SEQUENCE STRATIGRAPHY AND BIOTIC CHANGE IN MIDDLE PALEOZOIC MARINE FAUNAS OF THE APPALACHIAN BASIN

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The sequence stratigraphic paradigm and its corollaries provide a predictive framework within which to examine biotic changes and interpret their probable causes. Varied scales of biotic changes have been documented in the 60 million year Silurian-Middle Devonian stratigraphic interval of the Appalachian Basin that may be related to sequence stratigraphy. These include *ecological epiboles* (short-term, widespread proliferation of normally rare species), *outages* (absence of normally common species), longer-term (10s to 100s of Ky.) *community replacement*, and *major bioevents*, involving local extinction immigration and evolution of species. Replacement in Silurian-Devonian marine communities appears to involve lateral, facies-related shifting of broad biofacies belts, or *habitat tracking*. Tracking patterns may be nearly symmetrical in areas of low sediment input near basin centers. However, replacement cycles are commonly markedly asymmetrical reflecting the inequalities of preservation and sedimentary environments developed in similar depth ranges during transgressive vs. highstand (regressive) phases of cycles. The asymmetries involve both apparent and real effects; deletion of portions of facies transitions at sequence boundaries or condensed sections leads to artifactual asymmetries. However, in areas proximal to siliciclastic sources, tracking asymmetries arise from the markedly higher sedimentation rates during regressive (late highstand) than transgressive phases. Replacements may also involve *immigration* of "exotic" species into a sedimentary basin, either as short-lived events (*incursion epiboles)* or as wholesale faunal immigrations. The latter typically follow intervals of extinction/emigration of the indigenous faunas. Both large and small immigration events appear most commonly during highstands (transgressive peaks) which may alter climates, and permit migration pathways for nekton and planktonic larvae.

The Silurian-Devonian interval in the Appalachian Basin is divisible into several blocks of stability or ecological-evolutionary subunits (E-E subunits). Each is characterized by a relatively long interval (2-7 My) during which there is relatively little species level change and biofacies remain intact with little change in species composition or relative abundance. Habitat tracking was the major biotic response to fifth to third order fluctuations in sea level as recorded in parasequences, subsequences, and sequences. Major restructuring events that bound these intervals involve local extinction or emigration of long-lived lineages, *in situ* evolution, and immigration of "exotic" species from other biogeographic regions. Several of these bioevents in the Appalachian Basin correlate with global bioevents (e.g. the Kacak and *Pharciceras* events in the Middle Devonian), indicating widespread environmental changes. Most of the apparent abrupt turnovers can not be simply artifacts of incomplete preservation. Although a few E-E subunit boundaries do correspond to major sequence boundaries, there are many examples of third order sequence boundaries within E-E subunits; i.e. very little biotic change occurs across these unconformities. More significantly, several of the best documented faunal overturns (e.g. *base and top of the Hamilton-Tully fauna) do not occur at sequence bounding unconformities,* but instead are associated with highstands. These bioevents are demonstrably abrupt (e.g. within a single parasequence), even in expanded, conformable sections. Disruption of normal, tracking biofacies may have resulted from climatic changes and/or widespread anoxia developed during major eustatic/tectonic sea level rise. Furthermore, relatively high sea level may have linked otherwise isolated biogeographic provinces with the Appalachian Basin. Once established, new biofacies were rapidly stabilized and a long equilibrium phase ensued until the next major disruption. The situation is obviously complex, but sequence stratigraphy provides a heuristic framework for developing and testing models of macroevolutionary process.