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Distinguishing between domesticated pig breeds and wild boars using genetic approaches

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Introduction and Objectives

In pig production it is important to maintain purebred domesticated pig breeds and to consider the genetic background when cross breeding especially in developing countries. Recently there have been worldwide serious genetic introgression problems caused by crosses between domesticated pig breeds and wild boars. Therefore, the genetic purify of domesticated pig breeds should be identified accurately, and be managed appropriately. Here, we have developed methods to distinguish between domesticated pig breeds and wild boars based on genetic analysis using microsatellite (MS) polymorphisms and mitocondrial (mt) DNA variants.

Materials and Methods

We examined 176 samples: 30 Landrace sows (LR), 30 F_1 crossbred sows between Landrace and Large White (LW), and 116 wild boars (WB) which may mixed with domesticated pigs on Iriomote island in Japan. DNA was extracted from hair roots or muscular tissues. We analyzed the genetic properties of domesticated pigs and wild boars using a combination of 24 MS markers polymorphisms and mtDNA (part of D-loop region; 596bp) variants to develop phylogenetic trees by the neighbor-joining method.

Results and Discussion

The phylogenetic trees produced from MS and mtDNA analysis show that domesticated pig breeds and wild boars formed two distinct main groups, one composed of domesticated pigs and the other including wild boars (Fig. 1, 2). The domesticated pigs could be divided into Landrace and F_1 crossbred groups indicating that MS is a powerful tool to identify different domesticated pig breeds (Fig. 1). In addition, 4 of the 116 wild boars, with haplotype II, VII and VIII, were included in the domesticated pig breed group (Fig. 2). This result shows that these individuals were crossbreds of domesticated pig breeds and wild boars, suggesting that the use mtDNA variants can detect genetic introgression. Therefore, we conclude that these combined techniques can accurately identify pig breeds and should be able to detect any genetic contamination of purebred domesticated pig breeds.
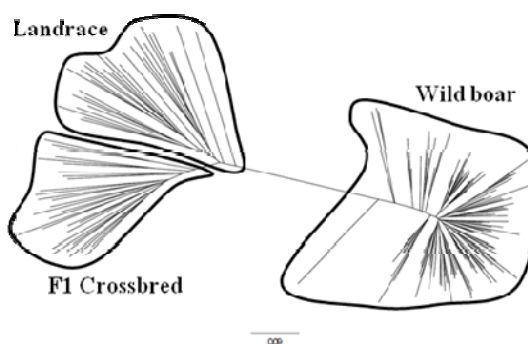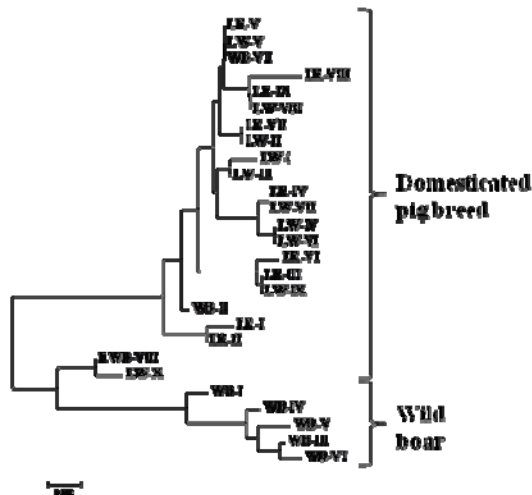

Fig.1 Phylogenetic tree using MS polymorphisms.

Fig.2 Phylogenetic tree using mtDNA variants. The Roman numerals show the haplotype.