

interval). We interpret this progradational stacking as the HST of DS2. The carbonate sediments of member 4 lower interval deposited from the middle to distal outer ramp. Consequently, this interval record a deepening-upwards trend. According to that, we hypothesise that member 4 lower interval represents the TST of DS3. A general shallowing-upwards tendency is recorded from member 4 middle interval (proximal outer-middle ramp) to the top of member 5 (deposited in tidal environments above fair weather base level). Consequently, we hypothesize that this tendency corresponds to the HST of DS3. In member 5, four parasequences have been recognized. We interpret them as related to tectonics-induced subsidence, because just in this part of the Triassic succession the occurrence of a strong syn-sedimentary extensional tectonics has recently been demonstrated (Martin-Rojas *et al.*, 2009).

The sequences identified correlate with those recognized in other sectors of the Alpujarride domain the Germanic- and Alpine -type Triassic.

References

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Application of numerical cladistic analyses to the Carnian-Norian conodonts: a new approach for phylogenetic interpretations

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The high intraspecific variability of conodonts in the upper Carnian-lower Norian interval and the proliferation of numerous species in this relatively short stratigraphical time generated many problems in the understanding of the Late Triassic conodonts phylogeny, systematic and taxonomy. The abundance of synonymies *per* species and the absence of an established phylogenetic model contribute to increase the issues concerning the conodonts systematic. Unfortunately, being natural assemblages of the Late Triassic conodont apparatuses still unknown, a multielement approach to the problem would just introduce more biases instead of solutions. The application of cladistic methods to the platform elements, instead, may provide an extremely valid methodology in the understanding of their evolutionary relationships. Platforms are in fact the most abundant conodont elements and they have well observable evolutionary patterns and, thus, they can be considered as the primary basis for the interpretation of the Late Triassic conodont phylogeny.

We applied numerical cladistic analysis to the species belonging to the five most widespread Late Triassic genera (*Paragondolella*, *Carnepigondolella*, *Metapolygnathus*, *Epigondolella* and *Norigondolella*) from the Pizzo Mondello section (Sicani Mountains, Western Sicily, Italy), GSSP candidate for the Norian (Mazza *et al.*, 2010 and references therein). This section provides several advantages for these kind of taxonomic and cladistic studies on conodonts: the section is a continuous succession of pelagic carbonate sediments (*Calcari con selce* or *Halobia Limestone auctorum*; Cherty Limestone, Muttoni *et al.* 2001, 2004; Guaiumi *et al.* 2007), characterized by uniform facies, high sedimentation rates and, more important, it has a rich conodont record which is representative of faunas spread in the entire Tethys.

A taxon-character data matrix describing the distribution of 68 characters among 2 outgroup and 32 ingroup taxa was

thus compiled and processed using PAUP* 4.1.

The analyses confirmed the validity of a series of evolutionary trends among the platform elements, evidenced the most important morphological characters for their classification and led to a reinterpretation of the phylogenetic position of the genera considered: *Metapolygnathus* and *Epigondolella* resulted the only two monophyletic groups and, thus, true phylogenetic genera; *Paragondolella* a polyphyletic assemblage of basal members of the ingroup; *Norigondolella* a paraphyletic series of taxa bracketed by *Paragondolella* and *Carnepigondolella* a paraphyletic group including all conodonts more derived than *Paragondolella* and *Norigondolella* but outside the *Metapolygnathus* and *Epigondolella* clades.

These results show the potentiality of applying cladistic methods also to parataxonomic taxa. Parsimoniously grouping by synapomorphies (shared derived characters) provides a more informative classification than using simple similarities (phenetics). A cladogram, in fact, describing more of the character state changes than a phenogram, gives a higher information content and provides a more natural classification.

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Paleoecological controls on Triassic flat clam biochronology

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The biochronologic significance and correlation potential of the Triassic flat clams *Claraia*, *Peribositria*, *Enteropleura*, *Daonella*, *Halobia*, *Eomonotis*, and *Monotis* is demonstrated at regional and global scales. Their biochronologic and paleogeographic utility is likely a result of a combination of their unique paleoautecology in combination with a genetic propensity for rapid evolutionary and turnover rates in a high-stress regime. Their evolutionary paleoecology can, in the absence of modern analogs or genetic information, be inferred from morphological adaptations, their unique facies occurrence, and analogous yet anecdotal similarities from other non-pelagic bivalves.

Most Triassic flat clams were likely either freely resting or reclining without byssal attachment (e.g. *Peribositria*, *Enteropleura*, *Daonella* and *Halobia*) or attached with a feeble or weakly functioning byssus (e.g. *Claraia*, *Eomonotis*, and *Monotis*). Although occurring across a spectrum of accumulation modes, many (but not all) of these bivalves occur within episodic monospecific or paucispecific shell accumulations. Triassic flat clam accumulations may be associated with a demonstrable pelagic fauna including ammonoids, radiolarians, conodonts and globochaets. Many of these shelly accumulations are clearly a result of significant biostratinomic processes, yet the most informative shell beds are those that represent occasional or episodic census assemblages (= life assemblages) or within-habitat time-averaged assemblages (= neighborhood assemblages). Shell beds vary considerably in thickness (some achieving thickness of several meters or more), their accumulation suggest density independence. These shell beds show a rapid increase in population numbers until saturation occurs and can extend for 10s and perhaps 100s of meters laterally. The abrupt upper surface of shell accumulations likely represents a mass mortality event due to reduction in one or more limiting factors or introduction of lethal pathogen.

Major constraints in the occurrence of marine bivalves are bathymetry, turbidity, availability of substrate, temperature, dissolved oxygen, and nutrition. Given that Triassic flat clams occur in a broad spectrum of marine environments mostly in relatively open marine settings at variable water depths, temperature and salinity levels are likely relatively constant and not likely significant inhibitors to their distribution or occurrence. Adaptations to dysaerobic environments alone cannot explain all mass occurrence (and mass mortality) of Triassic flat clams as they also occur in fully oxygenated marine settings (e.g.