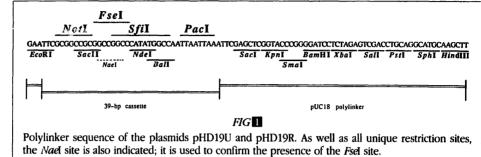


Extension of a pUC18-1ike polylinker by the octanucleotide recognition sites of NotI, FseI, SfiI and PacI

In anticipation that the recently described octanucleotide-recognizing restriction endonuclease $Fsel^1$ will soon be commercialized and thereby be as easily available as the other new rare-cutter enzyme Pacl (New England Biolabs), the vectors pTZ19U/pTZ19R² were engineered to contain the pUC18/19 polylinker plus the sites for the four known octanucleotide restriction enzymes – NotI, Fsel, Sfil and Pacl – as well as unique hexanucleotide sites for SacII, Ndel and Ball (Fig. 1).

Although the sites of Sfill and Fsel do overlap, cloning either into site does not affect the other recognition sequence. The expanded plasmids (pHD plasmids) still allow blue/white selection of recombinants, the creation of a singlestranded form via their f1 origin of replication, and the



translation of cloned DNA from the promoter for T7 RNA polymerase, situated directly adjacent to the polylinker. For the extension, a small DNA cassette was inserted (Fig. 1) similar to the one cloned into the plasmids of the pJDH series³, which already bear the *Sfil* and *Not* sites plus five unique 6 bp restriction sites in addition to the pUC18 polylinker⁴, but the *Apal* site was replaced by the *Fsel* site. This change also introduced a second *XmallII* site. Plasmids pHD19U and pHD19R were isolated and characterized as described³. The presence of the *Fsel* site was confirmed by the ability to cut the polylinker with *NaeI*, which has another site in the f1 origin.

The cassette could be inserted into any *Eco*RI site, thereby increasing the usefulness of many vector systems, and could be used, for example, for blunt-end cloning⁵, chromosome walking and jumping⁶, or as additional cloning sites in pYAC4 (Ref. 7), for instance.

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Casting multiple aliquots of agarose-embedded cells for PFGE analysis

We routinely cast multiple aliquots of cells embedded in agarose for pulsed-field gel electrophoresis (PFGE) analysis and have found that the following method offers several advantages. The well bottoms of a standard rigid polystyrene flat-bottomed 96-well microtitre plate (e.g. Flow Laboratories, catalogue number 76-307-05) are drilled out or removed by milling and the base is sealed with TitretekTM sealing strip (Flow Laboratories, catalogue number 77-420-00). Cells suspended in molten low melting point agarose (e.g. BRL ultraPURETM, final concentration of 0.5%) are dispensed into individual wells (typically in 100 μ l aliquots) from a reservoir (e.g. Flow Laboratories, catalogue number 77-824-01) using an 8-channel or 12-channel pipette. Bubbles are avoided by dispensing only to the first 'stop' on the pipette. The agarose plugs are allowed to set at approximately 4°C, and the sealing strip is then peeled back and the plugs transferred using a PTFE pusher, blunt-ended plastic pastette, or similar, to appropriate solutions for bulk processing before analysis by conventional electrophoresis or PFGE. The casting plate is recycled for further use by rinsing in 0.1 \bowtie HCl then distilled water. The plates can be sterilized by spraying with 70% ethanol. Air-dried plates are resealed with a fresh sealing strip and the casting process repeated.

The advantage of the method is its simplicity, as it involves cheap and readily available materials. Large numbers of plugs can be cast and set very quickly, ensuring that cells are evenly distributed within and between plugs. The cylindrical plugs formed by our method are more robust than cuboid plugs, which tend to lose their corners during processing. Our plugs can be picked up individually using standard sterile plastic bacterial inoculation loops. These 100 μ l plugs squeeze neatly into the slots formed by conventional gel slot combs. They can be easily sliced to reduce loading or to suit small comb sizes. The system is also suitable for simultaneous preparation of multiple plugs from several different samples within one plate, using the microtitre plate grid numbering system for unequivocal identification of each sample.

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