observing period of Wolszczan and Frail, are offset by a significant amount, about 170 and 500 μs, respectively. However, these offsets are not surprising given the number of parameters and uncertainties in Wolszczan and Frail's model. Our modelling of the spin and astrometric parameters shows that most of the growing residual in 1992 can be absorbed by small changes in the spin parameters and position. These uncertainties will need to be reduced before the small orbital perturbations predicted by Rasio *et al.*[7], which will confirm the planetary hypothesis, can be detected.

A further test was done at the suggestion of a referee by analysing the data with PSRTIME, an independent software package developed by A. Lyne at Jodrell Bank. This package also uses an independently generated ephemeris, JPL DE118. This comparison required rotating the timing position of Wolszczan and Frail by the known 0.4″ shift between the frames of the ephemerides (see ref. 8). A test using PSR1937+21 data showed microsecond agreement between the two analysis packages. Analysis of the Green Bank PSR1257+12 data with PSRTIME using Wolszczan and Frail's timing model also produces good agreement.

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Deep-sea amphipod swarms

SIR — Sustained and rapid swimming activity of deep-sea invertebrates is an unusual phenomenon. Even at hydrothermal vents, where food resources are enhanced through chemoautolithotrophic production, the dominant organisms are typically sessile or sedentary, though the swarming shrimp that crawl over surfaces of high-temperature (350 °C) black-smoker chimneys are an exception[1]. During *Alvin* dives at the Venture hydrothermal fields[2] along the East Pacific Rise (9°–10° N, 104° 14–17′ W; 2,520 m depth), we encountered a unique swarming behaviour in a previously undescribed pardaliscid amphipod (Fig. 1).

The amphipod swarms are monospecific and form schooling shoals just above the sea floor at densities sometimes exceeding 1,000 individuals per litre. This concentration of pelagic crustaceans surpasses all reported values from the deep sea that we could find, exceeding Smith's[3] estimate of copepod densities at another vent site by three orders of magnitude. The swarms, typically occupying a volume of less than 1 m^3, are invariably located immediately downstream of low-temperature (2–8 °C; ambient is 1.8 °C) flows of hydrothermal fluids emanating from cracks in the basaltic sea floor. Orientation of amphipods within a swarm was primarily, but not exclusively, polarized, with individuals facing into the low-temperature diffuse flow.

Using pulsed-dye injections and video records, we measured sustained swimming speeds of 5–10 cm s^{-1} (10–20 body lengths s^{-1}). The amphipods are constrained by a treadmill-like behaviour of net horizontal swimming upstream and passive movement downstream to a cycle length of the order of 2 m or less in an otherwise advective fluid environment. Using a conservative swimming speed of 5 cm s^{-1}, the maximum linear distance covered per day could be greater than 2 km. The swarms appear to be long-lived components of the vent community in that the swarms were first observed during dive operations in May 1991 and were found again at exactly the same sites (± 0.5 m) in December 1991.

FIG. 1 High densities of an undescribed pardaliscid amphipod swarm above a mussel (*Bathymodiolus thermophilus*) clump at a vent site. Swarms were found at numerous vent sites near 9° 50′ N and at 9° 17′ N. Unpublished records of 'crustacean swarms', almost certainly the same amphipod, are referred to in transcripts from *Alvin* dives at vent sites between 10° and 12° N on the East Pacific Rise (G. Thompson and W. Bryan, co-chief scientists; 1988).

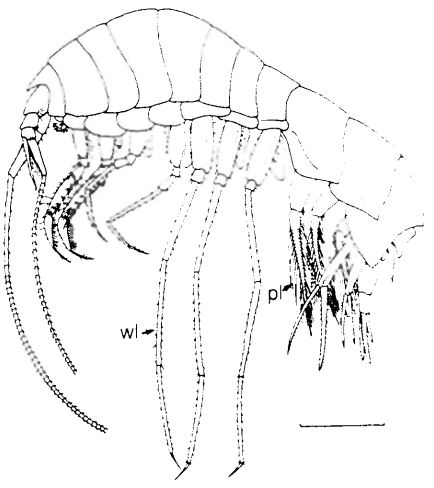

FIG. 2 The swarming amphipods are well adapted for swimming, with strong pleopods (pl) and delicate walking legs (wl), especially pereiopods 5–7. Scale bar, 1 mm. Until these observations, pardaliscid amphipods comprised 1% of the known amphipod fauna of vent sites, with 98% of the amphipods belonging to a single lysianassid species[5].

Not surprisingly, the morphology of the swarming amphipod is adapted for swimming, with well-developed pleopods and delicate walking legs (Fig. 2). Amphipod swarms were observed at numerous sites in association with mussels, clams and tubeworms, as well as in diffuse hydrothermal flows devoid of these megafaunal organisms.

Swarming in crustaceans is mainly reported in shallow-water species where light seems an important cue for swarm maintenance[4]. The significance of swarming in shallow-water taxa is most often associated with reproductive behaviour, feeding and avoidance of visually orienting predators. The adaptive significance of swarming behaviour in vent amphipods which live in complete darkness is not clear. Suspended microorganisms flushed in vent water from subsurface growth chambers may comprise their diet; it follows that individuals must maintain a position where the concentration of food particles is

sufficient to meet their metabolic demand. Although it is not possible to determine whether the swarming behaviour is more than an expression of optimal spacing of grazing individuals in an advective three-dimensional space, it is clear that the swarming amphipods must play a significant part in the bentho-pelagic coupling of chemosynthetic production.

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Tweaking the magnetosphere

SIR — Kurth's News and Views article[1] captures much of the excitement of the phenomenon of solar coronal mass ejections (CMEs) and their role in triggering terrestrial magnetic storms. But we wish to correct the impression that we do not yet know why some CMEs cause storms and others do not.

The necessary feature for the creation of major magnetic storms is the presence of an intense, long-duration (hours), southward, interplanetary magnetic field[2–4] somewhere within the high-speed (CME-related) stream structure. These southward fields efficiently interconnect with the Earth's magnetic field and allow energy transfer to the magnetosphere[5,6]. In a study of 55 (CME-related) shock-led high-speed solar wind-stream events occurring in 1978–79, 9 had such intense long-duration southward fields, 8 had predominantly northward fields and 38 had fields that were primarily in the ecliptic plane or had sufficiently out-of-ecliptic components, but were highly fluctuating in time[7]. Thus, only 9 of 55 shock-led, high-speed (CME-related) streams caused major magnetic storms.

For magnetic storms of lesser intensity, the requirements for the intensity of the southward field component and/or its duration are less[8]. These events are not necessarily associated with high-speed streams or shocks. At the lowest increment of magnetospheric energy, a substorm (thought to be an incremental part of a storm) is caused by even weaker and/or shorter-duration southward fields. Substorms are almost never associated with shocks and/or CMEs but with Alfvén waves[9] and discontinuities.

The level of the intensity of geomagnetic activity is ordered by the intensity and duration of the southward magnetic field. Velocity plays an important but not dominant role. Thus, CMEs are not a necessary and sufficient condition to cause intense magnetic storms, but long-duration, intense, southward interplanetary magnetic fields are.

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Emerging cytokine family

SIR — Our colleagues recently reported the cloning of a murine ligand (CD40L) to the CD40 antigen[1]. CD40 is a member of a family of at least nine transmembrane proteins[2], including the low-affinity nerve growth factor (NGF) receptor and two distinct tumour necrosis factor (TNF) receptors that each bind both TNF-α and TNF-β. Although Armitage *et al.* reported that screening of the CD40L sequence against the nucleotide sequence databases revealed no significant similarities[1], we have now found that CD40L is similar to TNF-α and TNF-β (see ref. 3 for a review), suggesting an emerging ligand family parallel to the TNF/NGF receptor family.

CD40L and pro-TNF-α are both type-II membrane proteins and sequence similarity is limited to the carboxy-terminal (receptor-binding) portion of the extracellular domains; in mature TNF-α (and in TNF-β, a secreted protein) the homologous region forms a β-sandwich which trimerizes[4,5]. CD40L thus presumably shares a similar tertiary structure and may be oligomeric, consistent with ligand-induced receptor cross-linking as a common activation mechanism.

Despite many other known ligands to members of the TNF/NGF receptor family are the neurotrophins (such as NGF), a set of homologous cytokines which bind low-affinity NGF receptor (and several *trk* proto-oncogenes)[6]. Although NGF is a homodimer whose protomer, like TNF-α and TNF-β, has an all-β structure[7], its topology differs from the TNF topology and no sequence similarity is apparent. The known ligands of the TGF/NGF receptor family thus fall into two structural classes. Because the remaining members of this receptor family (4-1BB, OX40, CD30, CD27 and FaS) reside chiefly on cells of the haematopoietic system, it seems their putative ligands are more likely to resemble TNF than the neurotrophins.

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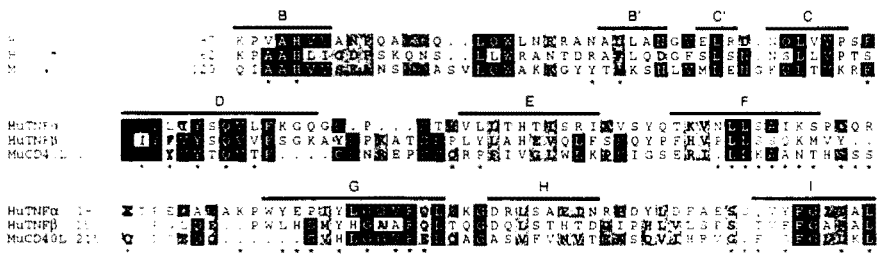

Region of similarity among human TNF-α and TNF-β and murine CD40L sequences. Identities and similarities between CD40L and each of the TNF sequences are highlighted. Asterisks, residues involved in the trimeric interface of TNF-α; B–I, β-strands of TNF-α (ref. 4).