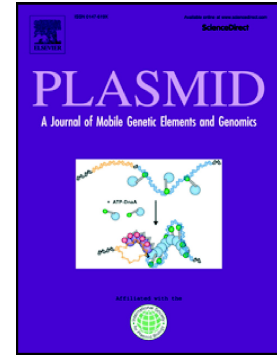


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Annotation of Plasmid Genes

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Abstract

Good annotation of plasmid genomes is essential to maximise the value of the rapidly increasing volume of plasmid sequences. This short review highlights some of the current issues and suggests some ways forward. Where a well-studied related plasmid system exists we recommend that new annotation adheres to the convention already established for that system, so long as it is based on sound principles and solid experimental evidence, even if some of the new genes are more similar to homologues in different systems. Where a well-established model does not exist we provide generic gene names that reflect likely biochemical activity rather than overall purpose particularly, for example, where genes clearly belong to a type IV secretion system but it is not known whether they function in conjugative transfer or virulence. We also recommend that annotators use a whole system naming approach to avoid ending up with an illogical mixture of names from other systems based on the highest scoring match from a BLAST search. In addition, where function has not been experimentally established we recommend using just the locus tag, rather than a function-related gene name, while recording possible functions as notes rather than in a provisional name.

Key words: genome; DNA sequence; gene names; gene function; replication; conjugative transfer

Highlights:

Review of current “issues” with plasmid annotation

Overview of annotation developments for other types of genome elements

Suggestions for good practice in plasmid annotation

Discussion of annotation in relation to replication, stability and conjugation functions

Previously unpublished annotation of IncX1 plasmid complete genome sequence as a model

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