

## Stratigraphic record of earthquake incidence

CISNE<sup>1</sup> uses the Lofer cycles of the late Triassic Dachstein Formation (Northern Limestone Alps, Austria and Germany) as an illustration of how stratigraphy may record histories of stick-slip movement and thereby of earthquake incidence along fault zones. As the discoverer of the emergence-submergence oscillations of the Lofer cycles, which I attributed to a sea-level oscillation<sup>2</sup>, I am very interested in Cisne's alternative tectonic way of producing periodic emergence of a platform margin. His model explains why the signs of emergence (microkarst, relict soils) should be restricted to the outer margin of the carbonate platform. But it necessitates some revision of current sedimentological and/or tectonic concepts.

It is necessary first of all to place these Triassic terranes into tectonic context. They are now part of the giant Oberostalpin ('upper Austride') klippe that extends for 450 km, from the Swiss border to Vienna, in itself a patchwork of thrust sheets and klippen of various facies, complicated by high-angle faults, and developed in a complex and controversial history<sup>3-7</sup>.

In Triassic time, the terrane was part of a tectonic trough, filled in the north with Triassic platform carbonates, while the southern part was open and accumulated the thin pelagic-hemipelagic Hallstatt beds<sup>5</sup>.

In several places, the toe of the reef complexes interfingers with ammonite-bearing, pink or greenish calcilitites of Hallstatt type. However, the bulk of the Hallstatt deep-water rocks are now found as discreet klippen masses emplaced on top of the platform facies and its deeper Jurassic/early Cretaceous cover.

Cisne's stick-slip fault would have defined the southeastern margin of the platform, separating it from the Hallstatt facies. It would have added to regional subsidence an additional component, either on the platform or on the Hallstatt side. Throwing the Hallstatt side down, relative to the platform, accelerates the subsidence of the platform margin during the 'stick' phase, leading through intertidal into subtidal conditions. The slip phase allows this margin to snap back into emergence, followed by truncation, and resubmergence in the next stick episode. In the alternative case, throwing the platform down slows the platform margin's subsidence during the stick phase, and sedimentation leads to progressive shoaling; then the margin snaps down in the slip phase. Thus, the Hallstatt-down model leads to upward deepening cycles, the platform-down model to upward shoaling cycles. One of the most distinc-

tive characteristics of the Lofer cycles is their generally upward-deepening character, which has seemed unusual to students of carbonate platforms. If these cycles were caused by stick-slip faulting, then the motion was down on the Hallstatt side.

It is here that difficulties develop. If the Hallstatt basin underwent more subsidence than the platform, it must have subsided by more than the thickness of Norian platform sediments (some 1.5 km) during Norian time. Since the Norian of the Hallstatt facies probably does not exceed a thickness of 150 m, the late Norian calls for a water depth of 1.5-2 km. This depth is about the limit to which pelagic aragonite shells persist on the present sea floor (the aragonite compensation depth). It seems that modern compensation depths go back to the dramatic rise in plankton carbonate productivity in late Jurassic time<sup>8</sup> earlier carbonate compensation depths lay at far shoaler levels. Thus, conventional wisdom assigns the Hallstatt carbonates with their ammonites to water depths of several hundred metres, not the required 2 km.

I can think of three possible ways to escape this dilemma—all of which would require revision of current concepts. One is that the oceans of the Triassic were saturated with calcium carbonate to much greater depths than those of the Jurassic, allowing preservation of aragonitic shells at depths of 1.5-2 km.

A second possibility is that the Hallstatt basin was oceanic, a Triassic antecedent of the Jurassic (Pennine) ocean strip, and that most of the Hallstatt beds were seamount deposits, scraped off during southward subduction of that oceanic basin, and emplaced over the margin of the platform as it began to be subducted in mid-Cretaceous time.

The third possibility is that the basin fronting the Loferite cycles was deep. The Hallstatt beds were deposited in a shoaler part of the trough, to the west. The Hallstatt facies was first brought to the longitude of the Lofer cycles by sinistral strike-slip displacements, probably in the mid-Jurassic when the Lammer-Torren zone underwent tens of kilometres of sinistral motion<sup>5</sup>, and were then emplaced by Juvavian (mid-Cretaceous) thrusting.

My preference is for the second of these models, which implies an 'accreted prism' origin for the entire stack of Alpine sediments.

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## Primary structure of the histidine-rich protein of *Plasmodium lophurae*

SIR—We wish to address the literature concerning the sequence of the histidine-rich protein (HRP) and the corresponding gene from the avian malaria parasite *Plasmodium lophurae*. Following publication of a DNA sequence derived from a *P. lophurae* genomic clone<sup>1</sup>, we were forced to reassess our own data, which differed extensively from the 3' half of the published coding sequence. Our results were derived from the complementary DNA clones<sup>2</sup> that were used to isolate the genomic clone. A corrigendum to the genomic sequence was published<sup>3</sup>; in the revised sequence, 120 base pairs (bp) were deleted and 90 bp were inserted. Our analyses<sup>4</sup> independently suggested that the published genomic sequence contained an insertion and a deletion, each of about 120 bp, together with a region of about 100 bp containing multiple insertions of one or two bp in the genomic sequence. The region of the genomic sequence between the insertion and deletion sites was not revised<sup>3</sup>. There is a significant difference in the amino acid compositions predicted by the two sequences, the most extreme being a fourfold difference in phenylalanine content.

What then are the most probable structures of the HRP and its gene? Making the assumptions that the published 5' DNA sequence<sup>1</sup> and corrections<sup>3</sup> to the numbers of downstream repeats not covered by the cDNA sequence are correct and that the 3' sequence from the cDNA<sup>4</sup> should take preference, a composite sequence can be constructed. The mature HRP (289 amino acids) predicted by this sequence has a molecular weight of 37,109 and contains 71.3% histidine, 7.2% proline, 7.0% alanine, 6.2% glutamic acid and smaller amounts of eight other amino acids. This composition is consistent with three independent determinations of the composition of purified HRP (cited in ref. 4).

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