GRAPH-PANGENOME ANALYSIS IDENTIFIES STRUCTURAL VARIATIONS ASSOCIATED WITH MEAT QUALITY TRAITS IN COMMON CARP

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Introduction

Currently trait dissection and breeding analysis in aquaculture species mainly rely on SNPs generated through aligning sequencing data to a single reference genome. However, it is far from enough to cover all genetic variations of germplasm (especially large structural variations). Pangenomic analysis played a key role in recent years in germplasm identification and breeding of plants and livestock animals, which used graphic genomes to accurately screen trait associated genes and variations.

Methods

We conducted PacBio third-generation sequencing and Illumina library construction for seven carp germplasm tissues, assembled the T2T genome of Longke 12 carp, and built a ten-germplasm graph pan-genome. Structural variations were identified, with PAVs intensively analyzed for their roles in domestication and trait formation.

RESULTS

This study constructed 7 chromosome-level genomes of common carp, then annotations and variation identification were carried out. Combined with the existing genomes of Songpu mirror carp, Heilongjiang carp, and Hebao red carp, a high-precision graphic pan-genome covering 10 species of common carp was constructed.

Table 1. Genome assembly of 7 germplasms of common carp

Germplasm	Genome size (Mbp)	Contig Number	Contig N50 length (Mbp)
mirror carp	1584.90	284	28.56
Huanghe carp	1552.37	228	27.83
Longke 12 carp(YZ)	1605.69	430	23.95
Furui carp	1565.84	228	29.33
Jian carp	1581.97	257	29.21
Longke 11 carp(KB)	1560.95	220	29.65
Yuanjiang carp	1547.67	222	29.82

Totally 40,852 genes were annotated, including core genome of 17,745 genes, dispensable genome of 21,714 genes, and germplasm specific 1,393 genes. Moreover, we identified 7098 PAVs (2738 deletions, 4360 insertions) in KB carp, which were associated with 3286 genes, while 37985 PAVs (16520 deletions, 21465 insertions) were identified in YZ carp, which were associated with 8117 genes. Functional annotation of these genes revealed that the PAV associated genes of KB carp were enriched in immune related pathways such as Th1 and Th2 cell differentiation, JAK-STAT signaling pathway, etc., while the PAV associated genes of YZ carp were enriched in various lipid metabolism related pathways such as steroid biosynthesis and inositol phosphate metabolism.

In summary, this study conducted comparative genomic analysis, annotation of large segment variations, whole genome association analysis, and gene functional identification, identifying functional variations and gene elements related to traits such as disease resistance, intramuscular fat, providing a solid foundation for subsequent breeding of common carp.

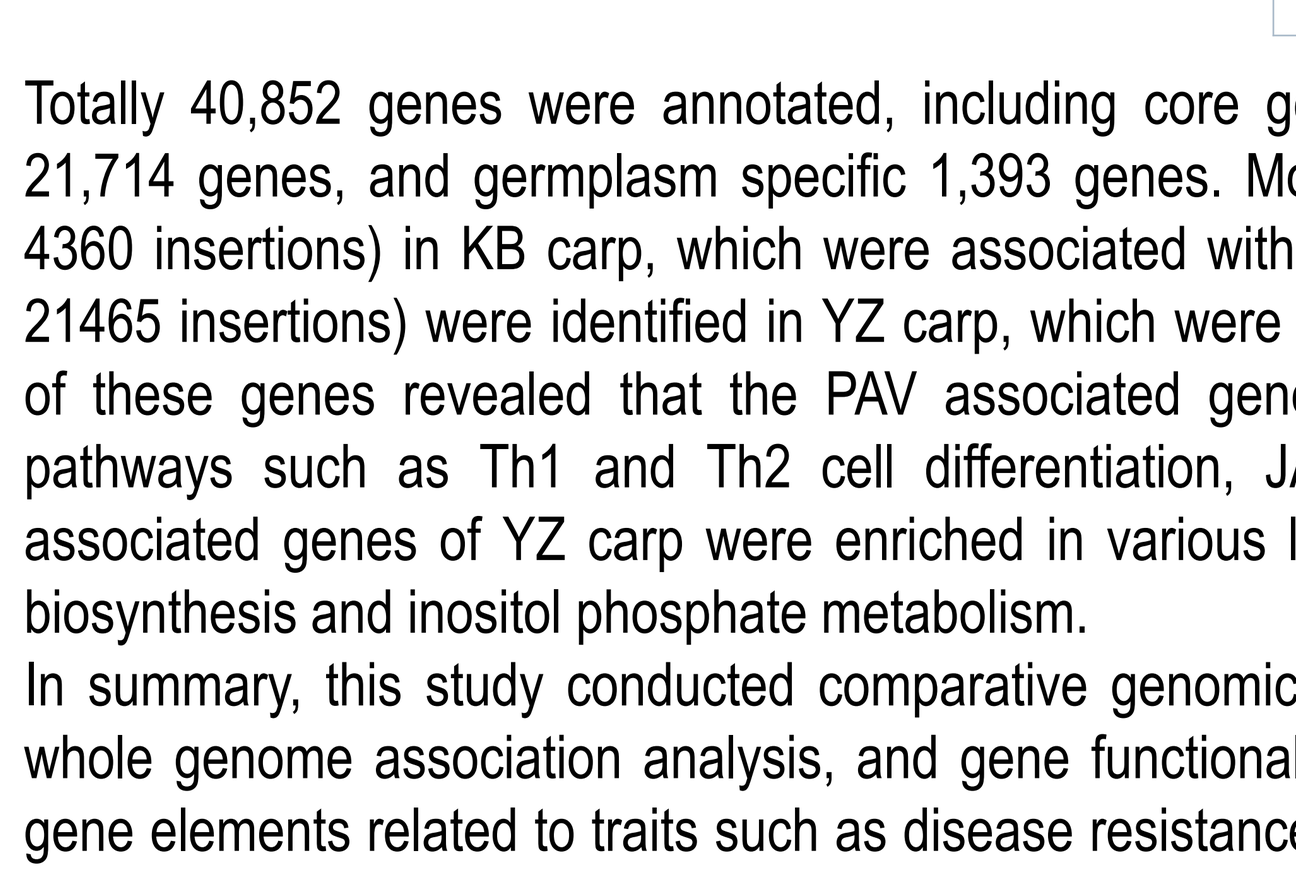


Figure 1. Pangenome covering 10 germplasms of common carp

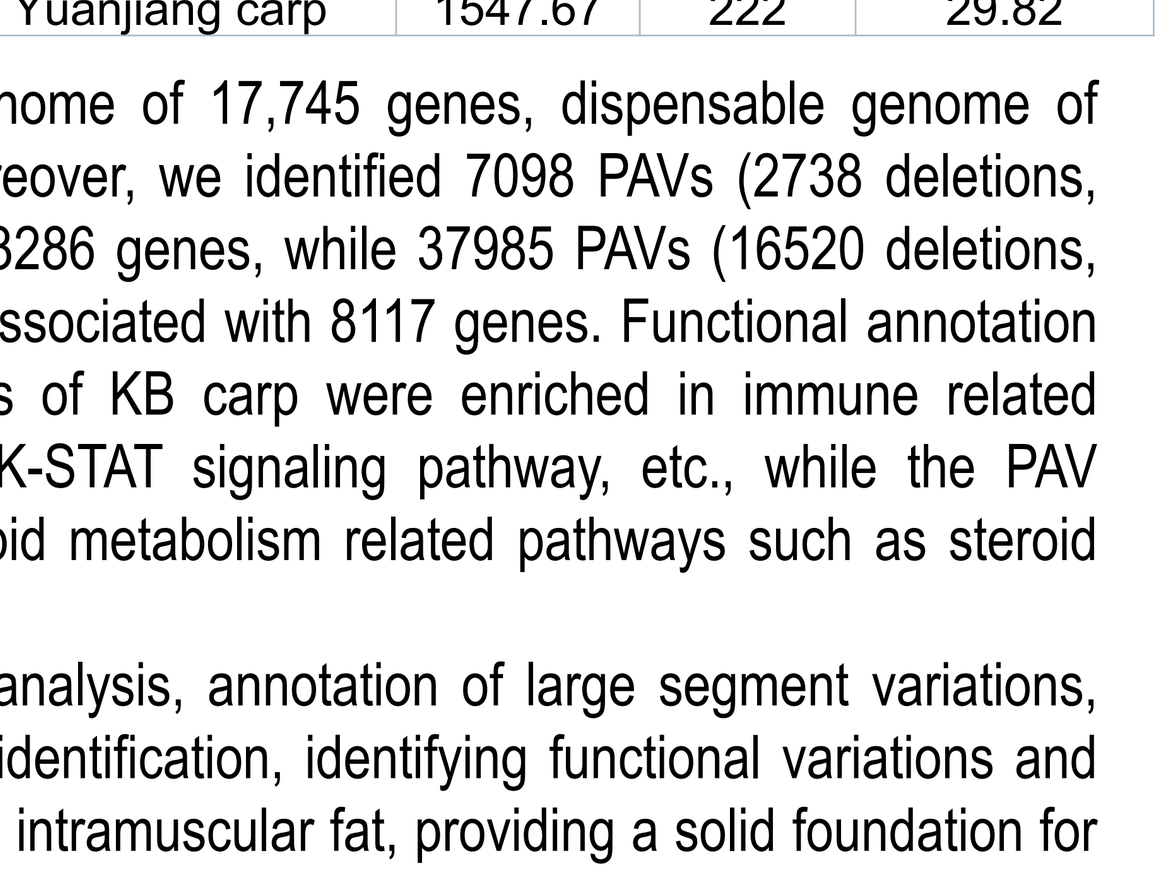


Figure 2. Functional annotation of specific genes and PAVs

Contribution

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