Microbiology Comment provides a platform for readers of Microbiology to communicate their personal observations and opinions in a more informal way than through the submission of papers. Most of us feel, from time to time, that other authors have not acknowledged the work of our own or other groups or have omitted to interpret important aspects of their own data. Perhaps we have observed results, although not sufficient to merit a full paper, add a further dimension to one published by others. In other instances we may have a useful piece of methodology that we would like to share.

The Editors hope that readers will take full advantage of this section and use it to raise matters that hitherto have been confined to a limited audience.

Jon Saunders, Editor-in-Chief

Reviews in Microbiology – less is more

Since its launch in 1994, Microbiology has published many lively and informative Reviews. These have provided an excellent resource for those engaged in microbiological research and teaching. In response to comments from readers and suggestions by the Editorial Board, the Editors have decided to build on the success of this section by establishing a new Mini-reviews series to highlight topics of breaking interest. Paul Rainey (University of Oxford) has recently been appointed as Reviews Editor for Microbiology and he will be responsible for establishing this new series. He will also co-ordinate the commissioning of regular full-length Reviews, which was formerly done by the Editor-in-Chief. Microbiology aims in the future to publish at least one Mini-review, plus, if possible, a full-length review, per monthly issue. The Reviews and Mini-reviews will cover the broadest possible range of topics of current interest.

The Reviews Editor will commission Reviews and Mini-reviews on subjects considered of importance and wide interest by the Editors and Editorial Board of Microbiology. However, unsolicited proposals for Reviews and Mini-Reviews are always welcomed: authors are advised to send their proposal before submitting a manuscript. Authors should bear in mind that Microbiology attracts a wide range of readers who are not necessarily specialists, and should pitch their text accordingly, providing enough background information to place the topic in the broader context of microbiology. All Reviews and Mini-reviews submitted to Microbiology, whether commissioned or unsolicited, will be subject to rigorous independent peer review.

Those with concepts for Reviews or Mini-reviews should contact:

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Jon Saunders, Editor-in-Chief

A pair of PCR primers for IncP-9 plasmids

Plasmids play a vital role in the rapid spread of genes throughout bacterial populations. They can function as vehicles for the transport of metabolic pathways that may be involved in bioremediation of xenobiotics, genes responsible for resistance to antibiotics, or the ability to carry out biotransformations. Hence, they are of environmental, clinical and industrial importance. Plasmids can be classified according to their incompatibility with one another, i.e. their inability to stably coexist in the same cell line. Incompatibility results from two plasmids sharing one or more elements of their replication or partitioning systems. DNA sequencing has also allowed plasmids to be grouped according to sequence similarity. Couturier et al. (5) have developed a system of replicon typing utilising probes specific for replicons from a number of well characterized incompatibility groups. Götz et al. (6) took this idea further, and used PCR primers specific for particular groups of plasmids to detect plasmid sequences in environmental DNA samples without a need to culture the bacterial host.

IncP-9 group members are broad-host-range plasmids originally isolated from Pseudomonas (4). The Pseudomonas genus is diverse, including species of agricultural and biotechnological interest, such as P. putida, a soil organism involved in a range of biodegradative and biotransformation functions; P. aeruginosa, an opportunistic pathogen found in clinical and aquatic environments; and P. syringae, a plant pathogen. IncP-9 plasmids can carry degradative functions (D plasmids), including TOL plasmid pWW0, NAH7 and SAL1, and/or genes encoding antibiotic resistance (R plasmids), such as R2, pMG18 and pM3. They are also widely distributed geographically. Despite this group containing the best studied of all the catabolic plasmids, TOL plasmid pWW0 (2), and the fact that some of the IncP-9 degradative pathways are now

GUIDELINES

Communications should be in the form of letters and should be brief and to the point. A single small Table or Figure may be included, as may a limited number of references (cited in the text by numbers, and listed in alphabetical order at the end of the letter). A short title (fewer than 50 characters) should be provided.

Approval for publication rests with the Editor-in-Chief, who reserves the right to edit letters and/or to make a brief reply. Other interested persons may also be invited to reply. The Editors of Microbiology do not necessarily agree with the views expressed in Microbiology Comment.

Contributions should be addressed to the Editor-in-Chief via the Editorial Office.
well characterized, very little is understood concerning the IncP-9 plasmid ‘backbone’, its distribution in the environment and the full range of phenotypes with which it is associated.

Reciprocal hybridizations between two D and two R plasmids belonging to the IncP-9 group suggested that although the overall relationship between the plasmids is not strong, a small ‘core sequence’ exists common to all four IncP-9 plasmids tested (3). Extension of these hybridization studies led to the proposal that homology between IncP-9 D plasmids TOL, NAH and SAL occurs between regions thought to carry replication and transfer functions (7). We have recently sequenced the minimal replicon of IncP-9 R plasmid pM3 (8)(A. Greated and others, unpublished data). Examination of the sequence and functional analysis allowed us to identify one of the ORFs as the pM3 \textit{rep} gene. FASTA results revealed 44 % identity with a proposed Rep protein from the broad-host-range plasmid pBBR1 from \textit{Bordatella bronchiseptica} (1). Neither the putative pMT2-Rep nor the predicted Rep protein from pBBR1 exhibited high similarity to any other proteins within the database. Incompatibility tests showed that pBBR1 does not belong to the IncP-9 group.

We have also recently sequenced the \textit{rep} ORF from the TOL plasmid pWW0 (A. Greated and others, unpublished data). Comparison of this with the pM3 \textit{rep} sequence demonstrated 84 % identity at the nucleotide sequence level. This allowed us to design PCR primers (5'-CCAGCGCGGTAC WTGGG-3'; 5'-GTCCGCAICTGCTTGAG CTT-3', where W = A+T and I = inosine) which should give a PCR product when an IncP-9 \textit{rep} gene is present. PCR products were obtained with both pMT2 and pWW0 purified DNA in addition to DNA obtained from the supernatant of boiled \textit{P. putida} and \textit{Escherichia coli} colonies harboring the plasmids. We have successfully applied these primers to DNA from mixed environmental cultures (unpublished data) and recommend them to anyone who is interested in monitoring IncP-9 plasmid behaviour in the environment.

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