ternative to the "exon shuffling theory," in which the mobile element precisely coincides with the limits of existing coding exons, thus restricting the evolutionary game to some sort of "card shuffling." The finding of the RPEs suggests a greater flexibility in the evolution of genes.

First, the insertions of RPEs realize a flow of genetic material across the boundary between noncoding and protein-coding sequences. In addition, we recently noticed that one of the RPEs (rpe22 of *R. conorii*) previously annotated as "intergenic" is located within the gene coding for tmRNA (the transfer/messenger RNA molecule used to rescue stalled ribosomes and to clear the cell of incomplete polypeptides) (*3*). Thus, the RPE appears capable of parasitizing both protein and RNA structures. The generality of such an influx of genetic material from noncoding to coding sequences deserves further study.

Second, the host proteins targeted by the RPE are different among the species in the same genus. This indicates that RPE insertions occurred after the divergence of those *Rickettsia* species and that the RPE proliferation might be continuing.

Third, the insertion of the RPE at sites that code for a part of the protein that is on the surface, but not necessarily in between domains or within the constraints of exon boundaries, argues for the possibility of a

significant evolution of preexisting protein domains and/or coding exons. For example, the RPE found in the DNA polymerase I of R. helvetica and R. felis is located on the surface of the exonuclease domain (4). Domain insertions within other domains have been described for other proteins, for example, the cat muscle pyruvate kinase, which consists of four different domains. One of the domains forming a  $\beta$  barrel is located within one of the loops of the other  $\alpha/\beta$ barrel domain (1PKM of Protein Data Bank). The structural and

functional consequences of such iterative insertions of domains within domains (a "Russian doll" evolutionary model) remain to be analyzed to better understand the flexibility of genes and genome, as well as the evolutionary modularity of genetic material.

## HIROYUKI OGATA, STÉPHANE AUDIC, JEAN-MICHEL CLAVERIE\*

Information Génétique & Structurale, CNRS-AVENTIS UMR 1889, 31 Chemin Joseph Aiguier, 13402 Marseille Cedex 20, France

\*To whom correspondence should be addressed. E-mail: jean-michel.claverie@igs.cnrs-mrs.fr

References and Notes

1. D. S. Dwyer, J. Theor. Biol. 194, 11 (1998).

- 2. H. Ogata et al., Science 290, 347 (2000).
- As suggested to us by K. P. Williams [see K. C. Keiler et al., Proc. Natl. Acad. Sci. U.S.A. 97, 7778 (2000)].
- See the supplemental figure associated with our report (2) available at Science Online at www. sciencemag.org/feature/data/1051142.shl

## **Scientific Whaling**

THE INFORMATION ABOUT THE HISTORY OF scientific whaling that R. L. Brownell Jr. and coauthors provide in their Letter is incomplete (1 Dec., p. 1696). Their comparison of the numbers of whales killed during the last decade under scientific permits to those taken under such permits in earlier times (thousands compared with hundreds, respectively) does not take into consideration that the tens of thousands of whales taken during the days of commercial whaling generally provided adequate material for whale scientists. Brownell et al. also mention the reported take of almost 5000 minke whales during a decade; however, this take is biologically insignificant when measured against a total population estimate of more than 700,000 minke whales for the Southern Hemisphere. The Japanese have provided the data from these scientific whaling operations on a regular and timely basis to the International Whaling Commission (IWC) and its Scientific Committee.

Like it or not, the Japanese scientific

"Like it or not, the Japanese scientific whaling program is operating legally." whaling program is operating legally. On the other hand, it is doubtful that the Southern Ocean Sanctuary, established by the IWC in 1994, would pass scrutiny if tested in international courts (1). As Brownell et al. note, Japan voted against establishment of the sanctuary and takes its annual catch of Antarctic minke from within sanctuary boundaries. The issue of scientific whaling is neither

scientific or legal. It is a cultural repugnance of some to the operations of others and has been described by an Irish delegate to the IWC as "cultural imperialism" (2).

## WILLIAM ARON\*

11809 NE 30th Place, Bellevue, WA 98005, USA. E-mail: waron@u.washington.edu

\*Former Science Director of the Alaska Fisheries Science Center, NOAA, former member of the Scientific Committee of the IWC in the 1970s, and IWC commissioner in 1977.

- References and Notes
- 1. W. Aron, W. Burke, M. M. R. Freeman, *Mar. Policy* **24**, 179 (2000).
- The Irish Minister of Culture and Tourism, in opening remarks for the 47th meeting of the IWC in 1995.

Need to amplify large full-length genes? Then GETLarge.

Introducing... GETLarge \*\* Full-length cDNA.

We've developed patented technology to overcome the limitations of conventional RT-PCR so that you can amplify large, full-length transcripts with confidence and ease.



The large, titin gene (7.0 kb) was successfully amplified using Human GLTLarge Full-length cDNA generated from different tissues; however, the titan gene was not amplified using non-enriched cDNA. Lane A: GLTLarge cDNA. Lanes B: non-enriched cDNA. Lane M: LkDNA blacks.

- Enriched cDNA using Gene Enrichment Technology
- Amplify large, full-length genes
- Select from different human tissues

For more information, call us at 1-877-GENEMED (1-877-436-3633) or visit our website at www.genemed.com

Od 1450 - De la la sectoria contra la Gambio de la

