# Unraveling gene duplication: Expectations of duplicate gene retention under the gene duplicability hypothesis.

**Vazquez Rochel***

Department of Plant Biotechnology and Bioinformatics, Ghent University, Ghent, Belgium

**Received:** *13-Dec-2023, Manuscript No. RNAI-24-126684;* **Editor assigned:** *15-Dec-2023, Pre QC No. RNAI-24-126684 (PQ);* **Reviewed:** *29-Dec-2023, QC No. RNAI-24-126684;* **Revised:** *05-Jan-2024, Manuscript No. RNAI-24-126684 (R);* **Published:** *12-Jan-2024, DOI: 10.35841/2591-7781.19.1000178.*

## Description

The evolution of gene duplications stands as a cornerstone in understanding the diversity and complexity of genomes across various organisms. Gene duplication, the process by which an organism's genome acquires extra copies of existing genes, has been a driving force in the evolution of biological complexity. The Gene Duplicability Hypothesis provides a theoretical framework to explore the fate of duplicated genes over evolutionary timescales. In this essay, we delve into the expectations surrounding duplicate gene retention under the Gene Duplicability Hypothesis, shedding light on the factors that influence the preservation and functional divergence of duplicated genes.

The Gene Duplicability Hypothesis posits that not all genes are equally likely to be retained following duplication events. Instead, it suggests that certain genes, due to their specific functional and structural properties, are more likely to be retained than others. This hypothesis proposes that duplicate genes can be classified into two categories: those that are functionally divergent (non-conserved) and those that are functionally conserved. The fate of duplicated genes is influenced by a complex interplay of factors, including the gene's functional importance, its dosage sensitivity, and the adaptive value of the duplicated function.

### Expectations of duplicate gene retention

Genes that play essential roles in cellular functions and survival are more likely to be retained following duplication. The redundancy provided by the duplicated copy allows for functional robustness, ensuring the organism's viability even if one copy undergoes functional divergence or loss. Dosage sensitivity refers to the organism's reliance on the precise dosage of specific genes for proper functioning. Genes that are dosage-sensitive, meaning their expression levels must be tightly regulated, are more likely to be retained as duplicates. The duplicated copy allows for the fine-tuning of gene dosage, preventing potential dosage-related disruptions.

### Functional divergence

The functional fate of duplicated genes is dynamic and can involve both neofunctionalization and subfunctionalization. Neofunctionalization occurs when one duplicate evolves a novel function, while subfunctionalization involves the partitioning of the original gene's functions between the duplicates. The extent of functional divergence is influenced by the selection pressures acting on the duplicated genes.

The adaptive value of duplicated genes plays a crucial role in their retention. Duplicates that confer a selective advantage, such as improved environmental adaptation or enhanced reproductive success, are more likely to be retained over evolutionary time. Positive selection acts as a driving force for the retention of duplicates with beneficial functions. Various evolutionary constraints, such as the effective population size, mutation rates, and recombination rates, impact the fate of duplicated genes. Small effective population sizes may lead to increased genetic drift, influencing the retention of duplicates. Additionally, recombination rates can affect the likelihood of preserving linked duplicated genes.

### Case studies and empirical evidence

Numerous studies across diverse organisms have provided empirical support for the expectations outlined under the Gene Duplicability Hypothesis. For example, in yeast, where gene duplicates are prevalent, essential genes have been found to be preferentially retained as duplicates, ensuring functional redundancy and robustness. Similarly, in plants, dosage-sensitive genes involved in developmental processes often exhibit a higher retention rate as duplicates. Furthermore, the examination of specific gene families has revealed instances of both neofunctionalization and subfunctionalization. For instance, the globin gene family in vertebrates has undergone multiple duplication events, leading to specialized functions for different globin genes, such as oxygen transport and signal transduction. Understanding the expectations of duplicate gene retention under the Gene Duplicability Hypothesis provides valuable insights into the mechanisms driving genome evolution. This knowledge not only enhances our understanding of the forces shaping genetic diversity but also has practical implications, especially in the context of molecular evolution, biotechnology, and medicine.

The identification and manipulation of duplicate genes with adaptive value hold potential for biotechnological applications. Engineered duplicates with enhanced functions could be utilized in various fields, such as agriculture and industry, to improve stress tolerance, yield, and product output.

Insights into the retention and divergence of duplicate genes can inform our understanding of genetic diseases and susceptibility. Dosage-sensitive genes that are prone to duplications may be implicated in certain disorders, highlighting potential targets for therapeutic interventions. Strategies for genomic engineering and synthetic biology can leverage the principles of duplicate gene retention to design organisms with tailored traits. By understanding the factors

influencing the fate of duplicated genes, researchers can optimize the engineering of genetic pathways for desired outcomes.

In conclusion, the expectations of duplicate gene retention under the Gene Duplicability Hypothesis provide a comprehensive framework for understanding the evolutionary dynamics of duplicated genes. The interplay of factors such as functional importance, dosage sensitivity, functional divergence, adaptive value, and evolutionary constraints collectively shapes the fate of duplicated genes. Empirical evidence from various organisms supports these expectations, offering valuable insights into the forces driving genome evolution.

The implications of this understanding extend beyond evolutionary biology, reaching into diverse fields, from biotechnology to medicine.

## *Correspondence to:

Vazquez Rochel*

Department of Plant Biotechnology and Bioinformatics,

Ghent University,

Ghent, Belgium

Email: Vazquezroch_e@psb.vib-ugent.be