



Polymorphism of *SLC11A1* gene in Doom pigs of Asom

BHANITA DEVI¹, S LASKAR², P BORAH³, D J KALITA⁴, G U ZAMAN⁵, A M FERDOCI⁶ and I HUSSAIN⁷

Assam Agricultural University, Khanapara, Guwahati, Asom 781022 India

Received: 27 September 2014; Accepted: 11 November 2014

ABSTRACT

The solute carrier family 11 member 1 (*SLC11A1*) also called as *NRAMP1* gene is found to be associated with the transport of iron and other bivalent cations. To find out polymorphism in *SLC11A1* gene in Doom pigs of Asom, 55 blood samples were collected randomly from Doom pigs and genomic DNA was extracted using the rapid isolation of mammalian DNA method. A fragment of 934 bp length of *SLC11A1* gene was amplified using polymerase chain reaction (PCR) with a pair of specific primers. The amplified PCR products of *SLC11A1* gene was digested with *SmaI* restriction enzyme, which produced 3 fragments (505bp, 231bp and 198bp), 4 fragments (505bp, 429bp, 231bp and 198bp) and 2 fragments (505bp and 429bp) for AA, AB and BB genotypes, respectively. At position 736, A $\leftrightarrow$ G transition was found for AB genotype. The present study revealed that the population of Doom pigs under study was polymorphic in respect of *SLC11A1* gene having 2 alleles with frequencies 0.8364 and 0.1636 for 'A' and 'B', respectively. The genotypic frequencies were 0.71, 0.26 and 0.03 for AA, AB and BB genotypes, respectively.

Key words: Doom pig, PCR-RFLP, Polymorphism, *SmaI* and *SLC11A1*

Pork has a lucrative demand in North Eastern States of India and hence there is a better prospect for expansion of pig farming, which is expected to uplift the economic status of the farmers. The doom variety of pig comprises a very small proportion of the total indigenous pig population in Asom. The animals are black with thick hairs on the neck and shoulder. This variety of pig is available mostly in the eastern region of India, in areas bordering Asom and West Bengal. They are reared in scavenging system and are considered to be quite hardy and resistant to many diseases. They produce the finest bristle that can be utilized for brush industry and so there is a need to conserve this unique germplasm.

The Solute carrier family 11 member A1 (*SLC11A1*) gene, formerly known as natural resistance-associated macrophage protein 1 (*NRAMP1*) was first isolated in mouse as a candidate gene for the Bcg/Ity/Lsh locus that conferred genetic resistance/susceptibility to inbred mouse strains to infections by *Mycobacteria*, *Salmonella* and *Leishmania* (Vidal *et al.* 1993). *NRAMP1* mainly exists in reticulo-endothelial cells and organs, such as outer white blood cells, spleen and lung, can resist several intracellular pathogenic microorganisms (Blackwell 1996, Supek *et al.* 1996). Tuggle *et al.* (1997) reported that the whole sequence

of *NRAMP1* gene in swine encodes 539 amino acids. *NRAMP1* gene in swine is located on q23–26 of chromosome 15 (Sun *et al.* 1998, Xiaoling *et al.* 2014). The *SLC11A1* gene also codes for an iron/divalent cation transporter (Blackwell *et al.* 2003). The sequence length of *NRAMP1* gene in swine is about 15 kb, containing 15 exons and 14 introns as that of human beings and *Mus musculus* (Govoni *et al.* 1995, Marquet *et al.* 2000, Wu *et al.* 2007). The present study was undertaken to identify polymorphism in the genomic sequence of *SLC11A1* gene and to estimate the gene and genotype frequencies in Doom pigs of Asom, India.

MATERIALS AND METHODS

Blood samples from 55 Doom pigs were collected randomly from animals of different districts of Asom, India, viz. Dhubri (Agamani and Golokganj area) and Kamrup (Bamunigaon and Chaygaon area) including animals from Conservation Unit of Doom pig at Livestock Research Station, Mandira, Assam Agricultural University, Kamrup, Assam.

Isolation of genomic DNA: Blood (5 ml) was aseptically collected from the anterior vena cava of the animal in vacutainer tube containing EDTA (2.7%) as anticoagulant. Genomic DNA was isolated from 600 μ l of blood by rapid isolation of mammalian DNA method using standard protocol (Sambrook and Russell 2001).

Gene amplification by polymerase chain reaction: A pair of specific forward (F: 5'- TGAACACTTCATTTAACA GAAGA - 3') and reverse (R: 5'-GCCTCTGAGCA

Present address: ¹, ⁷SRF (drbhanita@gmail.com, mdiftikarhussain@gmail.com), ^{2,3,5}Professor (laskarsubimal@gmail.com, borahp@rediffmail.com, gzaman60@gmail.com), ⁴Associate Professor (djkalita@rediffmail.com), ⁶Assistant Professor (ferdoci_a@rediffmail.com), Department of Animal Biotechnology, College of Veterinary Sciences.

GGGAAGACT-3') primers was used as per Tuggle *et al.* (2005) with slight modification and polymerase chain reaction was performed to amplify the 934 bp fragment of *SLC11A1* gene.

The PCR reactions were carried out in 25 µl reaction mixture containing 1.0 µl DNA template, 0.5 µl each of forward and reverse primers of concentration 20 pmol/µl, PCR master mix 12.5 µl and nuclease free water 10.5 µl. The PCR reaction was carried out in 0.2 ml PCR tubes in a thermal cycler under the following condition: initial denaturation at 94°C for 5 min, followed by 30 cycles of denaturation at 94°C for 30 sec, annealing at 55°C for 60 sec, extension at 72°C for 30 sec with a final extension step at 72°C for 5 min.

Polymorphism detection by PCR-RFLP: The PCR products (8.5 µl) was digested with 1.5 µl of *SmaI* enzyme, 3.5 µl of 10× Tango buffer and 6.5 µl of nuclease-free water. The mixture was incubated at 30°C for 4 h and inactivation was done at 65°C for 20 min in a thermocycler. The digested products were analyzed by 5% polyacrylamide gel electrophoresis (PAGE) and the gel was visualized in a GelDoc system. Identification of genotypes was done according to the restriction fragment patterns and it was confirmed by sequencing.

Sequencing and alignment: The PCR products from different genotypes were sequenced commercially. The nucleotide sequences obtained were confirmed through BLAST analysis. Alignments of the sequences were performed by using software BioEdit. The sequences were submitted to NCBI with Accession no KF31415, KF 934415 and KF 934416.

Genotype and allele frequencies: To find out the restriction site of *SLC11A1* gene, WEB CUTTER 2.0 software was used. The gene and genotype frequencies were calculated by using software POPGENE 1.32 (Yeh *et al.* 1999) and are presented in Table.1.

Table 1. Gene and genotype frequency of *SLC11A1* gene in Doom pig

Gene frequency		Genotype frequency			
		Genotypes	Obs.(O)	Exp.(E)	(O-E) ² /E
Allele A	(0.8364)	(A,A)	(39)	(38.4037)	(0.0093)
Allele B	(0.1636)	(B, A)	(14)	(15.1927)	(0.0936)
		(B,B)	(2)	(1.4037)	(0.2533)

RESULTS AND DISCUSSION

Genotype and allele frequencies: By PCR amplification, a 934 bp amplified product was obtained in all samples from Doom pigs (Fig.1). The PCR-RFLP analysis using *SmaI* on *SLC11A1* gene in Doom pigs yielded (Fig. 2) 3 fragments for AA genotype (505 bp, 231 bp and 198 bp), 4 fragments for AB genotype (505 bp, 429 bp, 231 bp and 198 bp) and 2 fragments for BB genotype (505 bp and 429 bp). A nucleotide transition (A→G) was observed at position 736 bp (Accession no KF31415). Double peak was observed

among the sequences of all the heterozygous Doom pigs having 4 unique fragments (505 bp, 429 bp, 231 bp and 198 bp), while among the homozygous single peaks were observed (Accession no KF 934415) with 3 fragments (505 bp, 231bp and 198 bp) for AA genotype and 2 fragments (505 bp and 429 bp) for BB genotypes (Accession no KF 934416). Comparable findings were also reported by Liu *et al.* (2011) in Chinese indigenous pig, Large white and Landrace pig using restriction enzyme *SmaI*. They found 3 banding patterns; 3 each for GG genotype (506 bp,232 bp and 198 bp), AG genotype (506 bp 430 bp and 232 bp) and 2 banding patterns for AA genotype (505 bp and 430 bp). Tuggle *et al.* (2005) made almost similar observations, who could find 2 banding patterns with 3 fragments (505 bp,232 bp and 198 bp) and 2 fragments (505 bp and 430 bp) with 2 alleles in intron 1 due to *SmaI* digestion in Chinese pig. However, Sun *et al.* (1998) using the restriction enzyme *HinfI* identified polymorphism in respect of *SLC11A1* gene with 3 alleles.

The frequency of AA, AB and BB genotype was 0.71, 0.26 and 0.03, receptively, in the population studied. Similarly, the allele frequency of A and B was 0.836 and 0.163, respectively. Liu *et al.* (2011) found that allele G is dominant in Large white, Landrace and Songalio black pig and allele A has lower frequencies and AA genotype is not detected in large white and Songalio black pig upon digestion with *SmaI*.

The animals showed 3 genotypes AA, AB and BB in

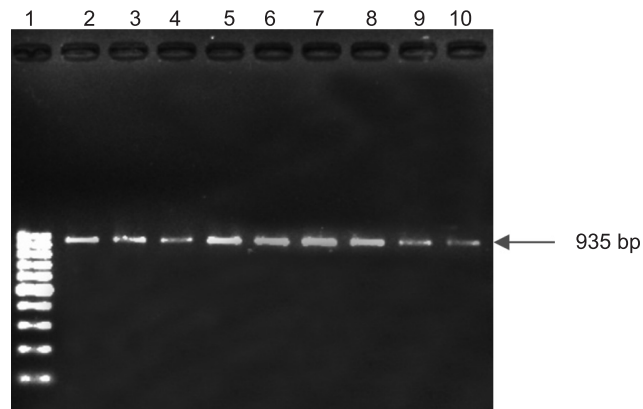


Fig. 1. Lane 1: 100 bp DNA Ladder; Lane 2–10: PCR Amplicons of *SLC11A1* gene.

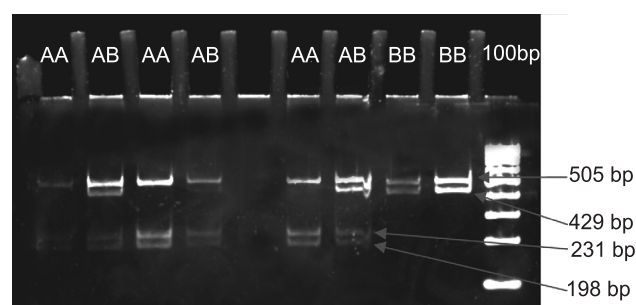


Fig. 2. PCR-RFLP OF *SLC11A1* gene in Doom Pig, DNA Ladder: 100 bp.

respect of the *SLC11A1* gene. The gene frequencies were estimated to be 0.8364 and 0.1636 respectively for A and B. The genotype frequencies for AA, AB and BB were estimated to be 0.71, 0.26 and 0.03 respectively.

In conclusion, the population of Doom pigs under study was polymorphic in respect of the *SLC11A1* gene, having 2 alleles with frequencies 0.8364 and 0.1636, respectively.

ACKNOWLEDGEMENT

The authors wish to place on record their sincere gratitude to the State Biotech Hub (Asom), College of Veterinary Science, Khanapara, Asom, India, funded by the Department of Biotechnology, Government of India and Core Lab, (NBAGR) Department of Animal Genetics and Breeding, College of Veterinary Science, Khanapara, Asom, India, for providing the facilities for the study. Authors are thankful to the Conservation Unit of Doom Pigs in Asom under the project 'Conservation of threatened species' for providing the samples used in this study.

REFERENCES

- Blackwell J M. 1996. Structure and function of the natural resistance- associated macrophage protein (*NRAMP1*), a candidate protein for infectious and autoimmune disease susceptibility. *Molecular Medicine Today* **2**: 205–11.
- Blackwell J M, Searle S, Mohamed H and White J K. 2003. Divalent cation transport and susceptibility to infectious and autoimmune disease: continuation of the Ity/Lsh/Bcg/*NRAMP1/SLC11A1* gene story. *Immunology Letters* **85**: 197–203.
- Govoni G, Vidal S, Cellier M, Lepage P, Malo D and Gros P. 1995. Genomic structure, promoter sequence and induction of expression of the mouse *NRAMP1* gene in macrophage. *Genomics* **27**: 9–19.
- Liu Y, Qiu X, Xu J, Hu Fang, Y Li, Li H, Gong Y and Zhang Q. 2011. Association Analysis between the Polymorphism of the *SLC11A1* gene and Immune Response Traits in Pigs. *Asian Journal of Animal and Veterinary Sciences* **6**: 580–86.
- Marquet S, Lepage P, Hudson T J, Musser J M and Schurr E. 2000. Complete nucleotide sequence and genomic structure of the human *NRAMP1* gene region on chromosome region 2q35. *Mammalian Genome* **11**: 755–62.
- Sambrook J and Russell D 2001. *Molecular cloning: A Laboratory Manual*, Third edition, 2: Cold Spring Harbor Laboratory New York.
- Sun H S, Wang L, Rothschild M F and Tuggle C K, 1998. Mapping of the natural resistance-associated macrophage protein 1 (*NRAMP1*) gene to pig chromosome 15. *Animal Genetics* **29**: 138–40.
- Supek F, Supekova L, Nelson H and Nelson N. 1996. A yeast manganese transporter related to the macrophage protein involved in conferring resistance to mycobacteria. *Proceedings of National Academics of Sciences* **93**: 5105–10.
- Tuggle C K, Schmitz, C B and Gingerich-Feil D. 1997. Rapid communication: Cloning of a pig full-length natural resistance associated macrophage protein (*NRAMP1*) cDNA. *Journal of Animal Science* **75**: 277.
- Tuggle C K, Marklund L, Stabel T J, Mellencamp M A and Stumbaugh A. 2005. Genetic markers for screening animals for improved disease resistance (*NRAMP*). United States Patent, 6844159B2. <http://ddr.nal.usda.gov/handle/10113/6983>.
- Vidal S M, Malo D, Vogan K, Skamene E and Gros P. 1993. Natural resistance to infection with intracellular parasites: isolation of a candidate for Bcg. *Cell*. **73**: 469–48.
- Wu Z F, Luo W H, Yang G F and Zhang X Q. 2007. Genomic organization and polymorphisms detected by denaturing high-performance liquid chromatography of porcine *SLC11A1* gene. *DNA Sequence* **18**: 327–33.
- Xiaoling D, Xiaodong Z, Yong Y, Yueyun D, Weiwei X, Yun M, Weihua Z and Zongjun Y. 2014. Polymorphism, expression of natural resistance-associated macrophage protein 1 encoding gene (*NRAMP1*) and its association with immune traits in pigs. *Asian-Australasian Journal of Animal Science* **27**: 1189–95.
- Yeh F C, Yang R C, Boyle T B J, Ye Z H and Malo J X. 1999. POPGENE version 1.32, the user friendly shareware for population genetic analysis. Molecular Biology and Biotechnology Centre, <http://www.ualberta.ca/Fyeh/>.