

Since its introduction in 1995, DNA microarray technology proved itself as an irreplaceable high-throughput technique providing valuable insights into the gene expression patterns and/or the genome identification of whole living organism. Unlike the traditional comparison of expression patterns from cells exposed to two different conditions, the transcriptional profiling of viral expression during time course study of host infection represent a unique technical challenge to a conventional approach. This book describes a global gene expression profiling of bacteriophage BFK20 infecting an industrial L-lysine producer *Brevibacterium flavum* CCM 251 determined by using the custom DNA microarrays in a loop design. New functions were assigned and/or proposed to several gene products of so far unknown function considering their co-expression pattern by utilizing 'guilt-by-association' algorithm. The study provided further insight into phage lifecycle and can be particularly useful to professionals in Virology, Molecular Biology & Biotechnology fields considering performing a viral whole genome time-course expression analysis.

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