Plastid genes across the Great Divide

A thesis presented in partial fulfilment

of the requirements for the degree of

Doctor of Philosophy

in Evolutionary Genetics/Bioinformatics

Institute of Fundamental Sciences

Massey University, Manawatu

New Zealand

Simon J.L. Cox

2014

Abstract

Nearly all life that is visible to the naked eye is arguably a direct consequence of one or both endosymbiotic events that took place early in evolution and eventually resulted in the mitochondrion and the chloroplast. The timing of the mitochondrial endosymbiotic event weighs argument around the nature of LUCA (Last Universal Common Ancestor) being complex or simple and challenge the commonly taught view of bacteria being the first kingdom to emerge from the primordial state.

The ancient metabolic pathways of amino acid and vitamin biosynthesis are examined and Ancestral Sequences constructed in order to discover the endosymbiotic signature within the nucleus of eukaryotes. Cyanobacterial and plant enzymes from these pathways are tracked as they cross from a prokaryotic coding environment to a eukaryotic one. If the eukaryote that took up the chloroplast ancestor was heterotrophic then it probably got some of its co-factors (vitamins) and essential amino acids from its diet. However, in order to become autotrophic it would have to be able to synthesise these amino acids and co-factors directly. The most likely source of these elements would have been the cyanobacterium; therefore cyanobacterial homologs should be found in the nuclear genome of plants.

Ancestral Sequence Reconstruction (ASR) had a negligible effect on uncovering deeper endosymbiotic homologs. However ASR did confirm ancestral convergence between chloroplast and cyanobacterial homologs and between eukaryote nuclear genes and their cyanobacterial counterparts for vitamin and amino acid biosynthetic pathways. The results, all significant, show that the convergence is much stronger between organisms from the same coding environment (prokaryote [chloroplast] versus prokaryote [cyanobacteria]) than from different coding environments (eukaryote [nuclear] versus prokaryote [cyanobacteria]).

Contents

Table of Figures

Tables

Photographs