The DNA polymerase from the archaebacterium *Pyrococcus furiosus* does not testify for a specific relationship between archaebacteria and eukaryotes

Patrick Forterre
Institut de Génétique et Microbiologie, Bat. 409, CNRS, URA, Université Paris-Sud, 91405, Orsay Cedex, France

Submitted February 12, 1992

Mathur *et al.* reported that the DNA polymerase from the hyperthermophilic archaebacterium *Pyrococcus furiosus* testify for the specific grouping of archaebacteria and eukaryotes in the tree relating the three domains of life (1), in agreement with the proposal of Woese *et al.* (2). Indeed, they have shown that amino acid sequences of regions 1 and 2a from *P.furiosus* DNA polymerase are more similar to homologous regions in a set of eukaryotic DNA polymerases than in a set of eubacterial and bacteriophage DNA polymerases (1). However, this report is misleading, since the prokaryotic and eukaryotic DNA polymerases used in their work belong to different families: family A in the case of eubacterial and bacteriophage DNA polymerases, and family B in the case of eukaryotic DNA polymerases (3). Since a prokaryotic DNA polymerase of the B family is known (*E.coli* DNA polymerase II), I align regions 1 and 2a from *P.furiosus* DNA polymerase with those from *E.coli* DNA polymerase II and eukaryotic DNA polymerases used by Mathur *et al.* (Human DNA polymerase α and Yeast DNA polymerases δ and REV3), together with regions 1 and 2a from Yeast DNA polymerase ϵ, which also belongs to the B family (Figure 1). In that case, the archaebacterial, eubacterial and eukaryotic sequences exhibit about the same level of similarity (Table 1). Accordingly, the data do not testify for a specific relationship between archaebacteria and eukaryotes. Interestingly, however, the finding of a DNA polymerase which belongs to the B family in the three domains of life strongly suggests that the separation between DNA polymerases A and B (which constitute a superfamily) occurred before the separation between eubacteria, archaebacteria and eukaryotes. Since DNA polymerases A and B contain homologous 3′ to 5′ exonuclease activities (3), this also suggests that the common ancestor of eubacteria, archaebacteria and eukaryotes was not a progenote but a complex DNA-cell containing already at least two DNA polymerases with proof-reading activity.

REFERENCES

1. Mathur,E.J., Adams,M.W.W., Callen,W.N. and Cline,J.M. (1991) *Nucleic Acids Res.* **19**, 6952.
2. Woese,C.R., Kandler,O. and Wheelis,M.L. (1990) *Proc. Natl. Acad. Sci. USA* **87**, 4576–4579.
3. Ito,J. and Braithwaite,D.K. (1991) *Nucleic Acids Res.* **19**, 4055–4057.
4. Blanco,L., Bernard,A., Blasco,M. and Salas,M. (1991) *Gene* **100**, 27–38.

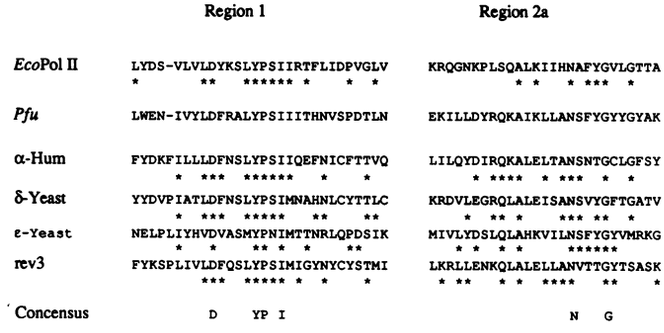

Figure 1. Alignments of regions 1 and 2a of *E.coli* DNA polymerase II (*Eco*Pol II), *Pyrococcus furiosus* (*Pfu*), human DNA polymerase-α (α-Hum), yeast DNA polymerases δ (δ-Yeast) and ϵ (ϵ-Yeast), and REV3 (Yeast). Amino-acids conserved in all sequences are in bold: (*)Identical amino-acids between *Pfu* and other DNA polymerases.

Table I. Number of identical amino-acids between the different couples of DNA polymerase sequences

	*Eco*Pol II	α-Hum	δ-Yeast	ϵ-Yeast	REV3
Pfu	19	23	23	18	23
*Eco*Pol II		20	21	15	15
α-Hum			27	14	25
δ-Yeast				15	28