Dataset

3D models related to the publication: Shape diversity in conodont elements, a quantitative study using 3D topography.

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Abstract
The present 3D Dataset contains the 3D models analyzed in Assemat et al. 2023: Shape diversity in conodont elements, a quantitative study using 3D topography. Marine Micropaleontology 184. https://doi.org/10.1016/j.marmicro.2023.102292. P1 elements represent dental components of the conodont apparatus that perform the final stage of food processing before ingestion. Consequently, quantifying the shape of P1 elements across the topographic indices of different conodont species becomes crucial for deciphering the diversity in feeding behavior within this group.

Keywords: Conodonts, Doolkit, Morphofunction, Scanning resolution, Topography

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INTRODUCTION

Conodonts, a successful group of early eel-shaped vertebrates, thrived in seas from the upper Cambrian (-500My) to the end of the Triassic (Clark 1983). Their presence in the fossil record is primarily marked by abundant phosphatic micro-remains known as conodont elements, functioning akin to teeth (Purnell 1995). These elements were intricately organized in a complex feeding apparatus, enabling conodonts to capture and process their prey (Aldridge 1987; Purnell and Donoghue 1997; Goudemand et al. 2011). Among these elements, the pectiniform elements (P1) stand out as the most robust and are typically well-preserved in the fossil record. Operating in pairs, the left and right P1 elements play a crucial role in the final stage of food processing before ingestion. Despite having no living representatives, the functional diversity of conodonts has been explored through nomenclatural descriptions, classification of P1 shapes (e.g., Sweet 1981, 1988; Over 1992; Purnell et al. 2000), morphometry (e.g., Girard et al. 2004; Hogancamp et al. 2016; Guenser et al. 2019), and analysis of platform element articulation kinematics (e.g., Donoghue and Purnell 1999; Martinez-Perez et al. 2014a, b; Suttner et al. 2017). As P1 elements are involved in food bolus processing, their shape may offer insights into diet preferences. While previous studies have investigated P1 element shapes using 2D and 3D morphometrics at the genus or species level, inter-species comparisons face challenges due to the wide morphological disparity and difficulty in finding homologous structures (Purnell et al. 2000; Jones et al. 2009). The advent of 3D imaging has introduced new tools for studying shape variations and diversity, enabling quantitative analyses on a larger scale. Dental topographic analysis, one such tool, divides an occlusal surface into smaller elements, such as points in digital elevation models (Ungar and Williamson 2000; Evans et al. 2007) or small polygons in 3D surfaces (Guy et al. 2013). Algorithms can then quantify the entire surface morphology using indices of complexity, orientation, or sharpness (Winchester 2016), eliminating the need for homologous structures and allowing a functional perspective on a wide range of morphologies (Evans et al. 2007; Prufrock et al. 2016; Li et al. 2020). While dental topographic methods have primarily been applied to mammal teeth for diet and morphofunctional assessments, applying these indices to conodont elements could facilitate a large-scale quantification of P1 element shape diversity. This approach may provide a better understanding of their morphofunctional role in the food processing of this extinct group, addressing poorly explored aspects such as sharpness, average slope, and complexity. This study aims to test the relevance and limitations of available indices for the quantitative segregation of shapes in several conodont P1 elements, considering the impact of 3D mesh processing on topographical results, including the initial voxel size and triangle homogenization. With that in mind, the topographical indices represent a promising toolkit for the quantification of conodonts shapes diversity as they allow to segregate sharp blade-like morphologies from wider platform ones (see Fig. 1). Its further implication to constrain the functional part of the P elements during food processing could bring a better understanding of feeding ecology in these groups.

METHODS

The specimens (see table 1) were scanned using the facilities of the SFR Bio-sciences (UMS3444/CNRS, US8/ Inserm, ENS de Lyon, UCBL) AniRa-ImmOs. The herein presented specimens were scanned using a voxel size of 1.6 µm. The surfaces were extracted slice-by-slice using AVIZO 9.0 (Visualization Sciences Group) resulting in polygonal meshes composed of triangle. To reduce the noise related to segmentation artefacts, surfaces were smoothed under Meshlab software using the Taubin

smooth method (Taubin, 1995). Then, in order to avoid any bias induced by the disparate sizes of the triangular polygons composing meshes, triangle size was homogenized on the base of the mean size of mesh triangle using the Isotropic remeshing of Meshlab software. Finally, topographical indices were calculated and mapped using Doolkit package in R (Thiery et al. 2021).

Inv nr.	Taxon
UM CTB 082	*Bispathodus aculeatus*
UM CTB 083	*Bispathodus aculeatus*
UM CTB 086	*Bispathodus aculeatus*
UM CTB 088	*Bispathodus ultimus*
UM CTB 089	*Bispathodus aculeatus*
UM CTB 090	*Bispathodus costatus*
UM CTB 092	*Bispathodus ultimus*
UM CTB 093	*Bispathodus costatus*
UM CTB 094	*Bispathodus spinulicostatus*
UM CTB 096	*Bispathodus aculeatus*
UM CTB 098	*Bispathodus ultimus*
UM CTB 060	*Bispathodus costatus*
UM CTB 073	*Bispathodus spinulicostatus*
UM CTB 049	*Branmehla suprema*
UM CTB 100	*Branmehla inornata*
UM CTB 101	*Bispathodus stabilis*
UM CTB 102	*Branmehla suprema*
UM CTB 103	*Branmehla suprema*
UM CTB 104	*Branmehla suprema*
UM CTB 105	*Branmehla suprema*
UM CTB 106	*Branmehla suprema*
UM CTB 072	*Branmehla suprema*
UM CTB 107	*Branmehla suprema*
UM CTB 108	*Branmehla suprema*
UM CTB 109	*Branmehla suprema*
UM CTB 110	*Bispathodus stabilis*
UM CTB 112	*Palmatolepis gracilis*
UM CTB 061	*Palmatolepis gracilis*
UM CTB 115	*Palmatolepis gracilis*
UM CTB 116	*Palmatolepis gracilis*
UM CTB 117	*Palmatolepis gracilis*
UM CTB 062	*Palmatolepis gracilis*
UM CTB 118	*Palmatolepis gracilis*
UM CTB 119	*Palmatolepis gracilis*
UM CTB 120	*Palmatolepis gracilis*
UM CTB 075	*Polygnathus communis*
UM CTB 121	*Polygnathus communis*
UM CTB 122	*Polygnathus communis*
UM CTB 123	*Polygnathus communis*
UM CTB 125	*Polygnathus communis*
UM CTB 126	*Polygnathus communis*
UM CTB 128	*Polygnathus communis*
UM CTB 130	*Polygnathus communis*
UM CTB 131	*Polygnathus communis*
UM CTB 132	*Polygnathus communis*
UM CTB 133	*Polygnathus communis*
UM CTB 139	*Polygnathus symmetricus*
UM CTB 140	*Polygnathus symmetricus*
UM CTB 141	*Polygnathus symmetricus*
UM CTB 142	*Polygnathus symmetricus*

Table 1. List of P element models. Collection: University Montpellier, Institut des Sciences de l'Evolution.

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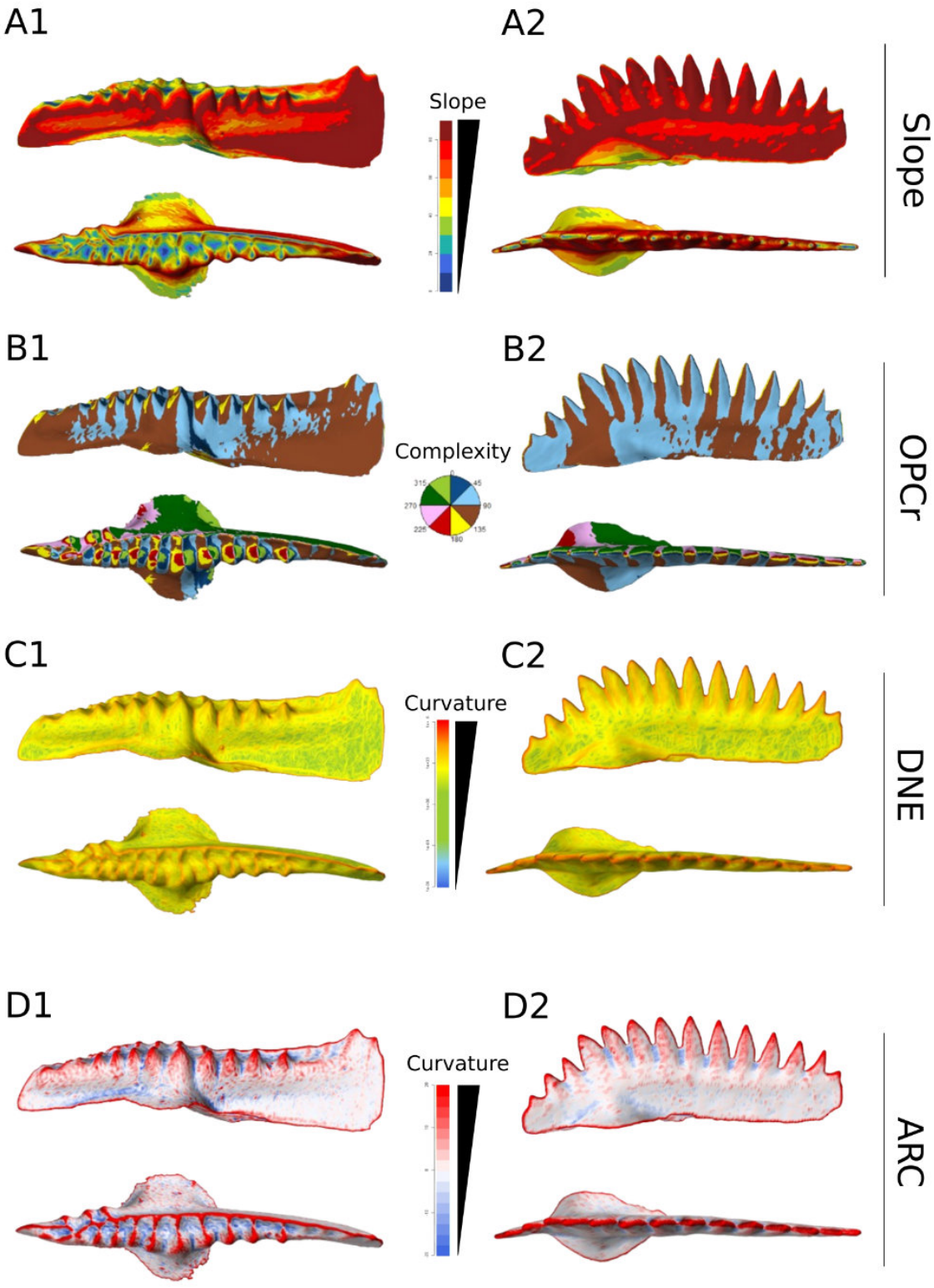

Figure 1. Mapping of topographic indices on P elements of two conodont taxa illustrating two different morphologies highlighting the differences between: 1- the wide platform *Bispathodus ultimus,* 2- the blade like *Branmehla suprema*. Indexes of complexity: A- Slope, B- OPCr. Indexes of curvature and sharpness: C- DNE, D- ARC

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