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## Kinship coefficient of Landlly pigs using porcine 60K SNP Beadchip and pedigree data

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### Abstract

Many genetic analysis require knowledge of biological relatedness between samples. In large-scale genetic association studies, the estimated kinship is used to remove cryptic relatedness, control for family structure and estimate heritability for trait of interest. However, estimation of kinship is challenging using conventional methods, such as pedigree and polymorphic microsatellites data. In the present study, Porcine SNP60K genotype and pedigree data were used to explore kinship analysis of Landlly pigs. Genomic kinship analysis of 69 Landlly pigs was done using a IBD-based coefficient and by setting of different levels of minor allele frequency and linkage disequilibrium. For pedigree based analysis a total 2462 Landlly pigs data has been utilized. Pearson's correlation coefficient was calculated between estimates of pedigree and genotyping kinship coefficients. In this study, the mean genotypic and pedigree kinship coefficient were  $0.061 \pm 0.01$  and  $0.055 \pm 0.008$ , respectively. Moderate correlation (0.362) was observed between pedigree and genomic kinship coefficient. This investigation provided an inference that genomic kinship coefficient might be used in place of pedigree-based kinship method effectively in Landlly population.

**Keywords:** kinship coefficient, Landlly pigs, porcine SNP60K Beadchip, pedigree

### 1. Introduction

Quantitative genetic revolve around studies of heritable traits. Therefore complete pedigree information is required for family-based studies. Kinship coefficient is defined as the probability that two homologous alleles drawn from each of two individuals are identical by descent (Falconer and Mackay, 1996) [3]. It is a classic measurement of relatedness and also called as coefficient of consanguinity. The kinship coefficient can be used to verify relationships, reconstruct pedigrees, detect pedigree errors and to identify unknown relationships among family members. Additive genetic relationship matrix (A matrix) calculated through pairwise relatedness based on pedigree is the key element of best linear unbiased prediction (BLUP) which is used for breeding value estimation (Henderson, 1975) [6]. In the last decade, genome wide association studies (GWAS) has incorporated genomic relationship matrix (G matrix) to model phenotype covariance through mixed models to estimate heritability for quantitative traits (Hong *et al.*, 2021) [7]. The genetic relatedness of samples helps to produce a more accurate estimate of each individual's haplotypes and also enhances the accuracy of imputation (Grossi *et al.*, 2018) [4].

Several studies have reported that kinship coefficient can be estimated from pedigree as well as highly polymorphic microsatellites (STR) markers data (Cotterman, 1940; Malecot, 1948; Harlizius *et al.*, 2011) [2, 8, 5]. By contrast, at least 15 variable STR genotypes are essential for estimating kinship coefficients in population-based studies. Moreover, in many situations, pedigree information may not be available or incomplete in animal breeding data. In order to derive the relationship matrix based on the pedigree, it is assumed that two full sibs from unrelated parents, have a kinship coefficient equal to 0.5. This means that they have 50% of all loci identical by descendent (IBD). However, this is not always true. Full sibs can share zero (kinship = 0), one (kinship = 0.25) or two (kinship = 0.50) IBD alleles due to Mendelian sampling.

The high-throughput genotyping presents opportunities for kinship coefficient estimation using millions of SNPs. In the recent years, SNP has become the alternative marker for kinship analysis using pedigree-free methods. For a more accurate estimation of pairwise kinship, SNP information is used to trace back all the relationships between the animals from a given population and the individual inbreeding coefficient is based on similarity of alleles without

using pedigree information.

Livestock rearing plays a significant role in ensuring the livelihood security of the human population all over the world. Pig farming is one of the main enterprises contributing to nutritional security with huge importance in developing nations. Courtesy of a high reproductive life and short gestation interval, pig rearing has recently received a boost in the north and north eastern parts of India. However, pig production suffers due to inadequate and/or inefficient selection and breeding strategies being applied most of the time. Pigs are mainly concentrated in North and North Eastern part of India. Total pig population in the country was 9.06 million as per Basic Animal Husbandry Statistics (2020) [1], which decreased by 12% over the previous census. Pigs constitute 1.7% of the total livestock population. Distribution of pig population across the country is not uniform. Among the Indian states, Assam has the maximum pigs (23.1%) followed by Jharkhand (14.1%), Meghalaya (7.8%), West Bengal (5.96%), Chhattisgarh (5.92%) and Uttar Pradesh (4.52%). Pork is rich in vitamins like riboflavin, niacin and thiamine and is highly preferred globally. The total meat production in the country is 8.6 MT wherein pig contributes to 4.82% (Basic Animal Husbandry Statistics, 2020) [1]. PorcineSNP60 BeadChip is being used worldwide to enable early and accurate genomic evaluation of pigs. However, research investigations on assessment of genomic kinship coefficient using porcine SNP data are very scanty in Indian crossbred pigs. In the present study, we evaluated the kinship analysis based on SNP genotyping data with identical-by-descent (IBD) related indices as well as based on pedigree information in Landlly pigs. This genomic information is expected to provide an insight towards effectiveness of genomic selection in crossbred pigs.

## 2. Materials and Methods

The present study was conducted on Landlly (75% Landrace & 25% Ghurrah) crossbred pigs at Swine Production Farm, Livestock Production and Management Section, ICAR–Indian Veterinary Research Institute (IVRI), Izatnagar, Uttar Pradesh, India; a unit of ICAR–All India Coordinated Research Project (AICRP) on Pigs.

To study the performance of exotic breeds of pigs under different agroclimatic conditions, AICRP on pigs was started in 1970. The ICAR–IVRI centre came into existence in 1971. This centre is situated at an altitude of 564 ft above mean sea level, 28 °N latitude, and 79 °E longitude. The climate of this place touches both extremes and relative humidity ranges between 45% and 85%. On the basis of temperature and relative humidity over the last 5 years, season was classified into 3 groups. Season 1 (November–February) had low temperature (12–18 °C) and high humidity (0.83–0.96), season 2 (March–June) had high temperature (23–30 °C) and low humidity (0.45–0.83), and season 3 (July–October) had high temperature (25–30 °C) and high humidity (0.85–0.89). The Landlly pig has been developed at ICAR-IVRI as a variety and can be reared in all types of breeding conditions with low cost feed resources. This variety has acceptable performance in North India. This farm follows a controlled mating system and most of the information is being recorded for individual and pedigree. Breeding of pigs starts at 7–8 months of age. The pigs were reared under similar feeding and breeding conditions. The pregnant animals were given a dry concentrate mixture (16% crude protein and 3200 Kcal) for proper growth of the fetus as well as for their own body

requirements. At birth, piglets were ear-tagged and information concerning their dam, birth date, and sex were registered. Piglets were injected 1mL iron dextran on the 4th and 14th days after birth. Creep ration rich in protein (protein 21%, lysine 0.89%, and ME 3.36 Mcal/kg) was started from 3rd week onwards and was continued up to weaning age (6 weeks of age). The piglets of each farrowing were maintained in separate pen (Pakka system) with their respective lactating sows'. Sufficient space was provided to each individual according to age. Weaning of piglets was done at 6 weeks of age. Weaned piglets were given ad-lib concentrate thereafter. The ration consisted of 20% protein, 0.78% lysine, and 3.17 Mcal/kg ME. Weaned piglets were housed in a group of 10 up to the age of 8 weeks.

Blood samples were collected from 69 Landlly pigs under aseptic conditions. The samples were genotyped using medium density PorcineSNP60 BeadChip platform (Illumina). SNP quality control was performed using PLINK v1.90 software (Purcell *et al.*, 2007) [9].

The pairwise kinship was estimated by using --genome flag in PLINK software (Purcell *et al.*, 2007). Furthermore, different minor allele frequency (MAF) value and linkage disequilibrium values were fixed to generate a pruned subset of SNP. In order to check the effect of MAF and LD, kinship coefficient was estimated for each data set. Pedigree-based kinship coefficient was estimated using the 'optiSel' R-package (Wellmann, 2018) within the R-version 4.0.4 (R Core Team 2021). For pedigree based analysis a total 2462 Landlly pigs data has been utilized. Pearson's correlation coefficient was calculated between estimates of pedigree and genotyping kinship coefficients.

## 3. Results and Discussion

The mean genotypic kinship coefficient was  $0.061 \pm 0.01$  (Table 1). Genotypic kinship coefficient ranged between 0 and 0.72. Out of all combinations, animal 5 has the showed highest genotypic kinship coefficient (0.72) with animal 6. Table 1 represents the descriptive statistics of genotypic kinship coefficient. Two LD levels (0.2 and 0.5) and three MAF (0.05, 0.1 and 0.2) were set to analyse the effect of MAF and LD on kinship analysis. At a constant LD value, the kinship coefficient was affected to a lower degree by changing MAF. Kinship coefficient remained same for MAF 0.05 and 0.1 for a constant LD level. However, it decreased slightly for a MAF 0.2. The value of genotypic kinship coefficient ranged from 0.06 to 0.063 for LD 0.2 and from 0.058 to 0.061 for LD 0.5. In the present investigation, genotypic kinship coefficient was in similar range irrespective of LD level. In this study, the average pedigree kinship coefficient was  $0.055 \pm 0.008$ . Although 2462 animals were used to determine the pedigree kinship coefficient, only 69 animals (genotyped) were utilised to calculate the average. Pedigree kinship coefficient ranged between 0 and 0.562.

A level of 0.5 was set to figure out the pair of Landlly pigs which has high kinship level. In the present investigation, out of 2346 combination, 20 pairs showed genomic inbreeding coefficient more than 0.5. The combinations were animal 5 and 6 (0.713), animal 20 and 21 (0.603), animal 66 and 67 (0.602), animal 66 and 65 (0.589), animal 52 and 53 (0.586), animal 63 and 61 (0.581), animal 26 and 27 (0.571), animal 67 and 65 (0.558), animal 48 and 53 (0.557), animal 55 and 54 (0.557), animal 4 and 6 (0.551), animal 49 and 50 (0.546), animal 14 and 15 (0.544), animal 56 and 57 (0.543), animal 44 and 45 (0.539), animal 62 and 61 (0.537), animal 47 and

51 (0.529), animal 50 and 51 (0.527), animal 59 and 58 (0.519) and animal 30 and 32 (0.513). The pedigree kinship coefficient for the above combinations were 0.5, 0.51, 0.27, 0.04, 0.27, 0.01, 0.5, 0.05, 0.05, 0.05, 0.25, 0.27, 0.52, 0.15, 0.09, 0.5, 0.27, 0.51, 0.26 and 0.31, respectively. Moderate correlation (0.362) was observed between pedigree and genomic kinship coefficient. The lower kinship coefficient in the present study is attributed to admixed inheritance of Landrace and Ghurrah breeds in Landlly pigs. This study also concluded that genomic kinship coefficient in Landlly population might be used in place of pedigree-based kinship method effectively.

**Table 1:** Descriptive statistics of kinship coefficient with variable parameters of  $r^2$  and MAF in Landlly pig population

LD	MAF	Kinship Coefficient
LD>0.2	MAF>0.05	0.063±0.01
LD>0.2	MAF>0.1	0.063±0.01
LD>0.2	MAF>0.2	0.060±0.01
LD>0.5	MAF>0.05	0.061±0.01
LD>0.5	MAF>0.1	0.061±0.01
LD>0.5	MAF>0.2	0.058±0.01

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