

**The
Palaeontological
Association**

63rd Annual Meeting

**15th–21st December
2019**

*University of Valencia,
Spain*

**PROGRAMME
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AGM papers**





Soft tissue associations reveal the influence of preservation on biodiversity in Burgess Shale-type fossil deposits

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Exceptionally-preserved fossil biotas of the Cambrian and Ordovician provide crucial data on early animal evolution, allowing for the reconstruction of stem lineages and informing on crown group character acquisition. However, a confounding factor to these phylogenetic analyses is information loss during fossil preservation. We compared the taphonomic signal of three Cambro–Ordovician Lagerstätten by classifying all eumetazoan genera based on presence/absence of different tissue types (biomineralized skeletons, sclerotized and unsclerotized cuticle, external and internal soft cellular tissue). Results show that preservation in the Ordovician Fezouata Shale is significantly different from the Cambrian Burgess Shale and Chengjiang Biota. In the Fezouata Shale, soft cellular structures are most commonly associated with partially mineralized and sclerotized tissues, which may be protecting the soft tissue, and soft, non-cuticularized organisms are unknown. Conversely, the Cambrian sites are remarkably similar, with both commonly preserving entirely soft cellular bodies and a higher diversity of tissue types per genus. This analysis allows for an exploration of the effects of taphonomic bias on phylogenetic analyses, which will be further constrained using decay experiments. Taken together, these approaches provide a coherent framework for reassessing biodiversity in Cambrian Lagerstätten and reanalysing character acquisition during the earliest evolution of animals.

Tracking the origin of an ancient genome duplication in teleost fishes using fossilized bone cell spaces

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Teleost fishes are a key model for genome evolution, because they experienced drastic changes in genome size in the course of their evolutionary history. Most notably, a whole-genome duplication occurred before the origin of modern teleosts, potentially triggering the evolutionary success of this enormous clade. However, exactly when in time and where in the phylogeny this occurred is unknown. Empirical quantitative studies have established a significant statistical relationship between the volume of osteocyte lacunae (spaces left by bone cells) and genome size. Since they fossilize easily, osteocyte lacunae have been used to infer genome size in a variety of fossil vertebrates, including non-avian dinosaurs and lungfishes. We assembled a dataset for teleosts and their close relatives, encompassing taxa with duplicated and non-duplicated genomes, Devonian to extant. Homologous bones have been CT-scanned with synchrotron light to three-dimensionally reconstruct osteocyte lacunae. This accounts for variations in cell shape and orientation, critical parameters not fully addressed by ‘classical’ 2D thin sections. Our results support an early occurrence of