

Copy Number Variations: A Key Factor in Genetic Variation and Phenotypic Expression

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[DOI:10.5281/TrendsInAgri.14019194](https://doi.org/10.5281/TrendsInAgri.14019194)

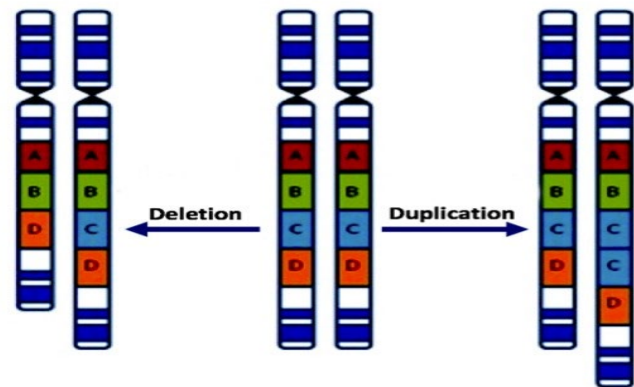
Abstract

Copy number variations (CNVs) are a crucial component of genomic diversity, characterized by the deletion or duplication of DNA segments that influence gene expression and phenotypic variation. These structural variations impact a wide range of biological traits, playing a significant role in disease susceptibility, growth and productivity across species. In livestock and poultry, CNVs have been associated with economically important traits such as disease resistance, reproduction, milk yield, meat quality and feed efficiency, offering new opportunities for improving genetic selection and breeding programs.

Keywords: CNV, Phenotypic variation, Resistance, Genetic selection

Introduction:

CNV is a genomic region that shows quantitative variants when compared to the reference genome and is comprised of deletion and duplication regarding copy number. A CNV is when the number of copies of a particular gene varies from one individual to the next. DNA CNVs are an important component of genetic variation, affecting a greater fraction of genome than single nucleotide polymorphisms (SNPs). CNV represents a copy number change involving a DNA fragment that is ~1 kilobases (kb) or larger (Feuk *et al.* 2006). A form of structural variation, are alterations of the DNA of a genome that results in the cell having an abnormal or, for certain genes, a normal variation in the number of copies of one or more sections of the DNA. For example; the chromosome that normally has section as A-B-C-D might instead have sections A-B-C-C-D or A-B-D (a duplication or deletion of C respectively.)



Most CNVs are stable and heritable, so CNV between individuals is largely a product of genetic heritage or de novo CNVs arise through diverse mechanism at various stage of development.



Mechanism of CNV:

DNA recombination, replication and repair processes are among the several mutational mechanisms that give rise to CNVs. Through the examination of CNV breakpoint junction sequences, mechanisms underlying changes in gene copy number have been thoroughly investigated. Because they are concentrated around breakpoints, repeated sequences both low-copy repeats, like segmental duplications and high-copy repeats, like SINEs, LINEs and endogenous retroviruses are a significant contributor to CNV instability. One of the main processes underlying the creation of recurrent CNVs, non-allelic homologous recombination (NAHR), is triggered by such sequence patterns (Chen *et al.*, 2014).

Recurrent rearrangements occur in several people, have a similar size, and exhibit breakpoint clustering. Non-recurrent rearrangements with dispersed breakpoints, on the other hand, vary in size but may share the lowest overlap region among patients and may be created by a number of distinct mechanisms: i) non-replicative processes, such as microhomology-mediated end joining (MMEJ) and non-homologous end joining (NHEJ); or ii) replicative mechanisms, such as microhomology-mediated break-induced replication, replication slippage, fork stalling, and template flipping (Hastings *et al.*, 2009).

Types of CNV:

Copy number variations (CNVs) are indeed classified based on the length of the repeated sequences, but the distinction between short and long repeats can be somewhat fluid and context-dependent. Here's a breakdown:

1. **Short repeats:** Short repeats are made up of comparatively tiny DNA segments, usually a few base pairs to a few kilobases in size. Microsatellites (short tandem repeats or STRs) and other tiny indels or duplications are a few examples. Short repetitions can be more prone to mistakes during DNA replication, which can result in copy number variation, and they are frequently quite varied between individuals.
2. **Long repeats:** Larger areas, usually tens of kilobases or more, are included in long repeats. Segmental duplications and bigger tandem repeats are two examples. Gene dosage effects and evolutionary adaptations are significantly impacted by long repetitions, which might encompass whole genes or sizable regulatory areas.

Applications of CNV:

Congenital heart disease (CHD) can be explained by a number of processes, including CNVs. Trio analysis, which enables the identification of de novo CNVs in CHD patients, is one of the most widely used techniques in CNV analysis. When use statistical techniques to evaluate the probability of causation of CNVs, comparison with control groups is also beneficial. The fact that monozygotic

twins can have distinct CNVs indicates that up to 12% of the human genome is thought to be susceptible to CNVs, which can happen during both meiosis and mitosis (Bruder *et al.*, 2008).

Copy number variation (CNV), which uses a wide range of mechanisms, including changes in transcript structure and gene dosage, to control organismal plasticity, may be one of the primary contributors to phenotypic diversity and evolutionary adaptation in plants and animals. Characterizing the genomic architecture of CNV in domestic species has advanced significantly in recent years.

Cattle, goats, sheep, pigs, dogs, chickens, ducks, and turkeys have had low-resolution CNV maps created for them, demonstrating that these structural polymorphisms make up a sizable portion of their genomes. CNVs have been linked to a number of morphological (late feathering and pea comb in chickens) and pigmentation (white coat in horses, pigs, and sheep) characteristics. They have also been linked to a variety of diseases and developmental disorders, such as osteopetrosis, anhidrotic ectodermal dysplasia, copper toxicosis, intersexuality, cone degeneration, periodic fever, and dermoid sinus, among others.

The capacity to identify CNVs has been greatly improved by developments in genomic technology. Conventional techniques like single nucleotide polymorphism (SNP) arrays and array-based comparative genomic hybridization (aCGH) have yielded important information about the incidence of CNV in various populations. Whole-genome sequencing (WGS) and paired-end mapping are two more recent techniques that have made it possible to find CNVs in high resolution throughout the whole genome. Through the use of these techniques, a comprehensive list of CNVs in cattle, pigs, poultry and aquaculture species has been discovered, demonstrating their impact on characteristics including feed conversion efficiency, disease resistance and reproductive success.

For instance, CNVs have been linked to characteristics of milk production in dairy cattle, such as lactation efficiency and fat content. CNVs have been connected to body composition and muscle growth in pigs, two characteristics that are essential for meat production. Similar to this, CNVs that affect disease resistance and egg-laying efficiency in chicken have been found, providing possible targets for genetic enhancement. Thus, by incorporating CNV data into genomic selection models, the capacity to identify and analyse CNVs in cattle genomes has created new opportunities for improving genetic gain in breeding programs.

Conclusion:

This article offers a thorough examination of CNV detection methods, from conventional aCGH to state-of-the-art NGS technologies, and how they are used in animal breeding. The potential of CNV-based selection techniques to speed up genetic improvement in livestock will be highlighted, along with the practical implications of CNV research for enhancing economically relevant



characteristics. CNV analysis is expected to become more significant in determining the direction of animal breeding and production in the future as genomic resources keep growing.

References:

- Bruder, C. E., Piotrowski, A., Gijsbers, A. A., Andersson, R., Erickson, S., de Ståhl, T. D., ... & Dumanski, J. P. (2008). Phenotypically concordant and discordant monozygotic twins display different DNA copy-number-variation profiles. *The American Journal of Human Genetics*, 82(3), 763-771.
- Chen, L., Zhou, W., Zhang, L., & Zhang, F. (2014). Genome architecture and its roles in human copy number variation. *Genomics & informatics*, 12(4), 136.
- Feuk, L., Carson, A. R., & Scherer, S. W. (2006). Structural variation in the human genome. *Nature Reviews Genetics*, 7(2), 85-97.
- Hastings, P. J., Lupski, J. R., Rosenberg, S. M., & Ira, G. (2009). Mechanisms of change in gene copy number. *Nature Reviews Genetics*, 10(8), 551-564.