Polymorphism of The Promote Region of Chicken Insulin like Growth Factor-1 and Association With Bone Abnormalities

التغايرات الوراثية في منطقة المشغل لجين*IGF-1* لعينات الدجاج وعلاقتها بتشوه العظام

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Abstract

The insulin like growth factor-1(*IGF-1*) is important regulators in stimulating growth, protein synthesis, cell proliferation and differentiation in a variety of cell types. To achieve this goal, blood samples were collected from 50 *Gallus gallus* affected from bone abnormalities (distortion) and 50 samples a control group from the Animal farm/ College of Veterinary medicine/ University of Baghdad. DNA was isolated and the IGF-1genewas amplified by using specific primers for promoter region and *5' UTR* of this genes, then DNA sequencing was performed by using AB13730XL, (Applied Bio system, Macro Gen company, USA). The DNA sequencing results of flank sense of *IGF-1*gene from a control group was found to be compatible 100% with wild type of *Gallus gallus* from the Gene Bank. On the other hand, sequencing results of the same gene from 35cases abnormalities (distortion) revealed of 99% compatible and score 1351 and expect 0.0 with the wild type sequences of gene bank. The minor differences could be attributed to two transversion substitutions of (G>T,T>G) and (C>T) on locations 404, 104, and 249 nucleic acid respectability. Fifteen cases of bone abnormalities (Distortion) of *Gallus gallus*, 99% compatibility have one Transversion substitution G>T on position 404 andone transition substitution (C>T) on 249 positions, under number Sequence ID: gb|JX414253.1|. In conclusion, our case study suggests that polymorphisms of *IGF-1*gene are strongly associated with vertebrate growth and development of some chicken breeds in Iraq. The aim of this study is to identify the genetic polymorphisms of *IGF-1*gene and its association with vertebrate growth and development of some chicken breeds in Iraq.

Key words: *Gallus gallus*, Expect Value, Score, and *IGF-I*

الملخص

يعتبر عامل نمو الانسولين من المنظمات المهمة في تحفيز النمو، تخليق البروتين، والتكاثر والتمايز في مختلف أنواع الخلايا. استخدمت عينات دم من 50 دجاجة جنس *Gallus gallus* من المصابين بتشوهات العظام و 50 عينه من الاصحاء من الحقل الحيواني/ كلية الطب البيطري/ جامعة بغداد. وعزل الحامض النووي الدي اوكسي رايبوزي (DNA) لهذه العينات وتم تضخيم جين عامل نمو الانسولين باستخدام بادئات متخصصه لمنطقه المشغل و 5' UTR لهذا الجين, ثم اجراء تسلسل الاحماض النووية باستخدام جهاز AB13730XL في شركة مايكروجين في الولايات المتحدة الامريكية. أظهرت نتائج تتابع الحامض النووي(الدنا) لجين عامل نمو الانسولين لعينات السيطرة تطابقا بنسبة 100% مع الحمض النووي(الدنا) لجنس *Gallus gallus* عند مقارنتها مع مثيلاتها في البنك الجيني العالمي, و كانت نتائج تسلسل جين عامل نمو الانسولين في 35 عينة من المصابين بتشوه العظام من *Gallus gallus* المعزولة من العراق بنسبة تطابق 99% (وسكور1351 والمتوقع 0.0 مع بنك الجينات العالمي) ويعزى الاختلاف نتيجه نوعين من الطفرات الانقلابية (G>T and T>G) وطفره انتقالية (C>T) في المواقع 404, 104 و 249 حامض نووي وعلى التوالي. لوحظ ان 15 عينة من المصابين بتشوهات العظام من جنس *Gallus gallus* ذات تطابق 99% لوجود طفره انقلابية واحدةG>T ضمن الموقع 404 و طفرة انتقالية (C>T) ضمن الموقع 249. تهدف الدراسة إلى التعرف على التغيرات الوراثية في جين *IGF-I* وعلاقتها بتشوه العظام في بعض السلالات.

الكلمات المفتاحية: دجاج *Gallus gallus*، القيمة المتوقعه، عدد النقاط، *IGF-I* جين

Introduction

The insulin like growth factor gene (*IGF-1*) in chickens is composed of four axons and three introns, spanning more than 50 kb on chromosome 1[1]. Six exons spanning over a large region of the chromosome from 73-85kb constitute the *IGF-I gene* in humans and rats [2]. The *IGF-I* gene in chickens is composed of four exons and three introns, spanning more than 50 kb on chromosome 1[1]. Mature *IGF-I* is spanning 210 bp and encodes a single-chain polypeptide of 70 amino acids. The structure of the *IGF-I* gene is variable among chicken breeds, but the association of this variability with

the phenotypic variation is not yet clear [3,4]. One of the major hormones required to support normal growth and muscle development is insulin-like growth factor I (*IGF-I*) [5]. *IGF-I* is a complex system of peptide hormones that bind to the IGF-I receptor (IGFIR) to activate their intrinsic tyrosine kinase domain activities [6]. Biological responses to *IGF-I* have effects on cell growth, proliferation, differentiation, and survival against apoptosis [7,8]. For example, the *IGF-I* gene can influence growth rate, body composition and lipid metabolism in poultry [9]. The objective of the present study was to identify genetic polymorphisms of IGF-I gene and to find a correlation between the genotypic polymorphisms and the phenotype of vertebrate growth and development of some chicken breeds in Iraq.

Material and Method

Approximately, 3ml venous blood was collected from 50 *Gallus gallus* affected from bone abnormalities (distortion) and 50 samples a control group from the Animal farm / College of Veterinary Medicine / University of Baghdad. DNA was extracted from samples by DNA extraction kit (Genomic DNA Mini Kit, USA, Catalog #:GB 100) according to the manufacturer's protocol. Detection of IGF1(chicken insulin like growth factor 1) gene was conducted by using primers for amplification of *IGF1*gene. A fragment 814bp of *IGF1*was amplified using a forward primer (IGF1F:5′-CATTGCGCAGGCTCTATCTG-3′) [10] and a reverse primer (IGF1R:5′-TGAAGAGAAGCCCTTCAAGC-3′). These primer sets were supplied by IDT(Integrated DNA Technologies) company, Canada. The PCR amplification was performed in a total volume of 25µl containing 1.5µl DNA, 5 µl Taq PCR PreMix (Bioneer, Korea), 1µl of each primer (10 pmol) then distilled water was added into tube to the total volume of 25µl. PCR amplification was conducted under the following conditions: 5 min at 95°C, followed by 35 cycles of 94 °C for 1min, 56°C for 45s, and 72 °C for 1min and a final extension of 72°C for 10 min using a thermal Cycler made by Labnet (Labnet international, Inc, Multi Gene OptiMax, Catalog #: TC9610-230, USA). The PCR products were separated on a 1.5% agarose gel electrophoresis and visualized by exposure to ultraviolet light (302nm) after ethidium bromide staining. Sequencing of IGF1 gene was performed by national instrumentation center for environmental management (nicem) online at http://nicem.snu.ac.kr/main/?en_skin=index.html, biotechnology lab, machine is DNA sequence 3730XL, Applied Biosystem. Homology search was conducted using Basic Local Alignment Search Tool (BLAST) program which is available at the National Center Biotechnology Information (NCBI) online at (http:// www.ncbi.nlm.nih.gov) and Bio Edit program.

Results

The results shown in Figure (1) indicated that a yield of single band of the desired product with a molecular weight of 814bp for promoter region and 5' UTR for IGF1 gene was obtained. The sequencing of IGF1gene amplified product from 50 *Gallus gallus* (control cases) appeared 100% compatibility with standard *IGF1*of Gene Bank results as shown in Figure (2A), (Sequence ID: gb|JF831880.1|), there was no any polymorphism in promoter region and 5' UTR, however, 35 cases of bone abnormalities (Distortion) of *Gallus gallus*, showed 99% compatibility as shown in Figure (2B), (Sequence ID: gb|JX414253.1|), and have low number score (1351) bits than control cases (1352) bits. The bit Score is defined as statistical measure of the moral similarity and the higher value indicates that the high degree of similarity, and if dropped from the class of 50 points, the sense that there is no similarity, shown in Table (1). There was polymorphism in the promoter region, where as two transversion (G>T and T>G) and one transition (C>T) on location 404, 104, and 249, respectability Table (2). And 15 cases of bone abnormalities (Distortion) of *Gallus gallus*, 99% compatibility have one Transversion G>T on position 404 and one transition (C>T) on 249 positions, (Sequence ID: gb|JX414253.1|). (Figure 2Cand Table 1 and 2). All 50 samples of control and 50 bone abnormalities (Distortion) of *Gallus gallus* have the same expectation value (0.0).The expectation value is defined to give an estimate of the number of times expected to get the same similarity coincidental and the lower the value of E. This indicates that the degree of similarity was high between a sequence which gives greater confidence. The value of a very close to zero means that these sequences are identical.

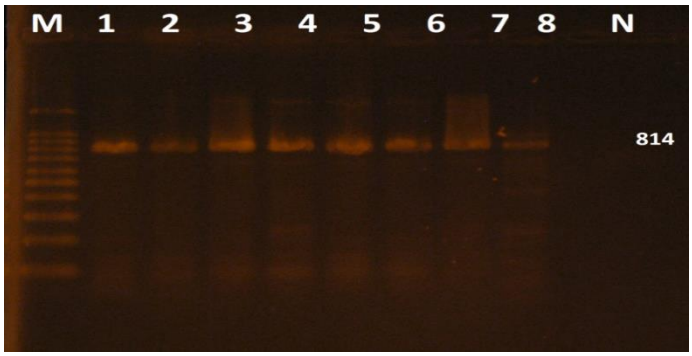

Fig. (1): Amplified *IGF-I* geneproduct run on a 1.5% agarose gel electrophoresis. Bands were fractionated by electrophoresis on a 1.5 % agarose gel (2 h., 5V/cm, 1X Tris-acetic buffer) and visualized under U.V. light after staining with ethidium bromide staining. Amplico sizes are 814 of the specific IGF-1 gene of the promotor region from chicken .Lanes :positive controls from 1,2,3.Lanes 4-8, samples from bone abnormalities from chicken.

A:*Gallus gallus IGF-I* gene, promoter region and 5' UTR, Sequence ID: gb|JF831880.1|

Score	Expect	Identities	Gaps	Strand
1352 bits(732)	0.0	732/732(100%)	0/732(0%)	Plus/Minus

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Query  1    ATTTAGAGAAAATCCTCACATTTATCTACATTACACAGACACTGTAGACAGGAAACAGCT  60
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Sbjct  752  ATTTAGAGAAAATCCTCACATTTATCTACATTACACAGACACTGTAGACAGGAAACAGCT  693
Query  61   GGGGGAGCATTTGCCTtctctctctctcCCTCTTCTGGCAAAGTTACCGAGTAAGGACTT  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  692  GGGGGAGCATTTGCCTTCTCTCTCTCTCCCTCTTCTGGCAAAGTTACCGAGTAAGGACTT  633
Query  121  TTTTGGGCATGGTGACAAATAACATCATACCTTTGCATTTTAAAACTAGAGCACAGAAGC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  632  TTTTGGGCATGGTGACAAATAACATCATACCTTTGCATTTTAAAACTAGAGCACAGAAGC  573
Query  181  ATATTTTTTCCCCTTTAAAAGAATGTGAATTAGTGACTGAGGGGTTAGCAGGCAAAAAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  572  ATATTTTTTCCCCTTTAAAAGAATGTGAATTAGTGACTGAGGGGTTAGCAGGCAAAAAAG  513
Query  241  CTTACGCTGCCACGGAAAATAAGGGAATGTATTCTGGTTAACTTTCGGGTGGCTGTGTGT  300
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Sbjct  512  CTTACGCTGCCACGGAAAATAAGGGAATGTATTCTGGTTAACTTTCGGGTGGCTGTGTGT  453
Query  301  ATATTTGCATTTTTGTGTGTATGTGTCTGCTTTTCAAATAGACAAAAACTTCCATAGGTG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  452  ATATTTGCATTTTTGTGTGTATGTGTCTGCTTTTCAAATAGACAAAAACTTCCATAGGTG  393
Query  361  AAGACATTGTCTGTATACCTTTATATTCCTGTGTACATCTGTGCACATTTCATTCATGCA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  392  AAGACATTGTCTGTATACCTTTATATTCCTGTGTACATCTGTGCACATTTCATTCATGCA  333
Query  421  GAGACACAGGTATTTTATTTATTTCAttttttttttAACCTAGAGAGACAGGCAGGCAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  332  GAGACACAGGTATTTTATTTATTTCATTTTTTTTTTTTAACCTAGAGAGACAGGCAGGCAG  273
Query  481  TTTACTTTGTTTTAAATGCATCTTTACGTTATTAAACTTGGCACGCCTACATGCTGACTA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  272  TTTACTTTGTTTTAAATGCATCTTTACGTTATTAAACTTGGCACGCCTACATGCTGACTA  213
Query  541  ACAATTAAAACCTCTGACTCTCTGTGCTATTAACCCTAAAATAGCAGTTTGTAATTTGCT  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  212  ACAATTAAAACCTCTGACTCTCTGTGCTATTAACCCTAAAATAGCAGTTTGTAATTTGCT  153
Query  601  AAAAGTAAAAGAGTTGTTGAGCACTGCTTGTAAATAGAGCAAAACAGCGCTGCGATCCTT  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  152  AAAAGTAAAAGAGTTGTTGAGCACTGCTTGTAAATAGAGCAAAACAGCGCTGCGATCCTT  93
Query  661  TAGCAACCACACAGAAGTCATGCAATTTCCTAGAATTTACAGTACTATGAATGTAGTAAC  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  92   TAGCAACCACACAGAAGTCATGCAATTTCCTAGAATTTACAGTACTATGAATGTAGTAAC  33
Query  721  TCAAGTAGCCCA  732
            ||||||||||||
Sbjct  32   TCAAGTAGCCCA  21
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B:*Gallus gallus* IGF1-2 gene, promoter region and 5' UTR, Sequence ID: gb|JX414253.1|

Score	Expect	Identities	Gaps	Strand
1351 bits(731)	**0.0**	**737/740(99%)**	**0/740(0%)**	**Plus/Minus**

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Query  1    GGGATTTAGAGAAAATCCTCACATTTATCTACATTACACAGACACTGTATACAGGAAACA  60
            |||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  753  GGGATTTAGAGAAAATCCTCACATTTATCTACATTACACAGACACTGTAGACAGGAAACA  694
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Query  61GCTGGGGGAGCATTTGCCTtctctctctctcCCTCTTCTGGCAAAGTTACCGAGTAAGGA  120
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Sbjct  693 GCTGGGGGAGCATTTGCCTTCTCTCTCTCTCCCTCTTCTGGCAAAGTTACCGAGTAAGGA  634
Query  121 CTTTTTTGGGCATGGTGACAAATAACATCATACCTTTGCATTTTAAAACTAGAGCACAGA  180
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  633CTTTTTTGGGCATGGTGACAAATAACATCATACCTTTGCATTTTAAAACTAGAGCACAGA  574
Query  181 ATCATATTTTTTCCCCTTTAAAAGAATGTGAATTAGTGACTGAGGGGTTAGCAGGCAAAA  240
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  573 ATCATATTTTTTCCCCTTTAAAAGAATGTGAATTAGTGACTGAGGGGTTAGCAGGCAAAA  514
Query  241 AAGCTTACGCTGCCACGGAAAATAAGGGAATGTATTCTGGTTAACTTTCGGGTGGCTGTG  300
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  513 AAGCTTACGCTGCCACGGAAAATAAGGGAATGTATTCTGGTTAACTTTCGGGTGGCTGTG  454

Query  301 TGTATATTTGCATTTTTGTGTGTATGTGTCTGCTTTTCAAATAGACAAAAACTTCCATAG  360
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  453 TGTATATTTGCATTTTTGTGTGTATGTGTCTGCTTTTCAAATAGACAAAAACTTCCATAG  394
Query  361 GTGAAGACATTGTCTGTATACCTTTATATTCCTGTGTACATCTGTGCACATTTCATTCAT  420
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  393 GTGAAGACATTGTCTGTATACCTTTATATTCCTGTGTACATCTGTGCACATTTCATTCAT  334
Query  421GCAGAGACACAGGTATTTTATTTATTTCAttttttttAACCTAGAGAGACAGGCAGGCA  480
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  333 GCAGAGACACAGGTATTTTATTTATTTCATTTTTTTTTAACCTAGAGAGACAGGCAGGCA  274
Query  481 GTTTACTTTGTTTTAAATGCATCTTTACGTTATTAAACTTGGCACGCCTACATGCTGACT  540
       |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  273GTTTACTTTGTTTTAAATGCATCTCTACGTTATTAAACTTGGCACGCCTACATGCTGACT  214
Query  541 AACAATTAAAACCTCTGACTCTCTGTGCTATTAACCCTAAAATAGCAGTTTGTAATTTGC  600
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  213 AACAATTAAAACCTCTGACTCTCTGTGCTATTAACCCTAAAATAGCAGTTTGTAATTTGC  154
Query  601 TAAAAGTAAAAGAGTTGTTGAGCACTGCTTGTAAATAGAGCAAAACAGCGCTGCGATCCT  660
       |||||||||||||||||||||||||||||||||| ||||||||
Sbjct  153 TAAAAGTAAAAGAGTTGTTGAGCACTGCTTGTAAATAGAGCAAAACAGCTCTGCGATCCT  94
Query  661 TTAGCAACCACACAGAAGTCATGCAATTTCCTAGAATTTACAGTACTATGAATGTAGTAA  720
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  93  TTAGCAACCACACAGAAGTCATGCAATTTCCTAGAATTTACAGTACTATGAATGTAGTAA  34
Query  721 CTCAAGTAGCCCAGCTTGAA  740
       ||||||||||||||||||
Sbjct  33  CTCAAGTAGCCCAGCTTGAA  14
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C:Gallus gallus IGF1-2 gene, promoter region and 5' UTR, Sequence ID: gb|JX414253.1|

Score	Expect	Identities	Gaps	Strand
1352 bits(732)	0.0	736/738(99%)	0/738(0%)	Plus/Minus

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Query  1   AGGGATTTAGAGAAAATCCTCACATTTATCTACATTACACAGACACTGTAGACAGGAAAC  60
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Sbjct  754 AGGGATTTAGAGAAAATCCTCACATTTATCTACATTACACAGACACTGTAGACAGGAAAC  695
Query  61AGCTGGGGGAGCATTTGCCTtctctctctctcCCTCTTCTGGCAAAGTTACCGAGTAAGG  120
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  694 AGCTGGGGGAGCATTTGCCTTCTCTCTCTCTCCCTCTTCTGGCAAAGTTACCGAGTAAGG  635
Query  121 ACTTTTTTGGGCATGGTGACAAATAACATCATACCTTTGCATTTTAAAACTAGAGCACAG  180
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  634 ACTTTTTTGGGCATGGTGACAAATAACATCATACCTTTGCATTTTAAAACTAGAGCACAG  575

Query  181 AATCATATTTTTTCCCCTTTAAAAGAATGTGAATTAGTGACTGAGGGGTTAGCAGGCAAA  240
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  574 AATCATATTTTTTCCCCTTTAAAAGAATGTGAATTAGTGACTGAGGGGTTAGCAGGCAAA  515
Query  241 AAAGCTTACGCTGCCACGGAAAATAAGGGAATGTATTCTGGTTAACTTTCGGGTGGCTGT  300
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  514 AAAGCTTACGCTGCCACGGAAAATAAGGGAATGTATTCTGGTTAACTTTCGGGTGGCTGT  455
Query  301 GTGTATATTTGCATTTTTGTGTGTATGTGTCTGCTTTTCAAATAGACAAAAACTTCCATA  360
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  454 GTGTATATTTGCATTTTTGTGTGTATGTGTCTGCTTTTCAAATAGACAAAAACTTCCATA  395
Query  361 GGTGAAGACATTGTCTGTATACCTTTATATTCCTGTGTACATCTGTGCACATTTCATTCA  420
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  394 GGTGAAGACATTGTCTGTATACCTTTATATTCCTGTGTACATCTGTGCACATTTCATTCA  335
Query  421TGCAGAGACACAGGTATTTTATTTATTTCAttttttttAACCTAGAGAGACAGGCAGGC  480
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  334 TGCAGAGACACAGGTATTTTATTTATTTCATTTTTTTTTAACCTAGAGAGACAGGCAGGC  275
Query  481 AGTTTACTTTGTTTTAAATGCATCTTTACGTTATTAAACTTGGCACGCCTACATGCTGAC  540
       |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  274 AGTTTACTTTGTTTTAAATGCATCTCTACGTTATTAAACTTGGCACGCCTACATGCTGAC  215
Query  541 TAACAATTAAAACCTCTGACTCTCTGTGCTATTAACCCTAAAATAGCAGTTTGTAATTTG  600
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  214 TAACAATTAAAACCTCTGACTCTCTGTGCTATTAACCCTAAAATAGCAGTTTGTAATTTG  155
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Query  601  CTAAAAGTAAAAGAGTTGTTGAGCACTGCTTGTAAATAGAGCAAAACAGCGCTGCGATCC  660
            ||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  154  CTAAAAGTAAAAGAGTTGTTGAGCACTGCTTGTAAATAGAGCAAAACAGCTCTGCGATCC   95
Query  661  TTTAGCAACCACACAGAAGTCATGCAATTTCCTAGAATTTACAGTACTATGAATGTAGTA  720
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Sbjct  94   TTTAGCAACCACACAGAAGTCATGCAATTTCCTAGAATTTACAGTACTATGAATGTAGTA   35
Query  721  ACTCAAGTAGCCCAGCTT                                            738
            ||||||||||||||||
Sbjct  34   ACTCAAGTAGCCCAGCTT  17
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Fig. (2): A: Sequencing of sense flanking the partialIGF1-2 gene, promoter region and 5' UTR for 50 cases *Gallus gallus* as compared with standard IGF1-2 gene, promoter region and 5' UTR obtained from Gene Bank. B: Sequencing of sense flanking the partial*IGF1-2* gene, promoter region and 5' UTR for 35 cases Bone Abnormalities (Distortion) of *Gallus gallus* as compared with standard *IGF1-2* gene, promoter region and 5' UTR obtained from Gene Bank. C: Sequencing of sense flanking the partial*IGF1-2* gene, promoter region and 5' UTR. for15 cases Bone Abnormalities (Distortion) of *Gallus gallus* as compared with standard *IGF1-2* gene, promoter region and 5' UTRobtained from Gene Bank. Query represents of sample; Subject represent of database of National Center Biotechnology Information (NCBI).

Table (1): Sequencing ID in gene bank, score, expect and compatibility of DNA sequences obtained.

	Organism	Sequence ID	Score	Expect	compatibility	No.Nucleotide
1	Gallus gallus (Control group)	gb|JF831880.1	1352	0.0	100	21-752
2	Gallus gallus (Bone Abnormalities)	gb|JX414253.1|	1351	0.0	99	14-753
3	Gallus gallus (Bone Abnormalities)	gb|JX414253.1|	1352	0.0	99	14-753

Table (2): Represent type of polymorphism in promoter region, 5UTR of *IGF1* gene for Bone Abnormalities (Distortion) of *Gallus gallus*.

	Change	Location of substitution	Type of substitution	No. of sample	Frequency 100%
1	G>T	704	Transversion	15	30
2	C>T	249	Transition	50	100
3	T>G	104	Transversion	50	100

Discussion

The *IGF* are important regulators in stimulating growth, protein synthesis, and cell proliferation and differentiation in a variety of cell types [11,12]. Single nucleotide polymorphisms (SNP), one base change including deletion, insertion, and substitution, play an important role in the transcription and translation of genes and affect function of protein, Laere, *et al*., [13] reported that a mutation in the *IGF2*gene acts as a major QTL that affects muscle growth in the pigs, Nagaraja, *et al.*,[14] to polymorphism in 5′-untranslated region of the chicken *IGF1* gene is significantly associated with lower egg weight and higher egg shell weight. Amills, *et al.*,[4] reported that polymorphism in the promoter region was associated with growth rate and feed efficiency. Zhou, *et al*., [15] showed that polymorphism in the promoter and 5'-untranslated region (5'-UTR) of the *IGF-I* gene was associated with growth and carcass traits. Also, Bian, *et al.*,[16] reported that haplotypes based on three *IGF-I* polymorphisms (5'-flanking, exon 3, and 3'-flanking regions) were associated with body weight traits, and Promwatee and Duangjinda [17] and Promwatee *et al.*, [18], found that polymorphism at 5'-UTR of the *IGF-I* gene was associated with body weight and carcass traits of synthetic chickens. Gouda and Essawy, [19], shown evaluate the transcript expression pattern of avian *IGF-I* polymorphism, and their effect on the growth traits of chickens by SSCP analysis of RT-PCR products. Consequently, the purpose of the present study was to investigate the possibility of using the *IGF-I* gene at promoter and the 5'-UTR for 1) studying the variation of the *IGF-I* gene; and 2) studying the associations of *IGF-I* gene polymorphism with vertebrate growth and development.

References:

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