

Exploring Marmosets: Evaluation of Model Animals in Disease Systems and Drug Systems

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Background

In recent years, the common marmoset (*Callithrix jacchus*) has gained significant recognition as a valuable experimental model in the field of disease research. This study explores the marmoset as a model for diseases with human parallels, highlighting its unique characteristics and its relevance in human disease research. Furthermore, we examined the distinct genetic features of the marmoset, identifying genes specifically associated with diseases in this experimental model and evaluating drugs that could target these diseases.

Methods

To assess the common marmoset's suitability as a disease model, we conducted a comprehensive comparative genomic analysis involving humans (*H. sapiens*), common marmosets (*C. jacchus*), crab-eating macaques (*M. fascicularis*), and mice (*M. musculus*). We focused on orthologous genes that play a pivotal role in human disease research and explored the benefits of utilizing marmosets as an experimental model, comparing them to other models.

Results

Our genomic analysis revealed that humans and common marmosets share over 90% of their disease-associated genes, making marmosets excellent models for human disease research. This genetic similarity extends to key pathways in cancer, neurodegenerative disorders, and metabolic syndromes, further solidifying the marmoset's relevance in disease research. Additionally, common

marmosets are expected to show drug responses more similar to humans than mice, due to their similar orthologous genes.

Conclusion

We propose that common marmosets offer a promising avenue for advancing our understanding of human diseases and facilitating the development of innovative treatments. By studying the marmoset, we can gain valuable insights into the genetic and molecular foundations of human diseases, identify novel drug targets, and enhance the efficacy of therapeutic interventions.