

GENES UNDER SELECTION IN CANCER

Technological advances in the analysis of single cells in tumors have made it possible to follow the evolution of cancer by applying concepts and software used in phylogenetic studies ([Navin et al. Nature 2011](https://www.nature.com/articles/nature09807)¹). However, many studies have been hampered by the usual high copy number heterogeneity of tumor cells. In a paper in Genome Research, [Hsu et al.](https://genome.cshlp.org/content/32/5/916.long)² propose a general analytic and evolutionary framework for the genotype–phenotype relationship. With this approach the authors were able to identify genes that had eluded prior genomic searches for positive selection.

They state: “The result ... is consistent with the ability of calculus to routinely solve otherwise seemingly intractable problems and is also consistent with the view that biology is likely to follow statistical thermodynamic rules for the large-scale behavior of complex systems that eschews details of internal structures and forces.

Indeed, we find that mutations in genes that are under no specific selective force follow a random distribution. In contrast, genes under selection such as those that drive a group of individuals to a specific location of the fitness landscape will be typified by a nonrandom distribution. In principle, this is a general approach to identify the genotype determinants of the phenotype specific to a population”.

1-<https://www.nature.com/articles/nature09807>

2- <https://genome.cshlp.org/content/32/5/916.long>