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Quantitative prediction for two-dimensional bacterial genomic displays JEAN-FRANCOIS MERCIER, CHRISTINE KINGSBURRY, University of Ottawa, BÉNÉDICTE LAFAY, CNRS-IRD, GARY W. SLATER, University of Ottawa — Two-dimensional bacterial genomic display (2DBGD) is a simple technique that allows one to directly compare complete genomes of closely related bacteria. It consists of two phases. First, polyacrylamide gel electrophoresis (PAGE) is used to separate the DNA fragments resulting from the restriction of the genome by appropriate enzymes according to their size. Then, temperature gradient gel electrophoresis (TGGE) is used in the second dimension to separate the fragments according to their sequence composition. After these two steps, the whole bacterial genome is displayed as clouds of spots on a two-dimensional surface. 2DBGD has been successfully used to distinguish between strains of bacterial species. Unfortunately, this empirical technique remains highly qualitative. We have developed a model to predict the location of DNA spots, as a function of the DNA sequence, the gel electrophoresis and TGGE conditions and the nature of the restriction enzymes used. This model can be used to easily optimize the procedure for the type of bacteria being analyzed.

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