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RELATIONSHIP BETWEEN SILENT MUTATIONS AND QUANTITATIVE TRAIT LOCI GENES IN CATTLE : A REVIEW

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Abstract

Silent mutation is one from many kinds of mutations occurs in code and non-code regions in different genes which keeping on protein function and sequencing leading to variance in one of amino acids in triplet code therefore, these happened with low percentages and non-significantly changing genetic code expressions that sometimes influence on protein sufficient function, folding so that, different types of insensitive mutation affect activity of mRNA intra cell in many cases so, secondary structure for mRNA will be alter and correlated with quantitative trait loci (QTL) which are part of DNA and associated with phenotype, quantitative trait variance, these can be identified by SNPs and related with polygenic genes so founded on different chromosomes that responsible on quantitative traits such as milk production and contents traits also growth which changed continuously thus, this view carried out to clarify importance of silent mutations and their relation with quantitative characteristics with performance of cattle.

Keywords : Silent mutation, QTL, genes, cattle.

Introduction

Phenotypic variance appeared as a result in participation and interaction several areas for genes with alleles effects that sensitive to environmental conditions so, QTL and silent mutations within genes impact on traits and complete work of each other which responsible on quantitative genetics (Trudy *et al*., 2009). Over than 20 years, it has been discovered that QTLs genes as Diacylglycerol O – Acyltransferase (DGAT), ATP binding cassette subfamily G member 2 (ABCG2), Insulin like growth factor 2 (IGF2), Growth hormone receptor (GHR) were linked with health, growth traits and immunity (Al-Samaraai and Ali, 2018) occasionally changes occure in some regions of genes refer to silent mutation which alter DNA without individual phenotype significantly that happened in non-codon regions out of genes or within introns or exons mostly, this mutation is the same meaning of synonymous mutation but the opposite is untrue synonymous mutation altering amino acid sequencing, transcription splicing, mRNA transcription, translation perform to change phenotype (Shalabina *et al*., 2006) silent mutation produced from additive, deletion or insertion causing different in reading encoding, mRNA may be effect on t RNA code at translation timing (Mueller *et al*., 2009) which break down protein resulting code will be changing to produce amino acid with similar function like lysine instead of isoleucine with same features of amino acid, this mutation not influence on protein function, however throughout several code, many of amino acids can be determined, this perform to same amine acid therefore, alternative mutation not change amino acid at mRNA translation (Khan, 2008) when codon alter from AAA become AAG, the same amino acids will be merging in peptide chain (Czech *et al*., 2010), whereas an area in CD18 gene which alter aspartic to glycine (Roy *et al*., 2012) another silent mutation replaces cytosine to thyamine at 775 position at 383, b p position and 880 b p $_C$DNA due to remove 105 b p within exon 4 for this gene (Mueller *et al*., 2015). If amino acid moved to ribosome lately, translation will be down slowly due to depression of gene expression which contains this mutation inside exon while ribosome waiting, if mRNA is un stable relatively, it will analysis in cytoplasm by enzymes (Patel *et al*., 2011). On other side, when mRNA is stable strongly with bands, gene may be still under expression, anyway, variance of mRNA splicing in cells influenced by mutations and this keep on protein codon which appeared via changing of gene expression throughout splicing, translation in case of mutation in exon 7 of survival of motor neuron 1 (SMN1) gene (Czech *et al*., 2010), that influence on accuracy and sufficient of splicing, stability of mRNA structure, function, whereas, there is a mutation lies beside splice area of intron flanking exon 10 for microtubule associated protein tau (MAPT) gene (Stylianos *et al*., 2013). Silent mutation occurs in the end 5¯ at site of ribosome and mRNA correlation has significant impact on expression levels of PETcGH2-7 which appeared 12–30% of total cell proteins expression while mutation PETcGH 8 -16 mutation reflects 30-53% of cell proteins expression so, mRNA transcription differences due to various in transcription levels which associated with free energy values of secondary structures in 5¯ area for mRNA so, unsensitive changes will be within nucleotides (Khan, 2008) for a long time to pick amino acid as well as may be translated at early time perform to change it or different one of three letters in triplet codon that stay without altering and similar in biological and chemical features (Calero *et al*., 2016), in the same side, triplet codon modifications impact on protein translation (Brooker, 2017), replacement one amino acid- weakend protein function also triplet structure or may be not affected depending on traits, correlated amino acids may be entering codon before limited time for stopping codon UGA thus, this mutation acting on produce incomplete protein, function, folding depending upon area of stopping codon on the same hand, there are two silent mutations founded at exon 9 in Chinese cattle for PRDM16 gene, first one is XM – 061788152 in A <G 1641T>· C 01881 when the other is AAA(Lys) <AAG(Lys), G> A on 627aa region (Xino *et al*., 2006). polymorphism at 348 position as a silent mutation not change amino acid aspargine AAT>AAC within exon 4 for Integrin beta chain – 2 (CD18) gene that correlated with milk production . However, QTL on 3, 6, 20 chromosomes for protein rate in addition 1, 3, 6, 9, 14 chromosomes for milk production (Patel *et al*., 2015). There are 36693 positions of quantitative traits for 492 traits in cattle including 5815

regions for milk fat, 3157 for milk protein contents, 1824 for milk production 550 for fatty acids contents and 1246 for mastitis (Albengha *et al*., 2016), silent mutation C > T at 775 p b position for Cluster of differentiation (CD1) gene codon is considered an indicator for higher milk production so, association between polymorphism of T < C 775 and milk yield performance a parameter to QTL (Czarnik *et al*., 2007) this mutation localized at 775 bp area for Integrin beta – 2 precusor (ITGB2) gene which associated with protein contents, while there are three regions for QTL on Betaine lipid synthase 1 (BTA1) gene that coupled with milk production (Czarnik *et al*., 2004), in the same hand, D 128 G mutation is a QTL index found within coding genes were related with lactation, milk content synthesis (Czarnik, 2000). Silent mutation revealed in exon 6 for pituitary – specific positive transcription factor 1 (POUIFI) gene which have polymorphisms acting on body contents, milk production. On the other hand Diacylglycerol O – Acyltransferase 1 (DGAT1) gene responsible on milk yield, fat contents also intra muscular fat composition a SNP in 5 UTR area for this gene related with high fat ratio in milk (Yang *et al*., 2013), Silent mutation from GCC Ala 487 to GCT Ala 487 available in exon 17 at 8539 b p in Chinese sheep (Xu *et al*., 2008), QTL influence on milk yield founded on twenty bovine chromosomes in the same side, there are 109 regions of genome linked with milk traits on chromosome 14 also have effect on milk fat, DGAT1 gene (Diacyl glycerol G – Acyl transferase 1), this gene contains 29 polymorphisms include two mutations in exon 6, first one R2S1L in Sanen goat with gene frequency 3.5% and second R396W in Sanen and Alpine goat with percentage 13% and 7% of frequency thus, contributed of 46% and 6% for genetic variance due to both mutations which correlated with milk fat content reduction (Martin *et al*., 2017). Arranz *et al*. (1998) proved that BTA20 has allelic effect for 308 kg milk yied, body weight at early age as well as carcass traits furthermore growth in beef cattle (Peter, 2004). However SNPs within 3, 4 and 5 introns of bovine gene POUIF1 proved as a silent mutation (Zhao *et al*., 2004).

on same direction, SNP 15 (9258 C > T) for Calcium dependent protease (CAPN1) gene considered a silent mutation in exon 4 on chromosome 29 which correlated significantly with meat quality (Kolikalapudi *et al*., 2014), QTL for growth traits and meat quality recorded at 0 – 30, 55 – 70 and 70 – 80 cμ on chromosome 5 including SNPs for myogenic genes in these regions (Patel *et al*., 2011). There are three Silent mutations for bovine GL1 family zinc finger 3 (GL 13) gene associated with body weight at birth and six months age in Nanyang cattle also Silent mutation in Inhibitor of growth family member 1 (INGI) gene linked with growth in Qinchuan cattle, furthermore, Non – SMC condensin 1 complex subunit G (NCAPG) gene coding condensing 1 protein which has important role in mitosis division organizing (Duan *et al*., 2015), moreover, primary effect of NCAPG mutation on progenitor cells correlated with phenotype, daily body weight in Germany Holstein (Proud and Roberts, 2007) also correlated with total body weight, hip width and carcass weight so that a significant differences reported between NCAPG with Ligand Dependent Nuclear Receptor Corepressor Like (LCORL) and DDB1 so as Cul4 associated factor 16 (DCAF16) with body muscular development in addition embryonic growth (Peter, 2004), Silent mutation of POU1F1 gene linked with milk production and birth weight (Lan *et al*., 2007), bovine NCAPG gene in QTL for body and carcass weight in cattle lies on chromosome 6 (BTA6), there is a variance in G < T NCAPG2c.1326 responsible on amino acid changing P112442 Met (Setoguchi *et al*., 2009), correlation between G < T NCAPGc1326 and birth with body weight (Weikard *et al*., 2010) in addition NCAPG besides of LCORL genes expressed on muscles longissimus acting on muscles growth organizing . Three silent mutations for bovine GL13 gene effect on body growth at birth and six months age in Nanyung cattle at QTL regions, these are : g47747:T > C and g52535:A > G and g53208:T > G moreover, these mutations not change amino acid component for protein expression in Nanyung cattle (Kolikalapudi *et al*., 2014). Furthermore, bovine gene INSIG1 linked with growth traits in Qinchuan beef cattle (Liu *et al*., 2012). on same direction, SNP 15 (9258 C > T) for Calcium dependent protease (CAPN1) gene considered a silent mutation in exon 4 on chromosome 29 which correlated significantly with meat quality (Kolikalapudi *et al*., 2014), in study of (Tijan *et al*., 2011) whom reported that QTL for growth traits and meat quality sited at 0 – 30, 55 – 70 and 70 – 80 cμ on chromosome 5 including SNPs for myogenic genes in these regions.

Silent mutation correlated with diseases or negative effects but there are advances because of creating genetic variation among different individuals so some of infections not appeared without one lethal gene available (Khan, 2008). Dopamine receptor (D2) gene is less stability and analyzing quickly resulting reduction of gene activity, in the other direction, silent mutation in Multi Drug Resistance (MDR) enabled cell membrane to set of drugs and reduced translation perform to abnormal folding in protein structure (Brooker, 2017). Silent mutation in apoptotic protease activating Apoptotic Peptidase Activating Factor 1 (APAF1) (Adams *et al*., 2016) which is an active element for cytochrome that modulated apoptotic cascade so that related with infections also this factor contributed in development of central nerve system. However, a silent mutation at 240 b p within exon 3 and 5 for Arginine Succinate Synthase 1 (ASS1) gene not effect on amino acids in Holstein cattle (Ghanem and Nishibori, 2018), while there are two silent mutations in Melanocortin 1 receptor (MCIR) gene on chromosome 14 their role are significant in skin colouring organisation in Chinese sheep, and these mutations are c.218 T > A.P.73 met > Lys. C.361 G > A, P. 121 Asp >Asn (Yang *et al*., 2013).

From previous information, silent mutation happened within genes and correlated with quantitative traits sometimes not affected by these changes anyway, these mutations can be dependent upon them as an active markers for selection and keeping on productivity balance in cattle.

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