How do new phytoplankton species form in the open ocean?

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Evolutionary genetic processes underpinning speciation process in marine phytoplankton are not well understood. Population size is a key parameter in evolutionary genetics and evolution may work in rather different ways in relatively small populations of terrestrial organisms and astronomically large populations of marine plankton. According to population genetics theory, natural selection works more efficiently in large populations. Thus, adaptation process is expected to be very efficient in large populations, such as found in marine microplankton, and we may expect the classic adaptation-driven Darwinian speciation scenario to play major role in evolution of new species in marine microplankton. However, our evolutionary genetic analysis of genome-wide DNA polymorphism data for five species in coccolithophore genus *Gephyrocapsa* (including *Emiliania huxleyi*) revealed the opposite trend – predominance of speciation driven by extrinsic barriers to gene flow rather than gradual evolution of intrinsic genetic species incompatibilities expected under the Darwinian speciation scenario. The best-fitting scenario for all speciation events analysed includes an extended period of complete genetic isolation followed by recent (last 14 kyr) secondary contact. This model supports the role of geographic or oceanographic barriers in population divergence and speciation. The coincidence of species emergence with glacial inceptions suggests stronger isolation between the ocean basins and increased segregation of low latitude ecological niches during glaciations are important drivers of isolation and speciation in marine phytoplankton. The similarity across multiple speciation events implies the generality of inferred speciation scenario for marine phytoplankton.