Corrigendum

A Population of Thermostable Reverse Transcriptases Evolved from *Thermus aquaticus* DNA Polymerase I by Phage Display

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After publication of this Communication, Dr. Fariborz Bahrami in our research group carried out a new fidelity assay. Instead of using commercially available rabbit globin mRNA (R1253, Sigma) as a template for the fidelity assay, a single clone was isolated and the corresponding DNA inserted into a pIVEX vector for in vitro transcription of the rabbit alpha globin gene into mRNA (V00875, NCBI). The high sequence diversity at positions 29, 48, and 49 of the alpha chain of rabbit globin was not observed in the new fidelity assay when using this in vitro transcribed mRNA as a template. We conclude that the sequence diversity at these positions did not result from polymerase-induced hotspot mutations during in vitro reverse transcription, but from distinct mRNA isoforms within the product R1253, which are not reported in the product specification sheet (Sigma), which have not been described at the nucleotide level (NCBI sequence database), and which were reported at the amino acid level.[1]

The estimates of the substitutions rates have therefore been revised. The natural and variant DNA polymerases have accordingly higher fidelities than previously estimated. The following two sentences replace the corresponding sentences on page 6135 (right column, penultimate paragraph) in the original publication.

"The substitution rates per base for RNA-dependent DNA polymerization of the most active variants, **5** (3.0×10^{-4}) and **14** (1.3×10^{-3}), were found to be similar or higher than that of avian myeloblastosis virus (AMV) RT (2.2×10^{-4}), which was used as a standard. Interestingly, the most abundant variant **21** (9.2×10^{-5}) had a fidelity which was about 2.5-times higher than that of AMV-RT."

The conclusions made in this Communication (last paragraph), however, remain unaltered. In particular, the observation that the catalytic efficiency of DNA polymerases can be improved by several orders of magnitude by using directed enzyme evolution by in vitro selection and phage display is unchanged.

[1] T. Hunter, A. Munro, *Nature* **1969**, *223*, 1270 – 1272.

