

P016 CAG·CTG repeat instability in *Escherichia coli*
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A number of human diseases such as Huntington's disease, myotonic dystrophy and spinocerebellar ataxias have been associated with the expansion of CAG·CTG repeats. To understand the processes involved in the instability of these repeats, we have developed a method to generate a library of repeats of different lengths that can be integrated in *Escherichia coli* chromosome. Instability is studied by measuring the lengths of repeat tracts using polyacrylamide electrophoresis based separation following PCR amplification.

Previous studies of trinucleotide repeat instability have been limited by the use of plasmid substrates where effects such as replicon size and copy number have complicated analysis. Our results confirm previous observations that CAG·CTG repeat instability is length and orientation dependent with repeats being more unstable when the CAG sequence is located on the leading strand template.

To investigate the pathways of repeat instability, we have analysed the behaviour of CAG·CTG repeat tracts in different mutants affected in pathways of DNA repair and recombination. This work is beginning to reveal the pathways of repeat instability, unencumbered by effects of plasmid biology.