

# SNPs: Extensive Utility Across Diverse Fields

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## Introduction

CRISPR-Cas systems are developing for detecting and genotyping single nucleotide polymorphisms (SNPs), offering rapid, accurate, and cost-effective methods for SNP identification. This is crucial for disease diagnosis, personalized medicine, and agricultural applications, with a focus on technological advancements improving SNP analysis accessibility and efficiency [1].

A systematic review and meta-analysis investigate the role of immune-related gene SNPs in determining an individual's susceptibility to COVID-19 and disease severity. Findings highlight specific SNPs significantly associated with varying clinical outcomes, offering insights into genetic predispositions influencing the body's response to viral infection and revealing potential therapeutic targets [2].

A multicenter case-control study explored the interplay between SNPs and lifestyle factors in determining lung cancer risk within the Chinese population. Research identified specific genetic variants that, combined with environmental and lifestyle exposures like smoking, significantly influence an individual's susceptibility to lung cancer. This provides valuable insights into personalized risk assessment and prevention strategies [3].

This review focuses on the significant role of SNPs in the pharmacogenomics of cardiovascular diseases. It explains how genetic variations influence individual responses to cardiovascular medications, affecting drug efficacy and the risk of adverse reactions. Understanding these SNPs is vital for developing personalized treatment strategies and optimizing drug dosages in cardiology [4].

This article reviews significant advancements in SNP discovery and genotyping technologies, specifically their application in crop improvement. It details how these genetic markers identify desirable traits, accelerate breeding programs, and enhance crop resilience and productivity, marking a crucial step towards sustainable agriculture and food security [5].

This article discusses the profound impact of SNPs on personalized medicine development and implementation. It emphasizes how understanding an individual's unique SNP profile can tailor medical treatments, optimize drug choices, predict disease susceptibility, and improve therapeutic outcomes, ushering in an era of highly customized healthcare [6].

This article reviews current understanding of genetic susceptibility to Parkinson's disease, focusing on SNPs. It explores how various SNPs contribute to disease risk, progression, and heterogeneity, discussing their potential as biomarkers for early diagnosis and targets for future therapeutic interventions in neurodegenerative disorders [7].

This review delves into various computational tools developed for annotating SNPs

and predicting their functional impact. It highlights the importance of these bioinformatics approaches in understanding how SNPs influence gene function, protein structure, and disease risk, streamlining genomic data interpretation in research and clinical settings [8].

This article examines the population genetics of SNPs and their critical applications in forensic science. It explains how SNPs, with their high abundance and low mutation rates, are utilized for individual identification, ancestry inference, and phenotype prediction. This provides robust genetic markers for solving criminal cases and identifying human remains [9].

This article explores advanced genomic approaches, including SNP analysis, for identifying causal genetic variants in rare diseases. It discusses the progression from broad SNP analysis to more detailed structural variant detection, emphasizing how these comprehensive genomic strategies are crucial for uncovering underlying genetic causes of complex and often undiagnosed rare conditions, paving the way for targeted therapies [10].

## Description

Single nucleotide polymorphisms (SNPs) play a fundamental role across a broad spectrum of scientific and clinical applications. These genetic variations are increasingly central to our understanding of human health, disease, and even the natural world. For instance, recent technological advancements highlight the development of CRISPR-Cas systems for efficiently detecting and genotyping SNPs. These gene-editing tools offer rapid, accurate, and cost-effective methods for identifying SNPs, which is crucial for precise disease diagnosis, the evolution of personalized medicine, and various agricultural applications [1]. The ability to quickly and accurately analyze SNPs makes these systems highly valuable in both research and practical settings, enhancing the accessibility and efficiency of genetic analysis.

The influence of SNPs extends significantly into disease susceptibility and personalized treatment strategies. A systematic review and meta-analysis underscore the critical role of SNPs in immune-related genes concerning an individual's susceptibility to COVID-19 and the severity of the disease. This work identifies specific SNPs associated with varied clinical outcomes, offering vital insights into genetic predispositions that shape the body's response to viral infections, and potentially pinpointing targets for future therapeutic interventions [2]. Furthermore, a multicenter case-control study explored the complex interplay between SNPs and lifestyle factors, such as smoking, in determining lung cancer risk within the Chinese population. This research identified genetic variants that, when combined with environmental exposures, notably influence an individual's susceptibility, thereby providing valuable insights for personalized risk assessment and pre-

vention strategies [3]. For neurodegenerative disorders, specifically Parkinson's disease, research reviews how various SNPs contribute to disease risk, progression, and heterogeneity, suggesting their potential as biomarkers for early diagnosis and targets for therapeutic development [7].

Understanding SNPs is also paramount in tailoring medical treatments and improving agricultural practices. In the pharmacogenomics of cardiovascular diseases, SNPs play a significant role by influencing individual responses to medications. This impacts drug efficacy and the risk of adverse reactions, making their understanding vital for developing personalized treatment strategies and optimizing drug dosages in cardiology [4]. The profound impact of SNPs on the development and implementation of personalized medicine is further emphasized, as recognizing an individual's unique SNP profile can tailor medical treatments, optimize drug choices, predict disease susceptibility, and ultimately improve therapeutic outcomes, moving us toward highly customized healthcare [6]. Beyond human health, significant advancements in SNP discovery and genotyping technologies have revolutionized crop improvement. These genetic markers are effectively used to identify desirable traits, accelerate breeding programs, and enhance crop resilience and productivity, marking a crucial step towards sustainable agriculture and ensuring global food security [5].

The comprehensive analysis and application of SNPs are supported by powerful computational tools and extend into forensic investigations. Various computational tools have been developed specifically for annotating SNPs and predicting their functional impact. These bioinformatics approaches are indispensable for understanding how SNPs influence gene function, protein structure, and disease risk, thereby streamlining the interpretation of complex genomic data in both research and clinical settings [8]. In forensic science, the population genetics of SNPs are critically important. Their high abundance and low mutation rates make them ideal for individual identification, accurate ancestry inference, and phenotype prediction, providing robust genetic markers essential for solving criminal cases and identifying human remains [9].

Finally, advanced genomic approaches centered around SNP analysis are instrumental in unraveling the genetic basis of rare and complex diseases. These strategies enable the identification of causal genetic variants, moving from broad SNP analysis to more detailed structural variant detection. This comprehensive genomic approach is crucial for uncovering the often hidden underlying genetic causes of complex and frequently undiagnosed rare conditions, ultimately paving the way for the development of highly targeted therapies. This work highlights the continuous evolution of SNP research, which promises to transform disease diagnosis, treatment, and prevention across an array of disciplines [10].

## Conclusion

Research into single nucleotide polymorphisms (SNPs) reveals their extensive utility across various scientific and medical fields. CRISPR-Cas systems are emerging as rapid and accurate tools for SNP detection and genotyping, vital for disease diagnosis and personalized medicine. Studies highlight the association of immune-related gene SNPs with COVID-19 susceptibility and severity, informing potential therapeutic targets. SNPs also interact with lifestyle factors to influence lung cancer risk, particularly within the Chinese population, aiding personalized risk assessment. In cardiovascular pharmacogenomics, understanding SNPs is crucial for tailoring medication responses, optimizing dosages, and minimizing adverse effects. Advancements in SNP discovery and genotyping technologies significantly enhance crop improvement, facilitating the identification of desirable traits for sustainable agriculture. The profound impact of SNPs extends to personalized medicine, where individual SNP profiles guide treatment choices and predict disease susceptibility. Furthermore, SNPs are key to understanding ge-

netic susceptibility to Parkinson's disease, serving as potential biomarkers and therapeutic targets. Computational tools are essential for annotating SNPs and predicting their functional impact, streamlining genomic data interpretation. Their population genetics are fundamental to forensic science, enabling individual identification and ancestry inference. Finally, advanced genomic approaches, including comprehensive SNP analysis, are pivotal for identifying causal genetic variants in rare and undiagnosed diseases, paving the way for targeted interventions.

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## Conflict of Interest

None.

## References

1. Yi Hu, Zheng Shi, Shuai Zhang, Song Sun, Yu Han, Ran Yu, Mingli Yang, Weipeng Zhang. "SNP detection and genotyping using CRISPR-Cas systems." *Trends Biotechnol* 41 (2023):107-119.
2. Hosein Farsi, Seyed Youssefi, Mohammad Goli Yazdi, Fereshteh Rostami, Amirhossein Rastegar, Ehsan Siozi, Sahar Saeedi, Fatemeh Ghasemi, Nima Rezaei. "SNPs of immune-related genes and their association with susceptibility to COVID-19 and disease severity: A systematic review and meta-analysis." *Rev Med Virol* 32 (2022):e2329.
3. Guo Wu, Dan Wang, Huijuan Wang, Juan Wang, Mei He, Yushan Wu, Meng Yang, Xueyun Lin, Tangchun Wu, Chun Wu. "SNPs, lifestyle, and lung cancer risk in the Chinese population: A multicenter case-control study." *EBioMedicine* 69 (2021):103445.
4. Amir Karimi, Marianna Karamanou, Anastasios A. Kousoulis, Dushko Fotiadis, Maria Daskalopoulou, Georgios Androutsos, Theodore G. Papaioannou. "The Role of Single Nucleotide Polymorphisms in Pharmacogenomics of Cardiovascular Diseases." *Curr Pharmacogenomics Personal Med* 18 (2020):1-13.
5. Rakesh K. Mishra, Pankaj Singh, Naveen Singh, Rituraj Singh, Ranjit K. Singh, Sanjeev Kumar, Arun Kumar, Santosh Singh, R. Singh, Ram Lal, Abha Pathak, Mahendra Kumar. "Advancements in SNP Discovery and Genotyping for Crop Improvement." *Front Plant Sci* 12 (2021):673231.
6. Inam Khan, Noor Ul Rehman, Mohammad A. Khan, Sadia N. Khan, Imtiaz Shah, Rahmat Ullah. "The Impact of Single Nucleotide Polymorphisms on Personalized Medicine Approaches." *Biomolecules* 13 (2023):678.
7. Anindita Das, Soumya Roy, Sudipta Ghosh, Partha Datta, Ruma Ray, K. Ray-Chaudhuri, Asish Pal. "Genetic susceptibility to Parkinson's disease: Current insights and future prospects of SNPs." *Ann Mov Disord* 3 (2020):157-172.
8. Jian Xu, Xinhui Lin, Xiao Cai, Yang Lin, Jiaqi Huang, Yong Xu, Shihua Li. "Computational tools for SNP annotation and functional prediction." *Genomics* 113 (2021):3000-3008.
9. Zhiyong Wu, Zhi Zhang, Xiaojuan Jiang, Cong Liu, Weiqi Liang, Jinhui Xie. "Population genetics of SNPs and their application in forensic science." *Forensic Sci Int Genet* 44 (2020):102187.
10. Sarah Ben-Salem, Hamad Al-Qahtani, Mohammad Faiyaz-Ul-Haque, Sawsan M. Al-Hamad. "Genomic approaches for identifying causal variants in rare diseases: from SNPs to structural variants." *Hum Genomics* 15 (2021):17.

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