A phylogenetically broad analysis of protist genomes unveils the ancestral eukaryotic complexity of the Ras superfamily of GTPases and novel aspects of eukaryotic cell biology

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The highly diversified Ras superfamily of GTPases is one of the central components of the molecular pathways underpinning the basic logistics in the eukaryotic cell. Different eukaryotic groups may differ substantially in the complexity of their complements of Ras superfamily paralogs due to lineage-specific duplications and losses, but it is clear this diversity stems from a certain number of ancestral paralogs that define the core cell biology of a prototypical eukaryotic cell. We have been engaged in a long-term project to reconstruct the evolutionary history of the Ras superfamily in eukaryotes, with a particular aim to define the actual set of paralogs that can be traced to the last eukaryotic common ancestor (LECA). The accumulation of genomic and transcriptomic data from phylogenetically diverse eukaryotes, particularly protists, has now enabled to draw a picture of the LECA's complement of Ras superfamily paralogs with an unprecedented accuracy. The LECA seems to have been endowed with up to around 60 different proteins of the Ras superfamily, which is a number substantially exceeding previous estimates. Whereas some of these ancestral paralogs have ever since remained an essential component of the eukaryotic cell, others have experienced more or less frequent losses. A notable category are paralogs correlated in their distribution with the capability of the organism to build a cilium. It includes not only well established cilium-associated GTPases, but also some paralogs hitherto lacking a clear functional assignment. Our analyses for the first time show wider taxonomic occurrence and apparent ancestral origin of some GTPases so far reported only from metazoans, and unveil novel, functionally uncharacterized ancestral paralogs with a sporadic distribution avoiding standard model organisms. These GTPases presumably indicate the existence of unknown functional pathways in the prototypical eukaryotic cell, making their study one of the priorities of evolutionary cell biology.