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Plant junk DNA: Useful or trash- A debate

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Abstract

Plant junk DNA was originally used to describe regions of the genome that do not code for proteins and were thought to have no biological function. Early studies revealed that only about 1–2% of the human genome encodes proteins, leaving the remaining 98–99% classified as non-coding DNA. However, advances in molecular genetics, genomics, and epigenetics have demonstrated that many non-coding regions play critical roles in gene regulation, chromosome structure, genome stability, and evolution. Although some DNA sequences may indeed be non-functional remnants of evolutionary processes, a significant proportion of so-called junk DNA is now recognized as biologically important. This review discusses the origin of the junk DNA concept, its major components, evidence supporting both functional and non-functional roles, and current perspectives on whether junk DNA is truly "trash" or an essential part of the genome.

Keywords: Junk DNA, trash, ENCODE, non-coding DNA, Marker-assisted selection

Introduction

Plant junk DNA or non-functional DNA is a DNA sequence that has no known biological function. Most organisms have some junk DNA in their genomes mostly pseudogenes and fragments of transposons and viruses but it is possible that some organisms have substantial amounts of junk DNA (Makalowski, 2003: Palazzo and Gregory, 2014) [10, 14]. Genomics. Not junk after all. Science 300: 1246–1247.). All protein-coding regions are generally considered to be functional elements in genomes. Additionally, non-protein coding regions such as genes for ribosomal RNA and transfer RNA, regulatory sequences, origins of replication, centromeres, telomeres, and scaffold attachment regions are considered as functional elements (Sean, 2012). It is difficult to determine whether other regions of the genome are functional or nonfunctional (Ponting and Hardison 2011) [16]. There is considerable controversy over which criteria should be used to identify function. Many scientists have an evolutionary view of the genome and they prefer criteria based on whether DNA sequences are preserved by natural selection. Other scientists dispute this view or have different interpretations of the data (Fagundes *et al*., 2022) [7]. The concept of junk DNA was introduced in the 1970s by molecular biologist Susumu Ohno, who proposed that much of the genome consists of non-functional sequences accumulated during evolution. Since protein-coding genes occupy only a small fraction of eukaryotic genomes, researchers initially assumed that the remaining DNA lacked biological significance (Havstad and Palazzo, 2022) [8]. With the advent of large-scale genome sequencing projects and functional genomic studies, scientists discovered that many non-coding DNA regions are involved in regulating gene expression, chromatin organization, and cellular processes. Consequently, the traditional view of junk DNA has been challenged.

Why it is Considered as "Junk"

Junk DNA refers to DNA sequences that do not code for proteins and were historically considered non-functional. These sequences include: Repetitive DNA (Satellite DNA, Minisatellites, Microsatellites), transposable Elements (Retrotransposons DNA, transposons, LINEs (Long Interspersed Nuclear Elements) and SINEs (Short Interspersed Nuclear Elements), pseudogenes, introns, intergenic Regions etc (Pennisi, 2012) [15]. it was considered "Junk" because they did not encode proteins mutations in many non-coding regions showed no obvious phenotypic effects, genome size varied enormously among organisms without corresponding increases in complexity (C-value paradox) and many repetitive sequences appeared to arise from selfish genetic elements. Thus, non-coding DNA was viewed as evolutionary baggage (Mattick, 2004; Eddy, 2012) [6, 11]. Junk DNA is useful or trash a comparison of traditional and modern perspective is presented in Table 1.

Table 1: Plant junk DNA: Useful or Trash: A comparison of traditional and modern perspective

Feature	Why It Was Considered "Trash DNA"	Evidence That It Is Useful
Definition	DNA that does not code for proteins and was thought to have no function.	Much of this DNA has important regulatory and structural roles.
Protein coding	Does not produce proteins.	Produces functional non-coding RNAs (miRNA, lncRNA, siRNA,

		snoRNA).
Gene regulation	Believed to be inactive.	Contains promoters, enhancers, silencers, and insulators that regulate gene expression.
Chromosome structure	Considered unnecessary DNA.	Telomeres and centromeres maintain chromosome stability and ensure proper cell division.
Evolution	Viewed as accumulated mutations and repetitive sequences.	Serves as a source of genetic variation and evolution of new genes.
Transposable elements	Thought to be selfish or parasitic DNA.	Influence gene regulation, genome evolution, and adaptation to environmental stress.
Pseudogenes	Regarded as non-functional gene remnants.	Some regulate expression of related genes and act as RNA decoys.
Development	No known role.	Controls developmental processes by regulating when and where genes are expressed.
Disease association	Considered biologically irrelevant.	Mutations in non-coding DNA are linked to cancer, cardiovascular diseases, and neurological disorders.
Current scientific view	Mostly regarded as "junk" until the 1970s–1980s.	Much of the non-coding genome has functional importance, although some repetitive DNA may still have no known function.

Evidence Supporting the Functional Importance of Junk DNA

The sequencing of the human genome has revealed that coding sequences cover only about 1.2% of the euchromatic genome. A big unknown of this is the estimate of non-coding sequences that are functional. A systematic approach to identification of the functional sequences was initiated in 2003 for this reason. Now, an encyclopedia of DNA elements (ENCODE) has been published for the human genome functional roles (Deng and Jiang 2013) [2]. Junk DNA acts as a genetic sensor, regulates gene expression, maintains chromosome structure, and drives evolutionary adaptability (Eddy, 2012) [6]. Key evidence for this functionality comes from several distinct biological mechanisms and large-scale research initiatives:

- **The ENCODE Project:** The Encyclopedia of DNA Elements (ENCODE) initiative found that at least (80%) of the human genome is biochemically active, operating to regulate genes and control when, where, and how proteins are produced (Ohno, 1972; Ecker *et al*, 2012) [5, 13].

- **Sensory Mechanisms:** Recent research reveals that newly discovered non-coding elements (like mechano-response enhancer elements) actively sense environmental changes, helping cells translate mechanical signals directly into changes in gene activity to promote tissue repair (Anonymous, 2012) [1].

Gene Regulation and Structure

Non-coding regions contain vital switches (promoters enhancers, silencers and insulators) that dictate where and when protein-coding genes are activated. These regions also support the functional integrity of centromeres, telomeres and meiotic cell division. Example, the β-globin gene cluster contains regulatory sequences far from the coding region that are essential for proper expression (Doolittle, 2013) [3].

Evolutionary Significance

Comparative genomics studies show that non-coding DNA evolves slowly and maintains genetic integrity and serves as raw material for evolution. Regions once labeled as junk contain unique regulatory sequences like Human Accelerated Regions (HARs) which control brain and nervous system development. Functions include gene duplication, emergence of new genes, evolution of regulatory networks Transposable elements contribute to genetic diversity and adaptation (Dunham *et al*., 2012) [4].

Production of Non-Coding RNAs: Non-coding DNA gives rise to several functional RNAs: MicroRNAs (miRNAs) which regulate gene expression post-transcriptionally. Small Interfering RNAs (siRNAs) participate in gene silencing. Long Non-Coding RNAs (lncRNAs) regulate chromatin structure and transcription. Example, XIST lncRNA is involved in X-chromosome inactivation in mammals.

Epigenetic Regulation: Many non-coding sequences participate in DNA methylation, histone modifications, chromatin remodeling etc. These processes regulate gene activity without altering DNA sequences (Linquist *et al*., 2020) [9].

The ENCODE Project and the Junk DNA Debate

The ENCODE (Encyclopedia of DNA Elements) project reported in 2012 [1] that approximately 80% of the human genome shows biochemical activity. Junk DNA has extensive transcription of non-coding regions, numerous regulatory elements identified and widespread protein-DNA interactions (Ecker *et al*., 2012) [5]. Critics argued that biochemical activity does not necessarily imply biological function. Therefore, the exact proportion of functional DNA remains debated.

Applications of Non-Coding DNA Research

Non-coding DNA research drives innovations in disease diagnostics**,** precision medicine and evolutionary studies. By decoding previously labeled "junk DNA", researchers uncover how regulatory elements, non-coding RNAs, and structural sequences impact cellular health and human uniqueness (Mercer *et al*., 2009) [12]. Key applications of this research include:

Disease Diagnostics and Therapeutics: Mutations in non-coding regulatory regions (like enhancers and promoters) often drive cancers and developmental disorders. Researchers utilize these genetic variants as biomarkers to create targeted therapies that modulate gene expression.

Gene Regulation Insights: Studies into elements such as microRNAs (miRNAs) and long non-coding RNAs (lncRNAs) explain exactly how cells control when, where, and how much protein is produced (Fagundes *et al*., 2022) [7].

Evolutionary and Ancestral Studies: Comparative genomics uses non-coding regions—which mutate more rapidly than coding genes to trace human origins and identify unique regulatory sequences that evolved after the human-chimpanzee divergence (Rinn and Chang, 2012) [17].

Understanding Genome Architecture: Structural non-coding DNA forms telomeres and centromeres, which ensure chromosomal stability. Research here advances anti-aging studies and treatments for age-related chromosomal degradation.

Medicine and Biotechnology

It will also beenused for cancer diagnosis, genetic disease studies and personalized medicine**.** Gene editing and synthetic biology is also a major function of it.

Agricultur

Use of Marker-assisted selection (MAS) for crop improvement for various traits like stress tolerance, disease tolerance and yield.

Conclusion

The traditional concept of junk DNA as useless genomic material has been substantially revised. Research over the past few decades has revealed that many non-coding DNA sequences perform essential functions in gene regulation, chromosome maintenance, epigenetic control, and evolution. However, evidence also indicates that some genomic regions may have little or no biological function and persist as remnants of evolutionary history. Therefore, rather than being entirely "trash," junk DNA represents a diverse collection of genomic elements ranging from highly functional regulatory sequences to potentially neutral evolutionary by-products. Continued advances in genomics and molecular biology will further clarify the roles of these enigmatic regions of the genome.

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