sequence has a G3:C70 pair (Fig. 3*b*), it is probably a $tRNA^{Ile}$.

Although it follows most of the rules for tRNA structure, this structure has one unusual feature (Fig. 3*b*). A very highly conserved purine-pyrimidine tertiary base pair, between position 15 and the last base of the extra arm, is a pyrimidine-purine pair in this sequence, a feature shared by only a few other tRNAs[10].

All three introns identified so far in eubacteria are in tRNA genes. This may be due to constraints of our detection method (which favours small, abundantly transcribed introns that self-splice efficiently *in vitro*, for example), or introns in tRNA may have been selectively retained during evolution. Although unrelated to group I, introns are frequently present in archaebacterial and eukaryotic tRNAs, within or next to the anticodon. Deletion of the intron results in failure to modify an anticodon uridine to pseudouridine in eukaryotic $tRNA^{Tyr}$ (refs 18–20). It is possible that introns also have a role in post-transcriptional modification of bacterial tRNAs.

Are group I introns ancient? If introns were present in the common ancestor of all cells, some should have been retained in the eubacterial lineage despite genome 'streamlining'[2]. Closely related introns have now been found in the anticodon loops of tRNA genes from widely divergent bacterial phyla. But as they are in different tRNAs, we cannot determine when these introns were acquired. One intriguing possiblity is suggested by the recent demonstration that the aminoacyl tRNA synthases for Leu, Ile and (unexpectedly) Arg are related[21], which raises the interesting corollary that their respective tRNAs may also have had a common ancestor. We must therefore consider the possibility that tRNAs were interrupted by introns before completion of the genetic code. Alternatively, the introns may have arrived recently at their present locations, for example by reversal of splicing[22] followed by reverse transcription.

Southern hybridization with the *Azoarcus* intron probe (Fig. 4) suggests that related introns are widespread among *Proteobacteria*. As more bacterial introns are sequenced, a comparison of the sequences of introns in homologous genes (for example, for the same tRNA) will provide conclusive evidence concerning the antiquity of group I introns. □

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CORRECTIONS

Evolution of ecological differences in the Old World leaf warblers

Adam D. Richman & Trevor Price

Nature **355,** 817–821 (1992)

IN Fig. 2*a* of the above letter the second and third rows were inadvertently interchanged. In addition, the sequence at position 15176 (ref. 1) for both *Sylvia* and *P. coronatus* should read 'A' and not 'T'. □

1. Anderson, S. *et al. Nature* **290,** 457–465 (1981).

Structure and expression of a human oxytocin receptor

Tadashi Kimura, Osamu Tanizawa, Kensaku Mori, Michael J. Brownstein & Hiroto Okayama

Nature **356,** 526–529 (1992)

WE have discovered an error in the DNA sequence of our pOTR gene in Fig. 1*b*. The nucleotides 714–717, CGGC should be GGCGGCG. The amino acids underneath should be Ala Ala Ala instead of Ala Gly. Accordingly, the complementary DNA encodes a 389 amino-acid protein with a relative molecular mass of 42,819. This error does not affect the conclusions of the paper. □

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