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Identification and association analysis of *PELP1, RFC2* and *ABHD11* polymorphisms with bodyweight and backfat thickness in large white Yorkshire pigs

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ABSTRACT

Genetic markers play a crucial role in enhancing selective breeding strategies for economically important traits in livestock. This study aimed to investigate the genetic variability and functional significance of single nucleotide polymorphisms (SNPs) in three candidate genes—*PELP1 RFC2, and ABHD11* and their association with growth performance traits in the Large White Yorkshire (LWY) pig population of Kerala. High-resolution melting (HRM) analysis followed by Sanger sequencing was employed to detect SNPs in the coding regions of the selected genes. Identified SNPs were evaluated for their potential impact on protein function and genotypic variation. Association analysis was performed using multinomial logistic regression to assess the relationship between gene polymorphisms and phenotypic traits such as body weight and backfat thickness. Three non-synonymous SNPs were identified: c.3514G>A in *PELP1*, c.905G>A in *RFC2*, and c.953A>G in *ABHD11*. Association analysis revealed significant correlations between the *RFC2* GA and *ABHD11* AA genotypes and higher body weight, suggesting a potential role in growth performance. No significant association was observed between *PELP1* polymorphism and either body weight or backfat thickness. These findings suggested that *RFC2* and *ABHD11* polymorphisms may serve as valuable molecular markers for selection in pig breeding programs.

Keywords: *ABHD11*, HRM analysis, LWY pigs, *PELP1, RFC2,* SNP

Pig farming is an integral component of the livestock sector, particularly in regions where land holdings are small and mixed farming systems predominate. In India, pig population stands at 9.06 million, contributing 3.72 per cent of nation's total meat production (BAHS, 2024). Besides contributing significantly to meat production, pig farming plays a vital role in ensuring livelihood and nutritional security, particularly among smallholder and socio-economically weaker farmers, owing to its low capital requirement and quick economic returns (Rajak *et al*. 2024). Furthermore, pig farming serves as a low-input livelihood option that provides income security and nutritional support to rural households, particularly empowering women and tribal communities, while acting as a buffer against crop failures and other agricultural uncertainties (Bharati *et al*. 2022). Among the transboundary pig breeds, Large White Yorkshire (LWY) is known for its superior growth rate, adaptability and reproductive performance. In Kerala, a southern peninsular state in India, pig farming has gained considerable traction in recent years as a sustainable enterprise, supporting rural livelihoods and catering to the growing demand for high-quality pork products.

Genetic improvement in production traits such as body weight and backfat thickness remains a pivotal goal in pig breeding programmes. These traits are economically important and serve as direct indicators of growth performance and carcass quality. Several studies have demonstrated significant associations between SNPs in candidate genes and economically important traits across livestock species. In pigs, genome-wide association and candidate gene studies have identified SNPs influencing growth, feed efficiency, carcass composition and immune-related traits (Tang *et al.* 2019, Ruan *et al.* 2021, Uemoto *et al.* 2021, Ballester *et al.* 2023). In this context, three genes -*Proline-, glutamic acid-and leucine-rich protein 1 (PELP1), Replication Factor C subunit 2 (RFC2)* and

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Abhydrolase domain-containing protein 11 (ABHD11)—have emerged as promising candidates due to their putative roles in cell proliferation, metabolic regulation, and fat deposition (Fontanesi *et al.* 2012; Chen *et al.* 2019; Bailey *et al.* 2020)

The *PELP1* gene encodes a nuclear receptor coregulator implicated in steroid signalling and transcriptional modulation, pathways critical to adipogenesis and muscle growth (Moseti *et al.* 2016; Bahmad *et al.* 2020). The *RFC2*, a component of the replication factor C complex, is involved in DNA replication and cell cycle progression, processes potentially linked to growth dynamics (Junghans *et al.* 2004, Gray *et al.* 2009). The *ABHD11*, a lesser-studied member of the alpha/beta hydrolase family, is hypothesised to influence lipid metabolism and energy homeostasis (Brown *et al.* 2012, Arya *et al.* 2017). While these genes have been studied in other mammalian systems, their relevance in swine remains unexplored.

Despite the recognized roles of *PELP1*, *RFC2* and A*BHD11* in cellular proliferation, metabolism and adipogenesis, information on the genetic variability of these genes and their association with economically important production traits in pigs remains limited. Therefore, the present study aimed to evaluate the polymorphisms in *PELP1*, *RFC2* and *ABHD11* genes and investigate their association with body weight and backfat thickness in Large White Yorkshire pigs reared in Kerala, India.

MATERIALS AND METHODS

Animals, data and sample collection: A total 108 LWY pigs (seven to nine months age) maintained at Centre for Pig Production and Research (CPPR), KVASU Mannuthy, Thirssur, Kerala were used in the present research. Body weight was measured in kilograms using an electronic weighing balance, whereas backfat thickness was determined at the last rib–lumbar region using a Renco Lean-Meater ultrasonic scanner (Renco Corporation, Minneapolis, USA) following the standard protocol**.** Venous blood (5 mL) was collected from ear vein of each and stored at 4°C until processing. Genomic DNA was isolated following phenol-chloroform extraction method as described by Sambrook and Russel (2006).

PCR amplification: The *PELP1, RFC2* and *ABHD11* gene sequences were retrieved from *Sscrofa* 11.1 Genome downloaded from NCBI (https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_000003025.6/). Specifically, exon 19 of *PELP1*, exon 10 of *RFC2* and exon 6 of *ABHD11* were selected for amplification and genotyping due to the presence of putative functional SNPs detected in these regions (Sadan, 2025). The primer sequences were designed to amplify exon 19 of *PELP1*, exon 10 of *RFC2* and exon six of *ABHD11* using the Primer-3 (V.0.4.0) software. Sequence and properties of primers designed are presented in Table 1. Annealing temperature was optimised initially by conducting conventional gradient PCR (Bio-Rad T100™ thermal cycler, USA) for each gene fragment. The PCR conditions were one cycle at 95°C for 10 min, followed by 40 cycles (30 sec at 95°C, 30 sec at 62.5°C for *PELP1,* 60°C for *RFC2* and 62°C for *ABHD11* and 30 sec at 72°C), followed by one cycle at 72°C for three min, hold at 4°C. Amplified PCR products were loaded into the wells of two per cent agarose gel with a standard 50 bp DNA ladder (GenerRuler, MBI Fermentas, Germany) as a marker to check the size of the fragment. Electrophoresis was carried out at the rate six V/ cm in 1X TBE buffer. Gels were stained with ethidium bromide and visualised under UV light and documented in a gel documentation system (Bio-Rad, USA).

High-resolution melting analysis and SNP identification: The HRM was performed in CFX-Opus 96 Real-Time PCR System (Bio-Rad). The protocol involved an initial denaturation step at 95°C for 15 s, followed by rapid cooling to 55°C for 15s. Subsequently, the final denaturation was carried out by incrementally increasing the temperature from 55°C to 95°C at a rate of 0.2°C per step. Fluorescence data acquisition was performed at each step until reaching 95°C. The resulting melting curve, analysed by precision melt analysis software (catalogue number:1845025), reflected the DNA's specific melting behaviour. Peaks in this curve corresponded to different DNA sequences or genotypes. The HRM software then identified variations like SNPs or mutations, enabling genotyping by comparing sample melting curves to known standard peaks (wild-type or mutant controls). All samples were plotted according to their melting profiles. Negative first derivative plots and difference plots were generated for the samples. Under the difference graph, melting profiles of the samples were compared to that of the reference genotype, which was converted to a horizontal line. Different genotypes formed distinct clusters in plots, distinguishable through visual analysis. Representative PCR products, from

Table 1. Sequence and properties of primers designed

Sl. No.	Gene	Primer sequence (5'-3')	Product size (bp)	Annealing temperature
1	PELP1 - F	5' – CCATGCTGGCTGACTTCATT - 3'	138	62.5°C
	PELP1 - R	5' – GCAGCAGTCACTATCCAAGG - 3'		
2	RFC2 - F	5' – CCTCCCTCACTTAATAACCAGAT - 3'	169	60°C
	RFC2 - R	5' – TGGTTCTCTGCTCTAACTGG - 3'		
3	ABHD11 -F	5' – CCTTCTCTCCGTTGGACAGT - 3'	168	62°C
	ABHD11 R	5' – CTCTGGCCGGCAACTTTTAG - 3'		

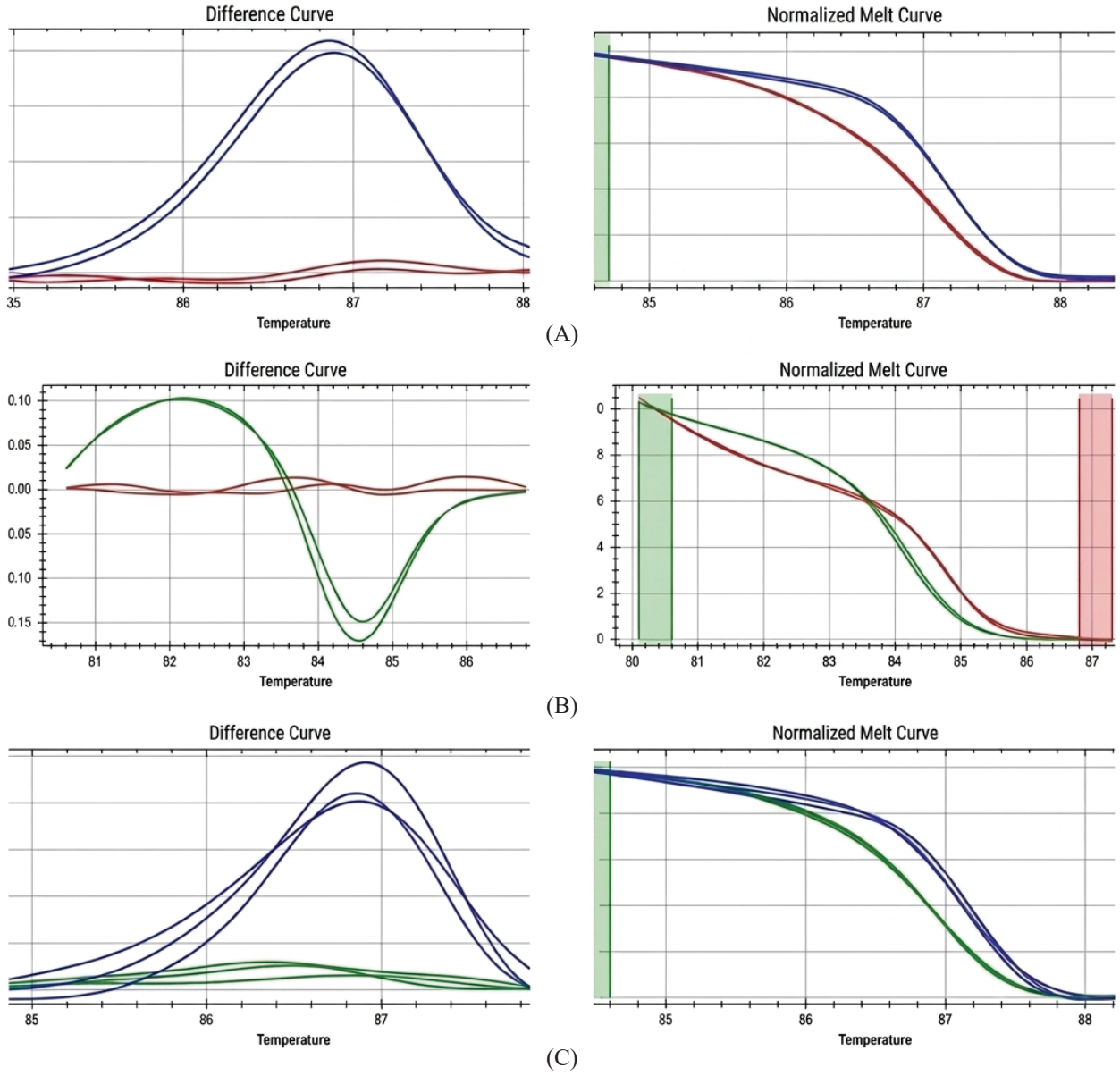

Fig. 1. Difference and normalised melt curve of HRM analysis
A – *PELP1* gene; B – *RFC2* gene; C – *ABHD11* gene

each genotype identified in the HRM assay were sanger sequenced to detect nucleotide variations and aligned with other sequences in GenBank employing BLASTn from NCBI.

Structural and functional implications of SNPs: The structural and functional consequences of SNPs on mRNA and protein structures were analysed using bioinformatic tools. The I-Mutant Suite web server was employed to assess the stability alterations of the resulting mutant protein variants (https://folding.biofold.org/i-mutant/i-mutant2.0.html). The RNA fold software was utilised to predict the minimum free energy (MFE) secondary structure of mRNA (http://rna.tbi.univie.ac.at/cgi-bin/RNAWebSuite/RNAfold.cgi). Gene sequences containing nonsynonymous SNPs were translated into protein sequences using the Expasy Translate tool (https://web.expasy.org/translate/). Secondary and tertiary structure of wild and mutant protein were predicted using SOPMA (https://npsa.lyon.inserm.fr/cgibin/npsa_automat.pl?page=/NPSA/npsa_sopma.html) and SWISS-MODEL (https://swissmodel.expasy.org).

Association analysis: For association analysis of body weight of LWY pigs, body weight was classified into four groups, very low (< "mean - 1SD"), low ("mean - 1SD" to mean), medium (> mean to "mean + 1 SD") and high (> "mean + 1SD"). For body weight categories, a multinomial logistic regression model was fitted with sex and genotypes of *PELP1, RFC2* and *ABHD11* as predictor variables.

$$\log (P(Y=j)/P(Y=Low) = \beta0 + \beta1(Sex) + \beta2(PELP1\ genotype) + \beta3(RFC2\ genotype) + \beta4(ABHD11\ genotype\ 3) + \varepsilon$$

where:

- P(Y=j) represents probability of body weight being in category j (Very Low ((≤75kg), Low (76kg-104kg), Medium (105kg to 134kg), High (≥135kg)).
- P (Y = Low) is the reference category.
- β0 is the intercept and β1, β2, β3 and β4 are regression coefficients.
- ε represents the error term.

For association analysis of back fat thickness of LWY pigs, back fat thickness was categorised into four different groups very low (< "mean - 1SD"), low ("mean - 1SD" to mean), medium (> mean to "mean + 1 SD") and high (> "mean + 1SD") based on the range. For back fat thickness categories, a multinomial logistic regression model was fitted with sex, body weight groups and genotypes as predictor variables.

$$\log(P(Y=j)/P(Y=Low) = \beta0 + \beta1(Sex) + \beta2\ (Body\ weight\ group) + \beta3(PELP1\ genotype) + \beta4(RFC2\ genotype) + \beta5(ABHD11\ genotype) + \varepsilon$$

where:

- P(Y=j) probability of back fat thickness being in category j (Very Low (≤11mm), Low (12mm-16mm), Medium (17mm-20mm), High (≥21mm)).
- P (Y = Low) is the reference category.
- β0 is the intercept and β1, β2, β3, β4 and β5 are regression coefficients.
- ε represents the error term.

RESULTS AND DISCUSSION

High-resolution melting analysis and SNP detection of PELP1 gene: The *PELP1* gene, known to act as a transcriptional co-activator for various nuclear receptors, notably peroxisome proliferator-activated receptor gamma (PPARγ), plays a central role in adipogenesis. Through its interaction with the co-activator domain of PPARγ, *PELP1* enhances transcriptional activity, thereby facilitating the expression of adipogenic target genes and promoting adipocyte differentiation, lipid accumulation and fat deposition (Moseti *et al.* 2016; Bahmad *et al.* 2020). HRM profiling of the PCR-amplified exon 19 fragment of the PELP1 gene revealed two distinct melting patterns (Fig. 1).

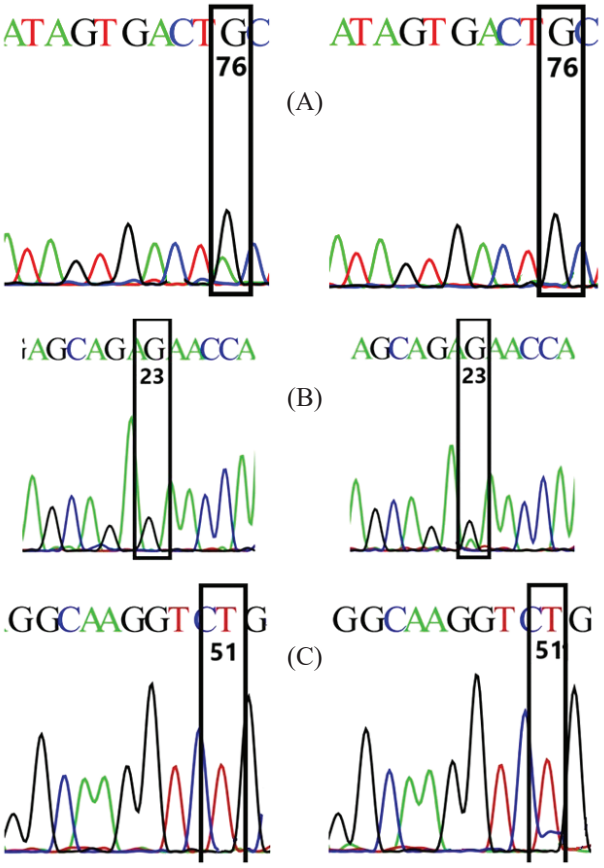

Fig. 2. Chromatogram of genes

PP and PQ genotypes of *PELP1* gene; GG and GA genotypes of *RFC2* gene; AA and AG genotypes of *ABHD11* gene

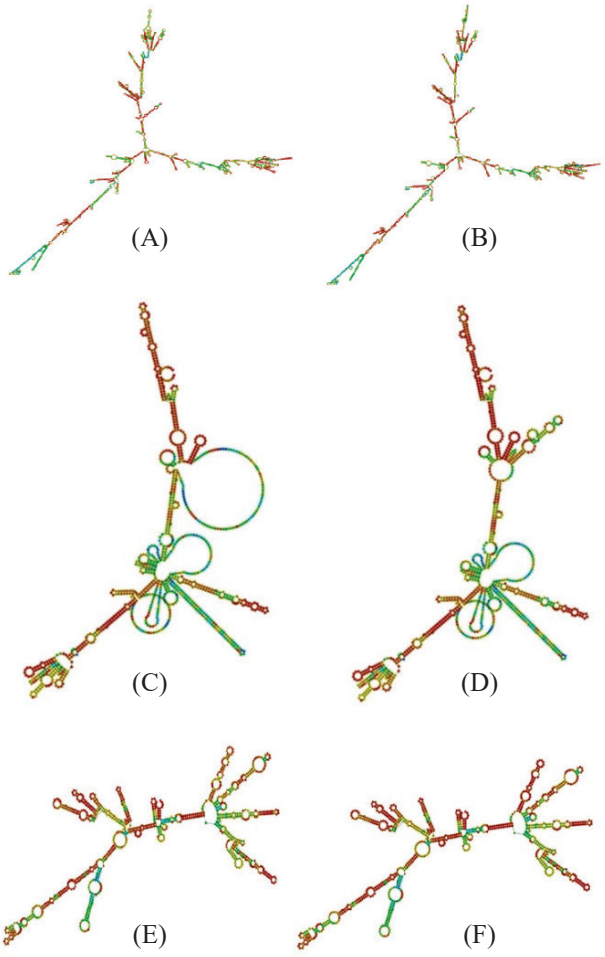

Fig. 3. Minimum free energy secondary structure of mRNA

A- Wild variant of *PELP1;* Mutant variant of *PELP1;* Wild variant of *RFC2;* Mutant variant of *RFC2;* Wild variant of *ABHD11;* Mutant variant of *ABHD11*

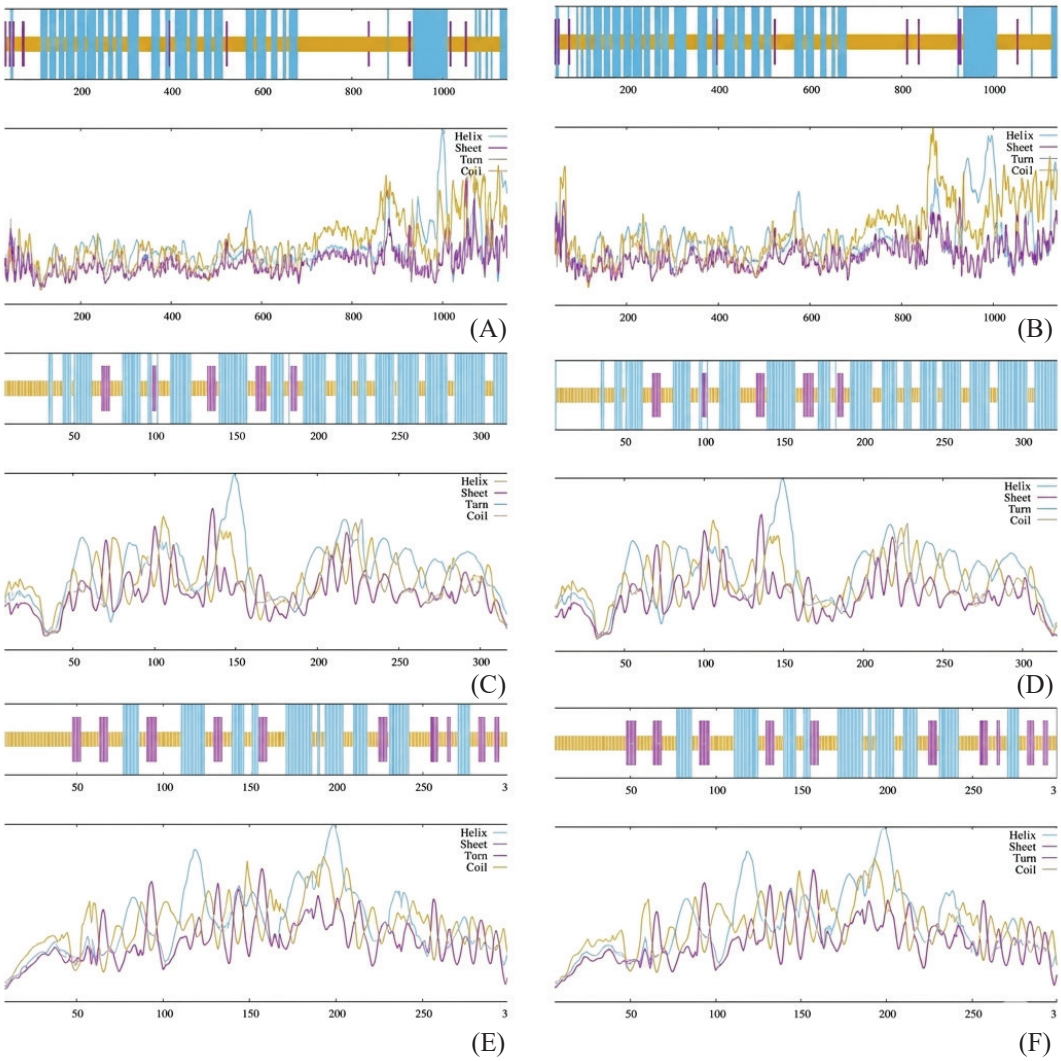

Fig. 4. Secondary structures of protein

Wild variant of PELP1 protein; Mutant variant of PELP1 protein; Wild variant of RFC2 protein; Mutant variant of RFC2 protein; Wild variant of ABHD11 protein; Mutant variant of ABHD11 protein

Subsequent Sanger sequencing of representative amplicons corresponding to each melting profile identified two genotypes, GG and AG. A single nucleotide polymorphism (SNP), characterized by a G>A transition at nucleotide position 76 of the amplified fragment in exon 19, was detected (Fig. 2). This variant, designated c.3514G>A, resulted in a codon change from GCA to ACA, leading to a non-synonymous amino acid substitution from alanine to threonine, which may influence protein function. Genotypic frequency analysis revealed that the GG genotype was predominant (0.74), whereas the AG genotype occurred at a frequency of 0.26. Correspondingly, allele G was the major allele with a frequency of 0.87, while allele A occurred at a frequency of 0.13.

The potential functional impact of *PELP1* c.3514G>A mutation was assessed using the I-Mutant prediction tool, which estimated a ΔΔG (Gibbs free energy change) value of -0.91, indicating decreased stability of the PELP1 mutant protein. The mRNA and protein structure predictions revealed structural differences between the wild-type and mutant variants (Fig. 3). Notably, the mutant variant exhibited a lower MFE (ΔG = -1587.50 kcal/mol) compared to wild (ΔG = -1587.30 kcal/mol), implying greater mRNA stability, as lower MFE values are generally associated with more stable mRNA configurations. To evaluate the structural implications of the c.3514G>A *PELP1* mutation at the protein level, both secondary and tertiary structures were analysed. Secondary structure predictions showed a reduction in alpha-helical content from 39.20% in the wild type to 37.93% in the mutant, accompanied by a relative increase in random coil regions, suggesting a modest increase in structural flexibility (Fig. 4). However, homology modelling revealed no overt changes in the tertiary structures between the wild-type and mutant forms of the PELP1 protein (Fig. 5), indicating that the substitution may exert its influence more subtly at

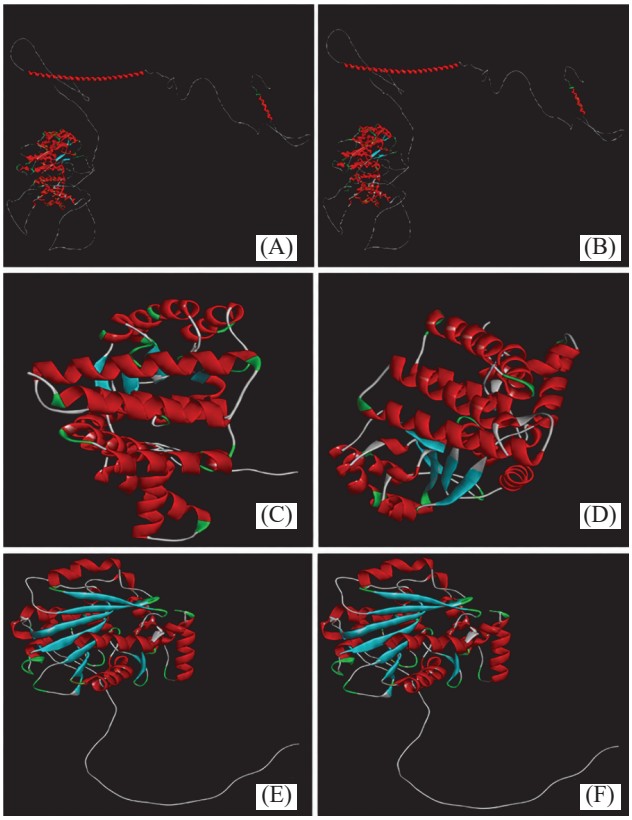

Fig. 5. Tertiary structures of protein

Wild variant of PELP1 protein; Mutant variant of PELP11 protein; Wild variant of RFC2 protein; Mutant variant of RFC2 protein; Wild variant of ABHD11 protein; Mutant variant of ABHD11 protein

the functional or dynamic level rather than inducing gross conformational changes.

HRM analysis and SNP detection of RFC2 gene: Given the high proliferative and regenerative capacity of muscle tissues, *RFC2* plays a pivotal role in maintaining genomic integrity during cell division. The HRM analysis of 169 bp fragment of *RFC2* gene yielded two distinct melting profiles (Fig. 1). Sanger sequencing of the corresponding PCR products confirmed the presence of two genotypes within the studied population: GG and GA. The identified SNP involves G to A substitution at position 23 of exon 10, designated as c.905G>A (Fig. 2). This mutation leads to a codon shift from AGA to AAA, causing a non-synonymous amino acid change from arginine to lysine, which may have structural and functional implications for the encoded protein. The GG genotype was predominant, observed in 65% of individuals, while the GA genotype accounted for 35%. Allelic frequency analysis showed a high prevalence of the G allele (0.82), whereas as the A allele had low (0.18).

To assess the functional consequences of the mutation, stability prediction using the I-Mutant tool indicated that the Arg→Lys substitution led to a decrease in protein stability, with a calculated ΔΔG of -1.59 kcal/mol. This negative value suggested a destabilising effect of the mutation on the RFC2 protein. The RNA secondary structure predictions demonstrated structural differences between the wild-type and mutant mRNA RFC2 transcripts (Fig. 3). The mutant variant exhibited a lower MFE ((ΔG = -253.80 kcal/mol) compared to wild (ΔG = -272.10 kcal/mol), indicative of enhanced mRNA stability, which might affect transcript processing or translation efficiency. Protein secondary structure analysis via revealed a reduction in alpha-helix content in the mutant variant (from 55.15% in wild-type to 54.55% in mutant), suggesting a marginal loss of structural stability (Fig. 4). Additionally, the random coil percentage was lower in the mutant, potentially implying reduced conformational flexibility, which might hinder proper protein folding. Finally, tertiary structure modelling using revealed discernible topological changes in the spatial conformation of the mutant RFC2 protein (Fig. 5). These changes included an extended overall structure and slight shifts in folding patterns. Such modifications might impair the efficiency of protein folding or its interaction with other subunits of the RFC complex, potentially impacting its biological function.

HRM analysis and SNP detection of ABHD11 gene: The *ABHD11* gene, a member of the α/β-hydrolase superfamily, plays a vital role in lipid metabolism, energy homeostasis and mitochondrial function (Bailey *et al.* 2020). Recent evidence has also implicated *ABHD11* in the regulation of body weight and metabolic efficiency through its involvement in 2-oxoglutarate metabolism, a critical intermediate of the tricarboxylic acid (TCA) cycle (Escoubet *et al.* 2020). This highlighted its functional relevance in maintaining cellular energy balance. The HRM analysis of a 168 bp region of the *ABHD11* gene uncovered two distinct melting curves (Fig. 1). Sanger sequencing of the corresponding PCR products confirmed the genotypes AA and AG. The SNP detected was A to G substitution at position 51 of exon 6, identified as c.953A>G (Fig. 2). This variant alters the codon from CAG to CGG, leading to change from glutamine to arginine. As a non-synonymous substitution, this change could potentially affect the protein's conformation, function, or its interactions with other molecules. Genotypic frequency analysis showed that the AA genotype was predominant, accounting for 78% of individuals, while the AG genotype was present in 22% with the dominance of the A allele (0.89).

To evaluate the functional consequence of the amino acid change, the I-Mutant tool was employed to predict the stability effect of the Gln→Arg substitution. The ΔΔG value was calculated as -0.48 kcal/mol, indicating a slight destabilising effect on the ABHD11 protein structure. The mRNA secondary structure predictions using RNA fold revealed no apparent structural differences between the wild-type and mutant ABHD11 variants (Fig. 3). However, the mutant variant exhibited a higher MFE, suggesting a less stable mRNA secondary structure. The SOPMA-based secondary structure prediction showed a minor increase in alpha-helix content in the mutant protein (from 33.12% to 33.44%), implying a possible enhancement in

Table 2. Effect of genotype and sex on body weight of LWY pigs

Effect	Model Fitting Criteria	Likelihood Ratio Tests		
	-2 Log Likelihood of Reduced Model	Chi-Square	df	Sig.
PELP1	57.088	1.297	3	0.730
RFC2*	65.877	10.085	3	0.018
ABHD11**	70.159	14.368	3	0.002
Sex	58.242	2.450	3	0.484

*p < 0.05 and ** p <0.01

local structural rigidity (Fig. 4). Additionally, the random coil content increased in the mutant, suggesting a gain in flexibility, while the extended strand content also rose slightly (from 14.47% to 14.79%), which could affect protein-protein or protein-ligand interactions. Tertiary structure modelling of both wild-type and mutant ABHD11 proteins using SWISS-MODEL revealed no substantial alterations in overall tertiary conformation (Fig. 5). This suggested that although the c.953A>G variant leads to minor changes in secondary structure, it does not cause large-scale structural disruptions.

Association of PELP1, RFC2 and ABHD11 genotypes with body weight of LWY pigs: The analysis revealed that genotypes of *RFC2* (p≤0.05) and *ABHD11* (p≤0.01) had significant effect while sex had no significant effect on body weight, which is likely attributable to the low number of male individuals within the studied cohort (Table 2). A notably low odds ratio (0.188) for the *RFC2* GG genotype in the high body weight category suggested that individuals with this genotype are 81.2% less likely (i.e., 5.32 times lower probability) to fall into the high body weight category compared to those with GA genotype (Table 3). Moreover, animals with the *RFC2* GA genotype had significantly higher mean body weight compared to the GG genotype group (Table 4). These findings aligned with Gray *et al*. (2009), who reported that increased *RFC2* expression in highly proliferative tissues, such as skeletal muscle, supports enhanced myocyte proliferation.

Similarly, the *ABHD11* genotype showed a significant (p≤0.01) association with body weight. The odds ratio of 0.136 for the *ABHD11* AA genotype in the very low body weight category indicates 86.4% reduced likelihood (7.35 times lower probability) of having this genotype in that category compared to the AG genotype (Table 3). Consequently, individuals with the AA genotype are more likely to exhibit higher body weight (Table 4). These observations are in agreement with prior functional studies, such as those by Escoubet *et al*. (2020), which demonstrated that ABHD11 knockout mice display a lean phenotype and resistance to diet-induced obesity. These findings suggest that *ABHD11* influences body weight regulation through

Table 4. Least square means for the effects of genotype of *PEPLP1, RFC2* and *ABHD11* on body weight of LWY pigs

Gene	Genotype	Mean ± SE (kg)
PELP1	GG	98.62 ± 5.32
	GA	101.70 ± 6.98
RFC2*	GG	91.69 ± 5.84[a]
	GA	108.62 ± 6.33[b]
ABHD11**	AA	110.83 ± 4.99[a]
	AG	89.49 ± 7.36[b]

*p < 0.05 and ** p <0.01; Mean values with different superscript differ significantly

Table 5. Effect of genotype, sex and body weight category on back fat thickness of LWY pigs

Effect	Model Fitting Criteria	Likelihood Ratio Tests		
	-2 Log Likelihood of Reduced Model	Chi-Square	df	Sig.
PELP1	113.035	2.426	3	0.489
RFC2	116.894	6.286	3	0.099
ABHD11	114.655	4.047	3	0.256
Sex	112.159	1.550	3	0.671
Body weight category**	157.627	47.019	9	0.000

** p <0.01

Table 3. Association analysis of genotypes of *PELP1, RFC2* and *ABHD11* with body weight of LWY pigs

Body weight category	Predictor	Coeff.	SE	Wald Chi-Square	p- value	Exp(B)	95% CI	
Very low	*PELP1* GG	1.073	1.150	0.871	0.351	2.924	0.307	27.827
	RFC2 GG	1.358	1.135	1.432	0.231	3.890	0.421	35.976
	ABHD11 AA**	-1.998	0.717	7.759	0.005	0.136	0.033	0.553
Medium	*PELP* GG	0.123	0.528	0.054	0.816	1.130	0.401	3.184
	RFC2 GG	-0.148	0.493	0.090	0.764	0.862	0.328	2.266
	ABHD11 AA	-0.230	0.602	0.146	0.702	0.794	0.244	2.587
High	*PELP1* GG	-0.224	0.667	0.113	0.737	0.799	0.216	2.956
	RFC2 GG*	-1.674	0.681	6.047	0.014	0.188	0.049	0.712
	ABHD11 AA	0.745	1.207	0.381	0.537	2.106	0.198	22.415

Note: Coeff. = coefficient; CI =confidence interval; Exp (B) = exponential odds ratio; ref =reference; SE =standard error. Reference - *PELP1* GA/*RFC2* GA/*ABHD11* AG, *p < 0.05 and ** p <0.01

Table 6. Association analysis of body weight group and genotypes of *PELP1, RFC2* and *ABHD11* with back fat thickness of LWY pigs

Backfat category	Predictor	Coeff.	SE	Wald Chi-Square	p- value	Exp(B)	95% CI	
Very low	*PELP1* GG	-0.034	0.720	0.002	0.962	0.966	0.236	3.961
	RFC2 GG	0.976	0.704	1.923	0.166	2.655	0.668	10.552
	ABHD11 AA	0.917	0.806	1.294	0.255	2.502	0.515	12.149
	Very low body weight**	20.158	1.079	349.063	0.000	5.7E+08	6.9E+07	4.706E+09
	Low body weight**	19.255	0.882	477.004	0.000	2E+08	4.1E+07	1.296E+09
	Medium body weight	17.681	0.000	-	-	5E+07	4.8E+07	4.8E+07
Medium	*PELP1* GG	0.995	0.901	1.219	0.270	2.704	0.462	15.810
	RFC2 GG	1.841	0.850	4.687	0.030	6.300	1.190	33.338
	ABHD11 AA	-0.484	0.923	0.275	0.600	0.616	0.101	3.760
	Very low body weight	-22.715	0.000	-	-	1.365E-010	1.365E-010	1.365E-010
	Low body weight	-1.977	1.013	3.806	0.051	0.139	0.019	1.009
	Medium body weight	-0.977	0.940	1.082	0.298	0.376	0.060	2.373
High	*PELP1* GG	0.402	0.819	0.241	0.624	1.494	0.300	7.436
	RFC2 GG	0.471	0.765	0.241	0.624	1.602	0.357	7.182
	ABHD11 AA	-0.401	0.932	0.186	0.667	0.669	0.108	4.156
	Very low body weight	-22.369	0.000	-	-	2.510E-018	1.929E-010	1.929E-010b
	Low body weight	-1.477	0.862	2.937	0.087	0.228	0.042	1.236
	Medium body weight	-1.902	0.894	4.527	0.033	0.149	0.026	0.861

Note: Coeff. = coefficient; CI =confidence interval; Exp (B) = exponential odds ratio; ref =reference; SE =standard error; Reference - *PELP1* GA/*RFC2* GA/*ABHD11* AG/High body weight, ** p <0.01

modulation of lipid metabolism and energy balance.

Overall, these results underscore the functional relevance of *RFC2* and *ABHD11* polymorphisms in influencing body weight and provide potential genetic markers for growth traits in commercial pig populations.

Association of PELP1, RFC2 and ABHD11 genotypes with backfat thickness of LWY pigs: Association analysis by multinomial logistic regression revealed that sex and the genotypes of *PELP1, RFC2* and *ABHD11* did not have a statistically significant influence on back fat thickness in LWY pig population (Table 5). These results suggest that, within this specific genetic background and environmental context, the examined polymorphisms may not contribute significantly to the variation in backfat thickness. However, these findings are in contrast with several earlier studies. Chen *et al.* (2019) reported a significant association between *PELP1* gene polymorphisms and back fat thickness in both Landrace and Yorkshire pig breeds. Similarly, Wei *et al*. (2022) demonstrated that *PELP1* expression is closely tied to fat deposition, possibly through alternative splicing events that lead to structural variations in the protein, thereby modulating its functional impact on adipose tissue metabolism. Fontanesi *et al*. (2012) identified a significant association between *RFC2* polymorphism and back fat thickness in Italian Large White pigs. Studies have implicated *ABHD11* in fat accumulation and lipid metabolism. Brown *et al*. (2012), Arya *et al*. (2017) and Liu *et al*. (2020) highlighted its involvement in lipid synthesis, degradation and signal transduction pathways that regulate metabolic efficiency.

Multinomial logistic regression analysis also revealed that body weight group was found to have a significant ($p < 0.01$) influence on back fat thickness in Table 5 and 6. These findings are consistent with earlier findings by Tummaruk *et al*. (2009), who demonstrated a significant correlation between body weight and back fat thickness in Landrace × Yorkshire gilts.

This study demonstrated genetic variability in *PELP1*, *RFC2* and *ABHD11* genes in LWY pig population of Kerala, India with notable implications on growth performance traits. Specifically, the non-synonymous polymorphisms detected in *RFC2* (c.905G>A) and *ABHD11* (c.953A>G) were significantly associated with body weight, indicating their potential utility as genetic markers in selection programmes aimed at enhancing growth traits in LWY pigs. Further functional analysis revealed the studied genetic variants in these genes could influence protein stability, mRNA structure, and overall gene function. All these findings emphasized the complex genetic factors influencing body weight and metabolic traits in pigs, highlighting the need for further research to explore breed-specific genetic effects and their application in pig breeding programmes.

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