

Mammalian Implantation and Subsequent Pregnancy – A Story of MiRNA Evolution and Co-option.

Nkem Nwaobi, Jonathan Fenn, Vladimir Ovchinnikov, James McInerney, Niamh Forde, Mary O'Connell

MiRNAs have long been associated with animal innovation. Specifically, it is known that bursts of miRNA diversity coincide with functional and morphological innovation. Indeed, placental mammals have over 13 miRNA families identified thus far that are unique to this clade. However, we know from gene regulatory network biology that “newer” miRNAs have fewer targets and major transitions such as the shift in reproductive strategy in mammals from oviparity to viviparity are most likely supported by a combination of new miRNAs and older miRNAs. Here we consider the role of “older” miRNAs (i.e., miRNAs that predate the origin of mammals) in the evolution and diversification of mammal reproductive strategies. Using a set of >400 mammal genomes, we have applied machine learning approaches to identify miRNAs and their homologs across all species in our set. From the large presence absence matrix, we extracted all miRNAs that are “older”, we mapped their evolutionary trajectories (e.g., expansions and contractions of miRNA gene families) and using independent methods have identified their targets, pre- and post-mammal origin, to explore shifts in the regulatory network through time and to identify key shifts that coincide with the origin of mammals. The likely impacts of these “older” miRNAs and their target profiles on mammal implantation strategies and subsequent embryonic development are investigated.