

Introduction

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Explanations of global variation in trilobite richness over the Paleozoic range from active displacement by brachiopod dominated environments to paleocontinental movement and its differing effects on various taxonomic ranks (Harper et al 2015; Westrop and Adrain 2001). I hypothesize that brachiopods and trilobites invaded adjacent geoplates at similar times due to a shared predation pressure. Primarily using the Paleobiology Database, determining covariance of invasion between the two clades will be possible. The objective is to create a method for modeling studies of faunal interaction and analyzing their possible causative factors.

Justification

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In a broad sense, this study will address how the rate of faunal overturn in paleocommunities affects long-term regional biodiversity change. Throughout the literature, studies have postulated many different possible explanations for perceived trilobite diversity fluctuation ranging from transgressive-regressive cycles and tectonics (Balseiro and Waisfeld 2013; Valentine and Moores 1970; Zhiyi *et al.* 2007) to sampling anomalies (Bambach *et al.* 2004; Connolly and Miller 2001; Peters and Heim 2011) and other biotic factors (Wright and Stigall 2013). Additionally, extensive analyses have already been performed on individual trilobite species distributions and stratigraphic ranges. Yet out of all these studies the sustained, the high level of contemporaneous brachiopod radiation has only been tangentially incorporated into the results and most are restricted to one or two well studied species, never having been generalized to the family level.

Predation on brachiopods and trilobites by a shared predator may have created a shared driver for cohabitation of and dispersal to geoplates. Specifically, predation by shell-crushing (durophagous) species helped to drive this relationship (Freeman and Miller 2011; Signor III and Brett 1984). This resultant indirect linking of trilobites and brachiopods via a commonly held predation pressure (i.e. *Anomalocaris* and nautiloids; Nedin 1999) influenced familial abundance change in specific localities throughout the Paleozoic.

Overall, this study will attempt to extend contemporary studies of species dynamics by providing a method for empirically determining the level of faunal interaction between clades. Although this has obvious relevance to fossil record data over millions of years, there is a more modern use for these methods at the species level. With increasing ease of global travel by humans comes a large number of species dispersing to new habitats over large distances, intentionally and unintentionally. While this may naturally occur over longer periods of time, species invasion could have major impacts on human agriculture and biofuel production. Effort must be given to extend research into the immediate threats posed by such organisms when invading potentially novel ecosystems over relatively short time scales. Lastly, this type of analysis could improve studies investigating the role of shared pressures (such as predation) on range alteration.

Research Plan

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All data for manipulation will originate from the Paleobiology Database. Initial data sets will be downloaded for both *Brachiopod* and *Trilobita* ranging from the Cambrian through the Permian. Soft culls and cleaning of the family level data will then be performed and rarefaction curves produced in order to reduce the sampling variability between geoplates. Familial presence and absence data will

then be generated by geoplate for each clade. All of this will be done in R, as can the creation and analysis of vectors. However, visualizing the resultant vector fields would be best accomplished in MATLAB.

Vector creation will be accomplished in four distinct steps. First, by differencing the presence and absence matrices of adjacent epochs, a new set of matrices will be formed (one less than the original number) that represent the changes in family richness between epochs for each geoplate. Next, the difference matrices will be subsetting to only include families that both were extirpated from one geoplate and invaded an adjacent one. This will require tabulating which geoplates were adjacent to one another in the PBDB, as well as comparing the original matrices for each epoch to determine extirpation and invasion. The third step in this process will be to place the vectors along the lines between adjacent geoplates, with the vector heads pointing to the plate being invaded. If there is no familial movement, and merely extirpation or arrival (with no evidence of coming from an adjacent geoplate), then no vector will be placed. If both plates display invasion the vector head will point to the plate with a higher number, and similar to the previous case it will not be placed if the magnitude of invasions is equal between adjacent geoplates. Finally, to determine the magnitude of each vector the R.M.S value of the family richness change for each geoplate will be taken. Effectively, the first three steps constitute direction, and the last constitutes magnitude; the two components of a vector. Combining these into a vector field bounded by paleolatitude and paleolongitude will create a gradient. Doing this for both clades across epochs will allow for the direct comparison between them using multiple regression on direction and position (latitude or longitude) variables, with the outcome variable being magnitude.

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