great sequence similarity. The identity of N-terminal amino acids of active and inactive TRDs F of *M.H2I* and *M.p11sI* suggests that the inactive TRD of *M.p11sI* derived from *M.H2I*. The inactivating mutation must have been a recent event, as the nucleotide sequences of the two regions differ only in the base causing the Glu to Gly change at position 291. The nucleotide sequences encoding the inactive TRDs (E) of *M.p11sI* and *M.H2I* differ from each other in five positions, three of which account for the amino-acid differences and two of which are null. Comparing the inactive E TRDs of *M.p11sI* and *M.H2I* to the active E TRD of *M.SPR* (Fig. 2b) shows that the evolution of the inactive TRDs from an active ancestor must have followed separate avenues.

These inert TRDs represent an intriguing case of preservation of nonfunctional genetic information. This information has been preserved in the absence of positive selective pressure, which in the case of the phage-encoded modification methyltransferases would be exerted by a bacterial restriction and modification system. Negative selection, counteracting the maintenance of genetic information encoding inactive TRDs in the phage genome, has also apparently not acted.

Thus the silent TRDs represent a reserve of genetic material of general evolutionary importance as suggested, for example, by the presence of 'pseudogenes' in some bacterial and eukaryotic genomes. The inactive TRDs described here—although 'expressed' within the context of the active methyltransferases—would operationally fulfil the role of pseudogenes. For this reason we term the inactive domains 'pseudo' TRDs. Considering the modular structure of the methyltransferases discussed here it is conceivable that maintenance of these pseudo domains is significant for the generation of new specificities. □

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CORRECTION

Identification of a G1-type cyclin *puc1*⁺ in the fission yeast *Schizosaccharomyces pombe*

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Nature **351**, 245–248 (1991)

WE have discovered an error in the DNA sequence of our *puc1*⁺ gene in Fig. 1 of the above paper. The CG pair at nucleotides 710–711 should be a GC pair. The amino acids underneath should thus be Leu Gln instead of Phe Glu. However, the protein sequence in Fig. 2 is correct. □

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