

## **Acid-loving Archaeon Reads DNA with Enzyme Strikingly Similar to Our Own**

Organisms that live in boiling acid read their DNA using enzymes surprisingly similar to our own, providing insight into the way in which the information stored in DNA is unlocked. In this week's issue of *PLoS Biology*, research by Dr. Nicola Abrescia and colleagues has shown that the enzyme that converts DNA into RNA is conserved between simple single celled microorganisms called *Sulfolobus* and more complicated 'higher' organisms, including human beings, despite a staggering 2 billion year evolutionary gulf. The paper explores how evolution has shaped our enzyme to accomplish more complex functions.

Life on earth is populated by organisms that can be grouped in three evolutionary domains: Eukarya (humans, plants, animals etc.), Bacteria (*E. coli*, *Chlamydia*, etc), and Archaea (including *Sulfolobus*). Many Archaea are extremophiles; living in high salt, acid or temperature environments. Transcription, the process of reading DNA to make RNA (which is in turn translated into proteins by ribosomes) is a fundamental process common to all organisms, and is carried out by the enzyme multisubunit RNA polymerase (RNAP). Eukaryotes have three different RNAPs, whereas Archaea and Bacteria have one. Archaea can serve as a wonderful model system because their simpler RNA polymerase machinery is related to the more complex eukaryotic RNAP. To start transcription, the archaeal enzyme requires two accessory proteins whilst the eukaryotic counterpart needs at least two more. This increased complexity prompts two important questions: how did our polymerase evolve from the ancestral enzyme; and how does Archaea bypass the requirement of further co-factor proteins?

New work, from a team of researchers from Spain, the UK and US and led by Dr. Abrescia, investigates the polymerase from the Archaeon *Sulfolobus shibatae* using X-ray crystallography. This reveals the enzyme's architecture which confirms its close evolutionary relationship with the eukaryotic RNAP. The research also identified a subunit novel to *Sulfolobus* which has no equivalent in the eukaryotic enzyme. The striking structural similarities suggest that the ancestral eukaryote used the same enzyme as the Archaeon, and that modern eukaryotic RNAP evolved by the addition of bolt-on proteins that regulate eukaryotic-specific processes. From the location and topology of the newly identified, Archaeon-only subunit, the scientists have suggested a mechanism by which Archaea do without the additional cofactors required by eukaryotes for initiating transcription.

The scientists also noted that the complete structure of the archaeal polymerase illustrates how the ancestral core enzyme was modulated by addition of novel subunits, an evolutionary process that has facilitated the complexity that we see today in Eukarya.