Sequence similarity of bacteriophage SPO2 DNA polymerase with E.coli DNA polymerase I

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All DNA polymerases known to date are classified into three families, based on evolutionary relatedness (1). The E.coli DNA polymerase I and the T7 phage DNA polymerase share sequence similarity for regions including DNA binding domain (2) and are classified as family A (1). Family B includes cellular and DNA virus polymerases of eukaryotes as well as polymerases of some bacteriophages including T4, φ29 and PRD1 (1,3). Members of this family show considerable similarity to each other, but show no appreciable similarity with those of the family A (1). Bacteriophage SPO2 DNA polymerase (4), designated family C, was thought to have no similarity with polymerases of both the family A and the family B (1). We found that the SPO2 DNA polymerase shares extensive similarities with E.coli and T7 polymerases for the DNA binding domain with 31% and 19% identities, respectively. The probabilities that these similarities occur by chance are less than $10^{-17}$ and $10^{-6}$, respectively (5), implying that the observed similarities are statistically significant and thus this DNA polymerase should be classified as a member of the family A.

References: