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Popular Article

## Pangenome analysis in domestic animals

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### *Abstract*

Pangenome constitutes of sequences that are unique to every individual along with the sequences common across the population. Recent developments in genomics highlighted that a single genome as reference does not portray the genetic diversity. Pangenome studies can aid in overcoming these limitations. They provide us with the structural variations (SVs) and missing genetic regions. Although this concept has originated with comparative bacterial genome analysis, advancements in next generation and third generation sequencing technologies have paved way for pangenome studies in humans, plants and animals. Till date very few pangenome studies were performed in domestic animals, but further studies in this field can significantly improve our understanding of domestication, migration and adaptability events in domestic animals.

### **Introduction**

Since the inception of sequencing technologies, several bacterial genomes have been generated. This led to the further identification of core genomes and non-essential genomes which laid the foundation of pangenome analysis. Bacterial pangenome studies indicates that the lack of information to completely explain the variation between individuals and there is a need for more genetic information (Tettelin et al., 2005). Due to the limitations in sequencing technologies and complex genomes, pangenome analysis in eukaryotes has begun later than prokaryotes. These studies began in complex organisms like humans began after 2009. Pangenome analysis in plants and animals began much later.

The pangenome is made up of three parts, a core genome present in all the individuals, accessory genome that is present in some individuals, and singletons confined to a single individual



(Figure 1). The genes present in the core genome involve fundamental metabolic processes like that of housekeeping genes and genes conferring drug resistance. Whereas, the accessory genome constantly undergo mutations and gene transfer is done horizontally to acclimatize to the novel niche.

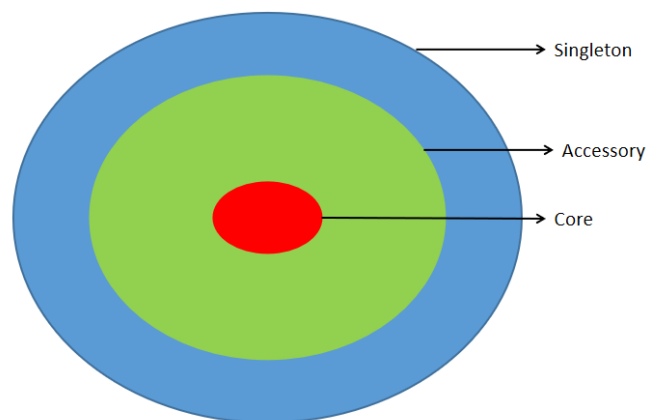


Figure 1: Constitution of a pangenome

There are three main methods to construct an eukaryotic pangenome. The first method is called iterative mapping and assembly. First, next generation sequencing reads are mapped to the reference, and then reads that are not aligned are extracted. These sequences are then used as a supplement to the reference genome and to build the pangenome. The second strategy is known as map-to-pan. To identify the non-reference sequences, *de novo* assembled contigs of each dataset are mapped to the reference. Next approach is based on *de novo* assembly, in which assembly and annotation is carried out first and then a comparative analysis is performed to define nonessential genes.

### Applications of pangenome analysis

- a. Redefining species and sorting based on genomic content
- b. Understanding evolutionary trends and phylogenomic diversity
- c. Microbial pangenomics aids in estimating pathogen transmission patterns
- d. Revealing genomic causes of important scientific issues
- e. Studying livestock adaptability, evolution and breeding
- f. Identification of hidden elements in prokaryote and eukaryote genomes
- g. Genotyping of structural variants
- h. Identification of molecular markers for genotyping studies
- i. Identification of novel functional genes
- j. Conservation and breeding of animal species



## Studies in domestic animals

The total number of research publications on animal pangenome is lower than that of plants, mainly due to population genetic processes and mutational generations. Till date, animal pangenomes focused on comparative genome analysis to reveal variations and selectively expressed genes that are related to phenotypes and evolution (Tian et al., 2020; Crysnanto et al., 2020; Wang et al., 2021).

Pangenome studies in domestic animals have unraveled various genetic variations in different populations. The first species among them was pig, in which a large number of novel genes involved in immune response and adaptability were identified. These studies in the domestic animals can aid in elucidating the hidden processes leading to different phenotypes. Table 1 enlists the salient features of the pangenome studies of domestic animals.

Table 1: Salient features in domestic animal pangenome studies (Gong et al., 2023)

Species	Year	Salient findings
Pig	2017	Variation between Chinese and European pigs
	2019	First pig pangenome; identified regions that are unique to chinese breeds and related to fat deposition
Goat	2019	38.3 Mb sequences missing from the reference identified Drawback of masking the true pan-sequences due to genomes of related goat species
Sheep	2021	SVs related to domestication identified Population stratified SVs effecting phenotypes and production traits identified
Cattle	2020	Showed the need for universal bovine pan-map
	2022	First one to show that pangenome can assist in downstream genomics analysis
Poultry	2020	Showed that hybridization affected the presence or absence variants than genetic drift during the events of domestication
	2022	Identified new regions involved in immune response and disease

## Conclusion

Advancements in the sequencing technologies have created a path for incorporation of pangenome studies for domestic animals. Recent discoveries in the pangenomes showed how SVs can be potential sources to study domestication, adaptation and migration events. Further



accomplishments like hybrid assembly, platinum genomes can expand the depth of pangenome and help in deep analysis. Sequencing costs may decrease in future and with greatly improved computational resources further pangenomes can be constructed and studies across different domestic animals.

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