Effectiveness of Denaturation Temperature Gradient-Polymerase Chain Reaction for Biased DNA Algorithms*

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DNA computing has been applied to a wide range of computational problems. Recently, challenging problems such as the SAT problem were solved, and various problem-solving strategies were suggested. The unique structures of nucleic acids, such as crossover or self-assembled molecules that are not found in nature can also be used to solve the logical problems and others. To expand the DNA computing field, it is important to develop not only efficient algorithms, but also the supporting biochemical experimental tools which are originally designed to implement the proposed algorithms.

In the previous work, the representation of weights on DNA sequences and the molecular algorithm to solve the graph problems with weighted edges was investigated [1]. A temperature-gradient based algorithm was suggested and implemented with experimental tools including two methods related with a melting temperature (T_m): the denaturation temperature gradient-polymerase chain reaction (DTG-PCR) and the temperature gradient gel electrophoresis (TGGE). We originally developed the DTG-PCR for amplifying the DNA with lower T_m more than the DNA with higher T_m. Since the specificity and sensitivity of the amplification is the first consideration in the conventional PCR, the denaturation temperature is fixed at a constant temperature for complete denaturation. However, when the weight is represented with a T_m of DNA, the denaturation temperature becomes a key factor in the PCR process. DTG-PCR allows us to amplify more or even isolate the most weighted (or the least weighted) paths among the candidate paths, so it is useful in that it can reflect the fitness easily and efficiently. Therefore, we can guide the search area by the DTG-PCR, and it plays an important role in the algorithm.

In this work, the effectiveness of DTG-PCR was shown with a series of DTG-PCR experiments under different denaturation gradient conditions. We also presented a mathematical modeling of the DTG-PCR and showed its effectiveness in experiment design for biased DNA algorithms. The accumulated product amount and the efficiency at each step of the PCR cycle were predicted, and the results were compared with real-time PCR results.

References

1. J. Y. Lee, S. -Y. Shin, S. J. Augh, T. H. Park, and B. -T, Zhang, Temperature gradient-based DNA computing for graph problems with weighted edges, *Lecture Notes in Computer Science*, **2568**:73-84, 2003

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