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Breeding of pigs with high meat quality using marker-assisted introgression

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Summary

We detected a QTL affecting the tenderness of meat in a pig F₂ family derived from a cross between Jinhua and Duroc and recognized that an allele from Jinhua increased the tenderness. Applying the technique of marker-assisted introgression for this QTL region, which attempted to introgress an allele of Jinhua at the QTL into the genomic background of Duroc, we produced pigs with high quality and productivity of pork meat.

Background and objective of the study

Jinhua pig is a native breed of small size in China. It produces tender meat with high intramuscular fat content but the productivity is very low. Duroc is a popular commercial breed, which shows higher growth rate and meat productivity, and is utilized as terminal sire for producing market pigs. However, the meat of Duroc, characterized as high lean content, is less tender than that of Jinhua and the meat quality remains to be improved. We established an F₂ experimental family derived from cross between Jinhua sows and a Duroc boar and performed QTL analyses for meat quality traits using this family. As a result of the analysis, we detected a QTL affecting the tenderness of meat. The allele originating from Jinhua increased meat tenderness. Based on the QTL information, we attempted to introgress the QTL allele of Jinhua into the genomic background of Duroc using the technique of marker-assisted introgression to create pigs with increased meat tenderness as well as high meat productivity.

Results

1. We detected a QTL on pig chromosome 2 (SSC2) affecting the shear force value of meat indicating the meat tenderness (Figure 1). The Jinhua allele increased meat tenderness.

2. The breeding scheme used for marker-assisted introgression is shown in Figure 2. F₁ individuals were crossed to a Duroc boar, which is the recipient line, to obtain backcross (BC₁) individuals. BC₁ individuals were selected for the Junhua allele at the target QTL based on the marker information in the region and were crossed to a Duroc boar to generate BC₂ individuals. The cycle of marker selection and backcrossing was repeated to generate BC₃ individuals. Moreover, we obtained BC₃F₂ individuals by intercrossing between selected BC₃ individuals possessing Jinhua allele at the QTL.

3. Except for the target QTL region, the genomic background of BC₃F₂ individuals was shown to be almost the same as that of Duroc pig based on the information of markers located

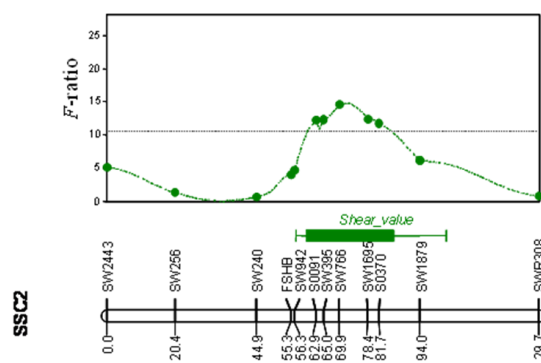


Fig. 1 QTL analysis of shear force value of pork meat on chromosome 2
Dotted horizontal line indicates the threshold value of F-ratio with genome-wide significance level $P=0.05$. The region including the position with the highest F-ratio ranging from SW942 to SW1879 was targeted for introgression.

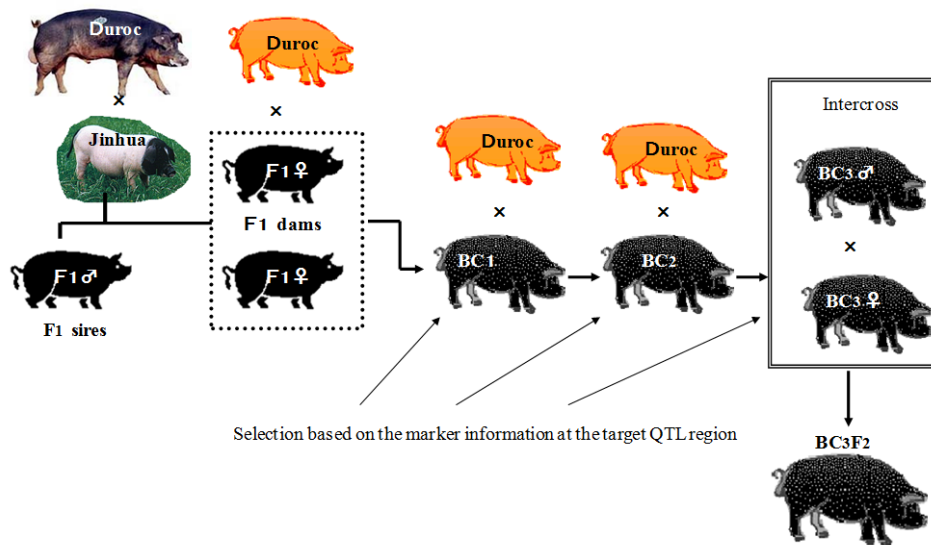


Fig. 2 Breeding scheme for marker-assisted introgression

across the whole genome (data not shown).

4. BC₃F₂ individuals were classified into three types according to the genotype at the target QTL: homozygote with Jinhua allele (JJ); homozygote with Duroc allele (DD); and heterozygote (JD). As shown in Figure 3, the three types were arranged in ascending order of shear force value, as JJ, JD and DD. The meat tenderness was significantly increased for the individuals of JJ type in comparison with the individuals of DD type.

Implication

1. BC₃F₂ individuals of JJ type showed high meat quality as well as high meat productivity, which are characteristics of Jinhua and Duroc, respectively. We plan to use BC₃F₂ males of JJ type as useful terminal sires for producing market pigs.

2. The identification of a gene responsible for the QTL will be attempted in further studies.

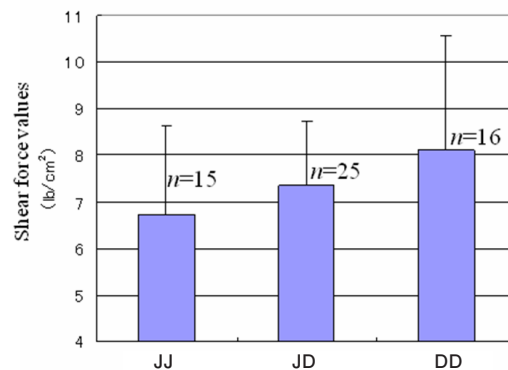


Fig. 3 Means of shear force values in three types of BC₃F₂ individuals
 Three types are denoted by JJ, JD and DD which indicate homozygote with Jinhua allele, heterozygote and homozygote with Duroc allele, respectively.