tized pulsar in supernova 1987A might nevertheless be detectable. The lowmagnetic-field millisecond pulsars would be weak sources in our scaling.

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Aluminium and global warming

SIR - The Intergovernmental Panel on Climate Change has overlooked two important greenhouse gases: CF_4 (CFC-14) and C_2F_6 (CFC-116). These gases have atmospheric residence times in excess of 10,000 years and have strong absorption bands in the atmospheric window near 8 μm (ref. 1). Of the chlorofluorocarbons, the radiative forcing of CF₄ and C₂F₆ during the 1980s was exceeded only by CFC-11, -12, -113 and HCFC-22 (ref. 2).

The only significant known anthropogenic source term for CF₄ and C₂F₆ is primary aluminium smelting. Various fluoride compounds, including CF4 and C_2F_6 , are produced during electrolysis of alumina (Al_2O_3) dissolved in a molten cryolite (Na₃AlF₆) bath³. A small, yet unidentified, natural source of CF4 is suspected. Fabian et al.4 estimated global emission rates of 28,000 tonne CF₄ and 3,200 tonne C₂F₆ per year in 1987. This suggests global average emission factors of about 1.6 kg CF₄ and 0.2 kg C₂F₆ per tonne of primary aluminium production. These emission rates are consistent with aluminium industry estimates of 1.5-2.5 kg of CF4 produced and emitted to the atmosphere per tonne of aluminium, and an order of magnitude or so less of C_2F_6 (ref. 5).

Using the band strengths reported by Hansen et al.², I estimate the global warming potential (GWP) to be between 10,000 and 11,000 for CF4 with 100-yr integration time and without correction for the overlapping of absorption bands of CH₄ and N₂O. F. Stordal, using a more detailed model, has estimated the 100-yr GWP of CF_4 and C_2F_6 to be about 8,400 (personal communication). Lashof and Ahuja estimated that CF4 was responsible for 1.7% of the total warming potential of all global anthropogenic greenhouse gas emissions in 1985⁶.

Average CF₄ and C₂F₆ emissions are thus equivalent to the greenhouse contribution of about 15-20 tonnes of CO₂ per tonne of aluminium. To the extent that CF₄ and C₂F₆ are produced during electrolysis cell anode effect, considerable variation in emissions from plant to plant would be expected as the frequency of anode effect varies by at least 10-fold between smelters7.

 CF_4 and C_2F_6 may be the most potent greenhouse gases being emitted in large amounts. Not only do they have a very large GWP, they also cause an essentially permanent alteration in greenhouse forcing. Aluminum smelting also results in large greenhouse gas emissions from production of the electricity consumed during smelting, and from CO2 produced during alumina reduction to aluminium metal. Alumina reduction, 2Al₂O₃ + $3C \rightarrow 4Al + 3CO_2$, results, in practice, in emissions of between 1.5 and 2.2 tonnes of CO₂ per tonne of aluminium. Aluminium smelters consume between 13 to 20 MWh of electricity per tonne of aluminium depending on efficiency. Greenhouse gas emissions from producing this electricity vary from at least 22 tonnes of CO₂ equivalent per tonne

of aluminium when the electricity is produced by a conventional coal-fired power plant to low levels for hydropower.

Cement is the only primary commodity, other than fossil fuels, specifically included in conventional tabulations of sources of greenhouse gas emissions. Yet the total greenhouse contribution from primary aluminium production appears to be greater than that from cement production on a global basis and can be tens of times greater in countries with a large primary aluminium industry based on fossil-fuel-generated electricity.

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Leukaemia/Drosophila homology

SIR — The sequence has recently been published¹ of a human complementary DNA clone encoded by a gene (designated AML1) that is rearranged in a translocation (t(8;21)) characterizing a subtype of acute myeloid leukaemia. No similarity was reported between the predicted polypeptide sequence and any known sequence. We find, however, that it is highly related to runt, one of the class of pair-rule genes that control morphogenesis in Drosophila melanogaster². The region of best alignment spans 118 amino acids from positions 60-177 in

intron boundary. It is tempting to speculate that it may represent a functional domain. Intriguingly, the t(8;21) breakpoints seem to cluster in the intron immediately downstream of this boundary.

Runt encodes a nuclear protein which is likely to be a transcriptional regulator, although it does not contain any of the structural motifs recognized in such factors, or a nuclear localization signal. AML1, however, does contain a cluster of basic residues at position 177-182 (four residues out of six being K or R) which is a 'minimal' motif in transcrip-AML1 and from position 115-232 in tion factors. This sequence would be

AMI.1	60	GELVRTDSPNFLCSVLPTHWRCNKTVPIAFKVVALGDVPDGTLVTVMAGNDENYSAELR
runt	115	GELAQIGSPSILCSALPNHWRSNKSLPGAFKVIALDDWPDGILVSIKCGNDENYCGELR

AML1 119 NATAAMKNOVARENDLREVGRSGRGKSFTLTITVFTNPPQVATYHRAIKITVDGPREPR 174 NCTTIMKNOVAKENDLREVGRSGRGKSFTLTITIATYPVQIASYSKAIKVTVDGPREPR nint

Region of best alignment between human AML1 and D. melanogaster runt.

runt. Within this region, 73% of aminoacid residues are identical, a further 23% are conservative replacements, and the percentage nucleotide identity is 68%. This is higher than the homology between the mouse proto-oncogene int-1 and its counterpart in Drosophila, wg (54% amino-acid identity over 468 residues³) and comparable to the homology between Drosophila and human homeoboxes. The region of homology also includes a perfect match of the A box of a putative ATP-binding site.

The region of homology between the Drosophila and the human sequences stops abruptly at a conserved exon/

disrupted by the t(8;21). Thus, AML1 seems to be a structural homologue of runt in man. Its role in human development, particularly in haemopoietic differentiation, remains to be established. ANTONIO DAGA

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