



E-ISSN: 2320-7078

P-ISSN: 2349-6800

[www.entomoljournal.com](http://www.entomoljournal.com)

JEZS 2020; 8(6): 880-885

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Received: 11-09-2020

Accepted: 20-10-2020

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## Comparative evaluation of economic traits/reproductive traits in Jharsuk Pigs and their parents

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### Abstract

The population of the crossbred pigs have increased from 14% in 1992 to 23.86% in 2012. Being one of the cheapest meat source in India, swine production is a choicest profession now at Pan-India level. Increase in population coupled with limited resources have augmented the need towards crossbreeding programmes in India to reduce the gap between demand and supply of protein source. Jharsuk (T&D) breed is well known for its good performance and adaptability due to 50% inheritance each of Tamworth and Desi respectively. Current study deals with (i) the effect of genetic groups on different growth traits like body weight at 0, 7, 14, 28, 42, 56 days and body weight gain between different ages and (iii) effect of Genetic groups, TLR 6 gene polymorphism and piglet titre on litter size at birth and litter size at weaning. Significant effect of genetic groups on Body weight at 42 days, 56 days, body weight gain between 42-56 days was observed. For TLR 6 gene polymorphism a total of nine sets of forward and reverse primers were taken for amplification of DNA samples for TLR6 gene loci. All eight primers produced amplified product except the fourth primer (TLR6-4). PCR products were subjected to polyacrylamide gel electrophoresis for the detection of single strand conformational polymorphism (SSCP). Different numbers of haplotypes, obtained with the eight primers were analyzed with the Spab software to see the association of these variants with important economic traits under study. Genetic group (Breeds) had significant effect on litter size at birth while, piglet titre (HA titre) had non-significant effect on litter size at birth and weaning. In many cases Jharsuk Variety (T&D) was found to be superior to or at par with its exotic F<sub>0</sub> breed i.e. the Tamworth breed. Current findings suggest the usefulness of Jharsuk and its superiority over Tamworth and Desi as a very profitable breed in Jharkhand and it could be further continued with increased sample size for each of the three experimental breeds taken. The research is important more so because it deals with threshold characters, which is very complex subject in itself and need to be studied more to know detail on its inheritance.

**Keywords:** Jharsuk (T&D), weaning, litter size, litter weight, heterosis, threshold characters, fecundity, MAS, haplotypes, SSCP

### Introduction

Distribution of Pig population across the country is not uniform. For instance thick population of pigs is recorded in eastern (2.8 million) and north eastern (4.5 Million) states, highest population is in Asom (2 Million), followed by Uttar pradesh (1.35 million), West Bengal (0.82 million), Jharkhand (0.73 million) and Nagaland (0.70 Millions) [[www.daahd.nic.in](http://www.daahd.nic.in)> NAP on pig]. Swine Production is an important profession in eastern and north eastern region of India. As per the Livestock Census 2012, the total pig population in India is 10.3 million, of which 76% is the indigenous breed. The population of exotic breeds has increased by 12.7% from 2003 to 2012. Eastern and North Eastern regions of India comprise of 63% of India's pig population. Jharkhand is the third leading state with a population of 0.96 million (nearly 10% of the India's total pig population) followed by Assam and Uttar Pradesh. As per NSSO 70th Round, at all India level, for every 1000 households, 18 households reported the ownership of pigs with average number of pigs owned to be 54.9 per 1000 households. Jharkhand demonstrates much higher density of pigs with respective figures at 64 and 202.9<sup>[12]</sup>. Naturally endemic infectious diseases provide selective pressures for pig populations and Toll-like receptors (TLRs) represent the first line of immune defense against pathogens and are likely to play a crucial adaptive role for pig populations<sup>[2]</sup>.

Due to the cheap and easy availability of pig meat, and the deficit between daily meat requirement and availability, the farmers need to be encouraged to keep cross bred swine for greater profitability as well [8]. Litter size at birth and weaning are two important economic traits for high profitability in swine husbandry. High litter size is an important contributor to maximize weaning capacity because it results in highest number and weight of piglets weaned. Average litter size at birth is 5-6 in Desi population. The corresponding value in crossbred like T&D is  $7.77 \pm 0.32$  [8].

Toll-like receptors (TLR) are crucial in innate immunity for the recognition of a broad range of microbial pathogens and are expressed in multiple cell types. There are 10 TLR genes described in the pig genome [1]. Considering these facts and figures, the current study was performed to assess the superiority of Jharsuk variety of pigs (and hence a crossbred) over its parental breeds namely Tamworth and Desi by considering growth and reproductive traits in Swine and to find the effect of TLR 6 gene polymorphism and piglet titre on the Litter size at birth and weaning in these three breeds.

### Materials and method

A total of Forty-eight Pigs belonging to three genetic groups namely Tamworth, Desi and T&D maintained at pig farm of Ranchi Veterinary College were taken for the current study. Under controlled managerial conditions, observations of different growth traits and reproductive traits under study were recorded for the experimental animals. Growth was measured in terms of body weight at different stages of growth, during pre-weaning period. Body weights of pigs were recorded at fortnightly interval from day of farrowing (0-day) to 56 days. Reproductive traits namely Litter size at birth, Litter Weight at Birth, Litter Size at Weaning and Litter weight at Weaning were also measured. Data pertaining to this study was analyzed by Least Square Analysis (Harvey, 1990) using SPAB. Further for the molecular part, DNA was extracted from a total of forty eight samples from the three breeds of pigs together. A total of nine sets of forward and reverse primers were taken for amplification of DNA samples for TLR6 gene loci. All eight primers produced amplified product except the fourth primer (TLR6-4). PCR products were subjected to polyacrylamide gel electrophoresis for the detection of single strand conformational polymorphism (SSCP). A total of nine sets of forward and reverse primers were taken for amplification of DNA samples for TLR6 gene loci. All eight primers produced amplified product except the fourth primer (TLR6-4). PCR products were subjected to polyacrylamide gel electrophoresis for the detection of single

strand conformational polymorphism (SSCP). Then Haplotyping was done based on the different patterns of bands obtained for different primers. The association of TLR 6 polymorphism with different economic traits was seen through association of haplotypes with different economic traits.

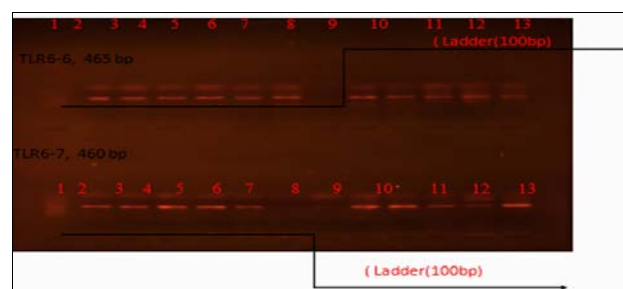


Fig 1: Standardization of Primer 6, 7

### Result and Discussion-

#### Effect of Genetic Groups on Growth traits

Least square analysis of variance showed non-significant effect of genetic groups on body weight at birth. The result presented in Table 1. indicated that the effect of genetic groups on body weight at birth, 7-day, 14-day and 28-day was non-significant while the effect was significant on body weight at 42-day and 56-day. In case of body weight at 42-day, Jharsuk weighed  $08.449 \pm 00.7254$  kg which was significantly higher than Desi and Tamworth. Significant effect was also observed for genetic groups on body weight at 56 day ( $p < 0.05$ ) with Jharsuk having significantly higher body weight ( $11.463 \pm 01.2215$ kg). Least squares analysis of variance showed non-significant effect of genetic groups on body weight gain between birth and 7-day, 7- and 14-day, 14- and 28-day and 28- and 42-day. Significant effect of genetic groups on body weight gain between 42- and 56-day was also observed.

Table 1. further indicated that Desi and Tx&D both differed significantly from each other whereas Tamworth varied non-significantly from Desi. The Relative superiority of Jharsuk (T&D) over both the parental breeds i.e. Tamworth and Desi might be due to Heterosis or Hybrid vigour in T&D [7].

It might be further attributed to inbreeding coupled with selection which negates the Inbreeding depression and also helps in accumulation of superior genes from both the parents.

Table 1: Effect of Breed on Different Growth and Reproductive Traits of Jharsuk (T&D), Tamworth and Desi

Economic traits	Jharsuk (T&D)	Tamworth	DESI	MSS
Body weight at Birth(Kg.)	01.140±00.106	01.349±00.148	0.943±00.177	0.025
Body weight at 7 days(Kg.)	02.417±00.468	01.476±00.652	01.097 ± 00.477	0.500
Body weight at 14 day(Kg.)	04.315± 00.665	03.065±.926	01.469 ± 01.105	1.590
Body weight at 28 days(Kg)	06.011± 00.693	04.063±00.966	02.177 ± 01.152	2.956
Body weight at 42 Days(Kg.)	08.449± 00.725 <sup>b</sup>	06.024±01.011 <sup>ab</sup>	03.456± 01.206 <sup>a</sup>	4.946*
Body weight at Weaning at 56 days(Kg.)	11.463± 01.222 <sup>b</sup>	06.999±1.702 <sup>a</sup>	03.945± 00.931 <sup>a</sup>	15.053*
Body weight gain between 0 and 7 days(Kg.)	02.345±00.8398	03.142± 01.1702	00.231 ±01.3961	1.853
Body weight gain between 7 and 14 days(Kg.)	01.898± 00.4351	01.589 ±00.6063	00.572± 00.7234	0.358
Body weight gain between 14 and 28 days(Kg.)	01.696± 00.324	00.998 ± 00.452	00.708 ± 00.539	0.230
Body weight gain between 28 and 42 days(Kg.)	01.764 ± 00.478	02.360± 00.532	01.963± 00.668	0.090
Body weight gain between 42 and 56 days(Kg.)	03.014± 00.641 <sup>b</sup>	00.975 ±00.895 <sup>a</sup>	00.489 ± 01.068 <sup>a</sup>	3.137*
Litter Size at Birth(Nos.)	09.856± 00.903 <sup>b</sup>	11.421± 01.259 <sup>bc</sup>	05.920± 01.200 <sup>a</sup>	6.556*
Litter Weight at Birth(Kg.)	10.727± 01.091 <sup>ab</sup>	14.276 ± 01.520 <sup>b</sup>	04.892± 01.813 <sup>a</sup>	9.672*
Litter Size at Weaning(Nos.)	08.535± 00.722 <sup>a</sup>	11.247 ± 01.006 <sup>b</sup>	05.556 ± 01.502 <sup>a</sup>	4.146*
Litter Weight at Weaning(Kg.)	94.610 ± 09.651 <sup>a</sup>	81.841 ± 13.4483 <sup>b</sup>	44.210± 16.045 <sup>c</sup>	511.473*

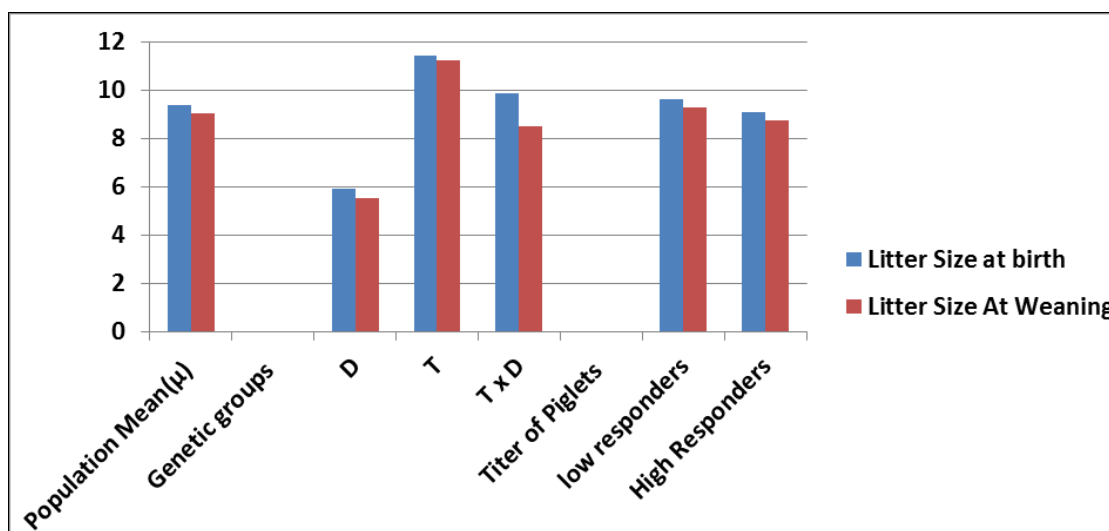
Scientists also reported non-significant differences among two (T&D and LR x D) and three breed crosses (T x LR x D) during pre and post-weaning periods up to 30<sup>th</sup> week of age

[13]. However literatures also mention significant effect of genetic groups on birth weight of piglets [15].

**Table 2:** Least squares means of litter size at weaning and litter weight at weaning

Factors	Litter Size at birth	Litter Size at Weaning
Population Mean ( $\mu$ )	09.378 $\pm$ 00.732	09.031 $\pm$ 00.585
Genetic groups		
D	05.920 $\pm$ 01.200 <sup>a</sup>	05.556 $\pm$ 01.502 <sup>a</sup>
T	11.421 $\pm$ 01.259 <sup>b</sup>	11.247 $\pm$ 01.006 <sup>b</sup>
T x D	09.856 $\pm$ 00.903 <sup>b</sup>	08.535 $\pm$ 00.722 <sup>a</sup>
Titer of Piglets		
2 -3	09.649 $\pm$ 00.855	09.288 $\pm$ 00.683
4 -7	09.107 $\pm$ 00.773	08.774 $\pm$ 00.617

\*Means with different superscripts differ significantly ( $p < 0.05$ ) within a column under a factor



**Fig 2:** Effect of Different Factors on Litter Size at Birth and Weaning

Scientists [9] also found significant ( $P < 0.01$ ) effect of genetic group on body weight at 4<sup>th</sup> and 8<sup>th</sup> weeks of age in *Desi*, LR, Tamworth and their two and three breed crosses. Significant ( $P < 0.01$ ) influence of genetic group at 4<sup>th</sup> and 8<sup>th</sup> weeks body weight was also recorded in crosses of Hampshire and indigenous pigs of Assam [3]. Significant effect of genetic group was also noticed in Tamworth, T&D and *Desi* piglets [10]. The present findings on the positive effect of crossbreeding are supported by research works by scientists [19]. According to him, the effects of offspring heterosis,

maternal heterosis and breed composition on individual pig performance and carcass merit were estimated with data from purebred, single cross, paternal backcross (single cross sires) and maternal backcross (single cross dams)pigs produced from matings among the Chester White, Duroc, Hampshire and Yorkshire breeds. Offspring heterosis was important for all weight traits, with highly significant estimates ranging from 3.5% (birth weight) to 10.5% (154-d weight). Maternal heterosis was small for most traits except 21-d weight (4.9%,  $P < .01$ ).

**Table 3:** Effect of genetic groups on reproductive traits

Primer	Hap.	Litter size at birth	Litter size at weaning	Primer	Hap.	Litter size at Birth	Litter size at weaning
TLR6-1	A	09.789 $\pm$ 00.822	09.157 $\pm$ 00.658	TLR6-7	A	09.310 $\pm$ 00.864	08.992 $\pm$ 00.670
	B	09.434 $\pm$ 00.950	09.225 $\pm$ 00.759		B	08.754 $\pm$ 01.635	08.648 $\pm$ 00.731
	C	10.001 $\pm$ 01.103	09.804 $\pm$ 00.881		C	09.296 $\pm$ 00.904	09.040 $\pm$ 01.198
	D	09.056 $\pm$ 01.666	08.874 $\pm$ 01.331		D	10.151 $\pm$ 00.933	09.443 $\pm$ 01.078
	E	10.249 $\pm$ 01.573	09.736 $\pm$ 01.256				
	F	07.737 $\pm$ 01.269	07.389 $\pm$ 01.0134				
TLR6-2	A	10.134 $\pm$ 01.136	09.290 $\pm$ 00.908	TLR6-8	A	09.019 $\pm$ 0.839	08.775 $\pm$ 00.742
	B	09.935 $\pm$ 01.226	09.577 $\pm$ 00.979		B	08.880 $\pm$ 00.915	08.850 $\pm$ 00.915
	C	08.225 $\pm$ 00.843	08.064 $\pm$ 01.055		C	10.082 $\pm$ 01.500	09.430 $\pm$ 00.813
TLR6-3	A	07.433 $\pm$ 01.392	07.303 $\pm$ 01.743		D	08.664 $\pm$ 01.349	08.358 $\pm$ 01.108
	B	07.995 $\pm$ 00.810	07.979 $\pm$ 00.647		E	10.172 $\pm$ 01.272	08.506 $\pm$ 01.106
	C	07.730 $\pm$ 00.836	07.236 $\pm$ 00.667		F	11.116 $\pm$ 01.906	08.601 $\pm$ 01.314
	D	10.904 $\pm$ 01.076	09.420 $\pm$ 00.860				
TLR6-5	E	13.087 $\pm$ 01.632	12.957 $\pm$ 02.043	TLR6-9	A	09.075 $\pm$ 00.671	08.686 $\pm$ 00.536
	A	09.774 $\pm$ 01.0165	09.526 $\pm$ 00.8121		B	09.638 $\pm$ 00.942	09.211 $\pm$ 00.752
B	08.922 $\pm$ 01.0288	08.746 $\pm$ 00.8219	C		09.420 $\pm$ 01.117	09.196 $\pm$ 00.892	
	C	08.990 $\pm$ 00.7421	08.847 $\pm$ 00.9289				

	D	09.969 ±01.1459	08.861± 00.9154
TLR6-6	A	10.491±01.0177	09.691 ±00.8130
	B	10.932±01.3873	10.212±01.1083
	C	08.682±01.6450	07.406±01.5920
	D	08.682±01.6450	08.158±01.3141

Effect of genetic groups (Table 1.) on litter size at birth was found to be significant ( $p < 0.05$ ). Least squares analysis of variance (Table 1.) showed the significant effect of genetic groups on litter size at weaning ( $p < 0.05$ ).

The effect of genetic group was non-significant on both the litter weight at birth and weaning [17]. In contrast, significant effect of genetic group on litter weight at birth and weaning was observed [14, 6, 16] in *desi*, LWY and their crosses as reported in the present study.

The effect of genetic factor on litter weight at birth and at weaning, age at first farrowing and mortality rate was found to be significant [21]. This result suggests the importance of genetic factor in improving reproductive efficiency of sows. The higher body weight of Jharsuk (T&D) piglets, higher litter size at birth and weaning and higher value of many other traits in T&D as compared to 75% Hampshire is an indication of better combining ability of Desi and Tamworth as compared to Hampshire for all these economic traits [8].

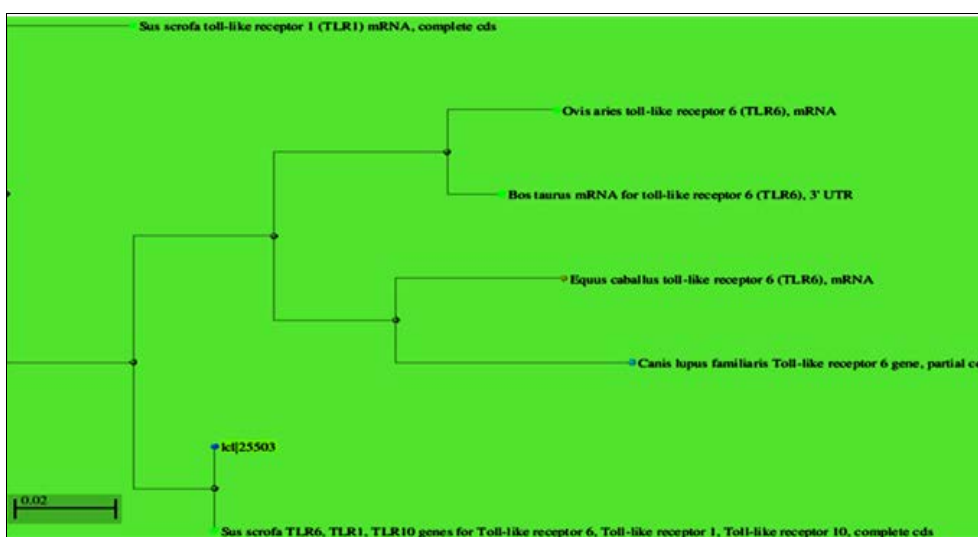
**Effect of TLR 6 gene polymorphism, piglet titre on Litter Size at birth and Litter Size at Weaning based on Table2 and 3**

The population means were observed to be  $09.378 \pm 00.7323$  and  $09.031 \pm 00.585$  for litter size at birth and litter size at weaning. Polymorphisms of all the primers (named as TLR6-1 to TLR6-9 with different numbers of haplotypes) had non-significant effect on litter size at birth and litter size at weaning. Genetic group (Breeds) had significant effect on litter size at birth and litter size at weaning. While, piglet titre (HA titre) had non-significant effect on litter size at birth and weaning.

The PCR-SSCP method is one of the method employed for detection of SNPs and nucleotide base change [4]. Molecular

studies (using PCR-SSCP) assessed the occurrence of polymorphism of TLR6 gene in human and animals [20]. Further SSCP variants were sequenced to construct phylogenetic tree and detection of SNPs under five different primers of TLR6 gene. In consonance with the current study, the expression of distinct sets of TLRs and the corresponding difference in reactivity to microbial molecules among subsets of pre-DCs and DCs support the concept that they have developed through distinct evolutionary pathways to recognize different microbial antigens [5]. Although in the current study, the polymorphisms in TLRs have a profound influence on responses to a wide range of pathogens and are associated with resistance and susceptibility to diseases [11]. A few candidate genes on chromosome 4 related to immune response, with a strong focus on the variants in Toll-like receptor (TLR) genes [18]. TLRs play an essential role in initiating the immune response against pathogens and can recognize a wide variety of pathogen associated molecular patterns from bacteria, viruses, and fungi.

**Phylogeny and Sequencing-**Phylogenetic analysis based on TLR6 gene fragment was studied and compiled for all the eight primers Figure 3 contained the genetic distance among the different species of animals with reference sequence ICI / 25503 of TLR 6-9 gene fragment. It was found to be nearest to *EquusCaballus* and most distant from *BosIndicus* and *Bos Taurus* among all. Sequencing result shows SNPs for all the primers. Here the same has been shown for primer 3 (Figure 4).



**Fig 3:** Phylogenetic Trees under TLR6-9





Fig 4: Sequencing report of the samples with Primer -3 (Page1, 2)

**Conclusion**

The current study shows the superiority of Jharsuk (T&D) over both its parental breeds and also the importance of crossbreeding in increasing the profitability of Pig rearing in India for all the sections of society. The current study could be further done in field condition with larger number of pigs on the same breeds and crossbreeding may be encouraged for indigenous breeds. Litter size is an important economic trait for the swine and hence much emphasis is given to this character during selection. Although the effect of TLR 6 gene polymorphism in the current study was not significant, other genes of the family can be studied to see the effect.

The current research could be continued further to larger number of animals for more applications and the result on phylogenetic studies and sequencing could be further explored to unravel many mysteries related to evolutionary studies and TLR family. The research is important more so because it deals with threshold characters, which is very complex subject in itself and need to be studied more to know detail about its inheritance.

**Acknowledgement**

The author is extremely thankful to the major advisor Dr. L. B. Singh, Ex. Chairman and Head, Department of Animal Breeding and Genetics, Ranchi Veterinary College, B.A.U. The author is also obliged to the members of her advisory

committee, Dr. D. K. Singh Dron, Ex. D.A, B.A.U., Dr. S. K. Singh (Sant), Ex. Dean R.V.C., Dr. R. L. Prasad for providing financial assistance and support for my research, Present Dean, R.V.C., Dr. Sushil Prasad and Honorable Vice Chancellor, B.A.U., Dr. O. N. Singh for constant support.

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