phosphoramidites suitable?

Standard trimer codon phosphoramidite mixes are currently optimized around E. coli codon abundances, with the most abundant codon used to code for a given amino acid selected for inclusion. This optimization is reasonable, given that their expected use is for oligos slated for generation of E. coli-based libraries for protein engineering. Other organisms (e.g., yeast or Drosophila) have different codon abundances/usage patterns (Codon Usage in Different Organisms). Thus, when performing codon-directed mutagenesis in an organism other than E. coli, it is important to compare the codon usage pattern of that organism with that of E. coli to ascertain the suitability of the standard mixes.

II. Phage Display Library Construction for Protein Engineering: dut/ung method

After synthesis of a mutagenic oligonucleotide using Trimer Phosphoramidites, the oligo will have a randomized trimer codon region with fixed sequences on each side. For protein engineering applications, such mutagenic oligos typically are cloned into E. coli to construct a phage display library. The dut/ung method is one such construction method that is highly efficient in this regard (6).

Background: Dut is a gene in E. coli that encodes for dUTPase, which degrades dUTP. A dut(-) strain lacks this enzyme, so an elevated concentration of dUTP accumulates, resulting in incorporation of U in place of T at some base positions during DNA replication. The ung gene encodes uracil N-glycosylase, which normally excises U from DNA. A ung(-) strain lacks this, so U bases are not excised from DNA in the bacterium. Thus, in a dut(-)/ung(-) double mutant, any U bases that are incorporated into DNA during replication are not repaired. However, because U and T have identical base-pairing properties, the T-to-U conversion is not mutagenic. Basic steps of the method

(1) A dut(-)/ung(-) strain is infected with M13 phage, and a circularized dU-containing M13 ssDNA template is obtained.

(2) The mutagenic oligonucleotide is annealed to this template in vitro via the fixed regions of the oligo (the mismatched randomized trimer codon region itself does not bind to the template).

(3) T7 DNA polymerase and T4 ligase are added, and the mutagenic oligo now functions as a primer for in vitro DNA replication, as the complementary strand is generated and the ends ligated together. The result is covalently closed circular dsDNA (CCC-ds DNA), with a dU-containing strand and a non-dU-containing strand (which contains the randomized trimer codon region).

(4) The CCC-ds-DNA is transformed into ung(+) E. coli. Uracil N-glycosylase excises U from the dU-containing strand, leaving apyrimidinic sites in it, which are recognized and cut by endonucleases. Thus the dU-containing strand is preferentially destroyed, and only the mutant strand is replicated, leading to its enrichment.
Codon-Based Mutagenesis Applications

As described in the Introduction, the main use of trimer phosphoramidites is for developing partially randomized gene libraries based on the concept of codon-based mutagenesis. Because trimer codons cover all 20 natural amino acids, their use avoids problems associated with random point, or saturating, mutagenesis. In a random point mutagenesis approach, because the use of single base mutations generated by error-prone PCR produces only about six amino acid substitutions on average, concurrent mutation of adjacent nucleotides must occur; this requirement often makes it very difficult to find a clone with the desired amino acid change. For example, in a 100 aa protein, the likelihood of converting Tyr (TAC) to Asn (AAC) is only 1/900, the likelihood of converting Tyr (TAC) to Met (ATG) is $1.37 \times 10^{-9}$ (3). In saturating mutagenesis, pools of degenerate oligos are used with N’s at the site(s) of the codon(s) to be mutated. However, because some amino acids are represented by higher numbers of codons than others (for example, six for Arg, one for Trp), there will be large differences in the relative amounts of oligos containing particular amino acid mutations, leading to substantial undesired codon bias. Also, about 5% of the oligos will contain stop codons that will cause improper chain termination (3). By contrast, use of trimer phosphoramidites allows the incorporation of an equimolar mix of all 20 natural amino acids, or any subset, into any position of a sequence. This advantage eliminates codon bias, presence of unwanted stop codons or frameshift mutations, and makes searching a clonal library for desired mutants much more efficient. Multiple amino acids within a protein can be modified at the same time while the overall tertiary structure is maintained. Trimer phosphoramidites have been used to develop phage display libraries with greater diversity (as much as 10x greater) than by traditional methods, with a high degree of amino acid uniformity (4). Trimer phosphoramidites were also used to maximize the diversity of a partially randomized library for use in developing streptavidin variants with altered specificities for desthiobiotin, a biotin analog, by directed evolution (5).
References