



Randomised Peptide Libraries

Scientists at Aston University have developed an improved protein randomisation method which eliminates redundancy in the randomisation process, improves the yield of DNA and enables the production of contiguous randomised codons. This useful technique improves the efficiency and reduces the cost of producing randomised proteins for screening for novel functionality. Aston's Business Partnership Unit is now actively seeking commercial partners to exploit this new invention.

Highlights

- Virtually no redundancy in the codon randomisation process
- Improved DNA yield
- Enables production of contiguous randomised codons
- More efficient than existing techniques

Background

Proteins are used in a number of industrial applications. Examples include their use as biocatalysts and in screening for novel drug candidates. Where suitable proteins do not exist in nature there is a tremendous need to engineer the production of novel proteins that can function in an industrial setting. This "engineering" of proteins is usually carried out by random mutagenesis. Randomised libraries are produced containing variations of a gene or gene fragment which are screened for novel activity. While a number of methods have been developed for introducing this diversity, none are without their drawbacks.

One widely used method is codon randomisation (saturation mutagenesis), which generates a library of mutants (a randomised gene library) in a single experiment. For full randomisation, key codons are typically replaced with NNN (64 sequences) or NN^G_{CorT} (32 sequences). This obligates cloning of redundant codons alongside those required to encode the 20 amino acids. As the number of randomised codons increases, there is therefore a progressive loss of randomisation efficiency; the number of genes required per protein rises exponentially. The redundant codons cause amino acids to be represented unevenly, and the organisation of the genetic code makes it impossible to encode functional subsets of amino acids (e.g. polar residues only) in a single experiment. Scientists at Aston have previously developed a method of randomisation which eliminates this redundancy and bias. However, even using this method the production of more than two contiguous randomised codons proved problematic.

The Technology

Further work at Aston University has now led to the development of an improved protein randomisation method which virtually eliminates the presence of unwanted sequences whilst also enabling the production of contiguous randomised codons with little additional effort. The method uses simple and easily performed cleavage, ligation and amplification reactions and can be carried out sequentially to produce contiguous randomised codons if required. Use of the Aston method should substantially improve the efficiency and reduce the cost of producing randomised proteins for screening for novel functionality.

Intellectual Property Protection

This technology is the subject of patent applications in the US, Europe and Canada:

<i>Title</i>	<i>Application Number</i>	<i>Priority Claimed</i>	<i>Our Ref</i>
Randomised Peptide Libraries	US 11/989,087 EP 06765007.7 CA 2616252	June 22, 2005	PAT-2005-009

Further Information

Further information can be made available and commercial discussions commenced on entering into a non-disclosure agreement.

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