Abstract

Existing methods for detecting the molecular drivers of convergent evolution suffer from either high false discovery rates or high computational costs. We sought to improve on existing phylogenetic screening methods which are inherently computationally efficient. Our method incorporates specific tests of these alternate mechanisms which could produce the convergent molecular signal solely by chance. We apply our method to a novel study of the evolution of herbivory among fruit flies and repeat an analysis of convergent evolution in marine mammals. Our method eliminated approximately 80% of the convergent genes identified by standard methods indicating a substantial reduction in false discovery rate (point estimate and 95% CI). Our method should significantly improve the pace of scientific discovery in genome studies, including those investigating the etiology of diseases with a genetic component such as cancer.

Tweet

We found a better way to discover the genetic drivers of evolution with applications to disease etiology.