Genomic Analyses Reveal Evidence of Extreme Alkali-saline Environment Adaptation of Amur ide (*Leuciscus waleckii*)

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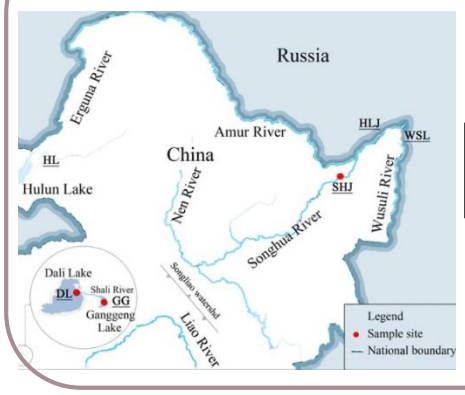
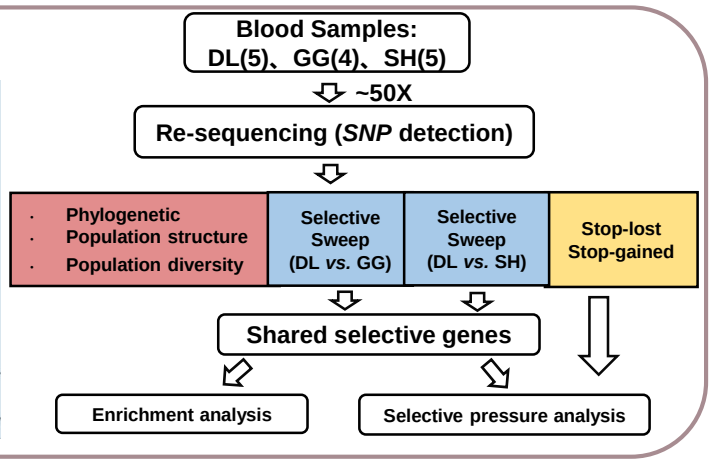
Introduction

- **Amur ide (*Leuciscus waleckii*) is a fish in the Cyprinidae family. Compared with other Amur ide living in freshwater ecosystems, the Amur ide population in Lake Dali Nor is famous for its high tolerance to the alkaline conditions of 54mM (pH 9.6).**

- **Amur ide provides an excellent model for understanding the genetic basis of alkaline adaptation evolutionarily from the genomic level. Here, in order to eliminated spatial background differences interference (geographical isolation, water system, genetic exchange) and focus on contrasting environments alone (alkaline water and freshwater), we re-sequenced genomes of three populations of Amur ide inhabiting different environments to disclose the adaptative mechanism under extreme alkali-saline environments.**

Materials & Methhods





Results

SNP identification & nucleotide diversity

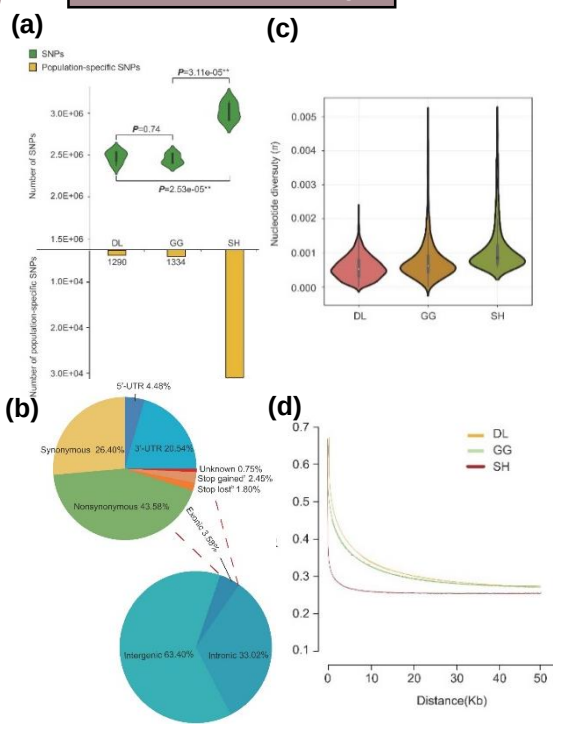


Fig.1 (a) The number of SNPs and populati on-specific SNPs identified in each popula tion. (b) Functional classification of the ca ndidate SNPs. (c) Nucleotide diversity (*π*). (d) LD decay.

Population structure

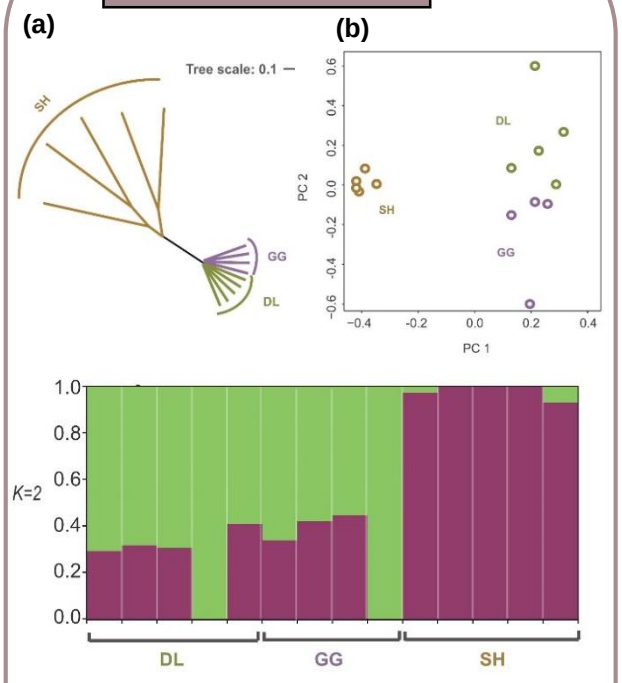


Fig.2 (a) Maximum-likelihood phylogenetic tree. (b) Principal component analysis. (c) Population structure

Selective candidate genes in DL

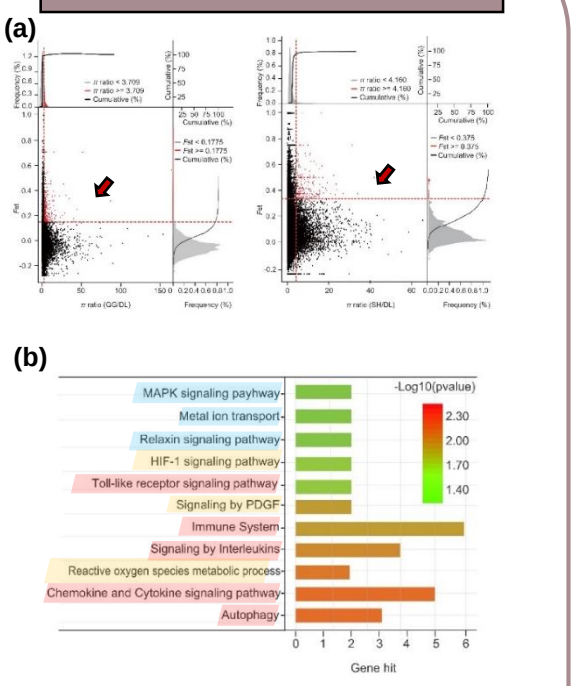


Fig.3 (a) Distribution of the *F*st and *π* ratio values (DL *vs.* GG / DL *vs.* SH). *(b)* KEGG category analysis of positive selected gene (PSGs) in the DL population.

Stop lost & Stop gained analysis

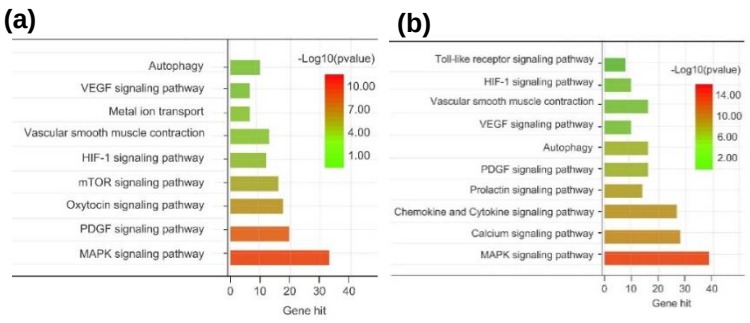


Fig. 4 (a) KEGG category analysis of genes in stop-lost SNPs that are similar to PSGs. (b) KEGG category analysis of genes in stop-gain SNPs that are similar to PSGs

Selective pressure & Protein structure

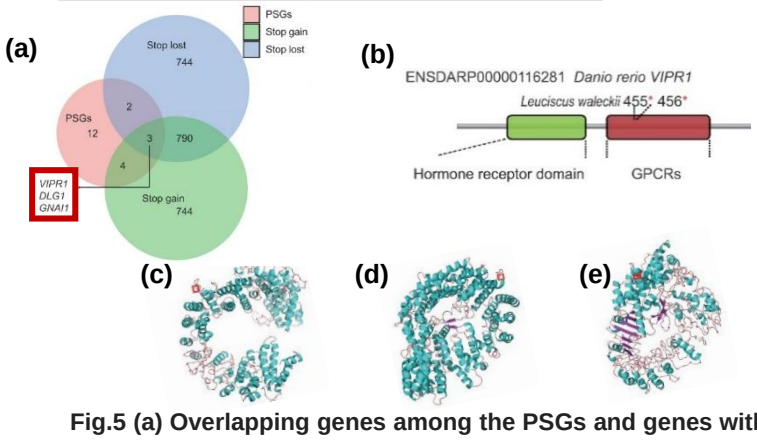


Fig.5 (a) Overlapping genes among the PSGs and genes with stop-lost and stop-gained in DL. (b) Structural analys of the t wo positively selected sites of VIPR1. (c–e) 3D structure for Amur ide VIPR1 in DL (c), GG (d) and SH (e)

Conclusion

- **Positive selected genes with alkaline adaptation involved in osmoregulatory regulation, inflammation and immune responses, and cardiorespiratory development with key roles in the local adaptation of alkaline Amur ides population to alkali environment.**

- ***VIPR1* were identified to experience strong positive selection, which probably play important roles in keeping hydromineral balance through relaxing muscle actions in the digestive tract of alkaline Amur ides population during alkali adaptaion.**