# In silico Analysis of "Interferon Beta 1" In some Selected Animal Species

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## Abstract

Type I interferons (IFNs), are considered as a main host immune system cytokines effector against infectious virus. In addition to ‖i‖nnat‖eim‖munerecep‖torbac‖teriallig‖ands and/or bact‖erial infections. Furthermore, th‖e development o‖f kinds I‖F‖Ns are a‖ls‖o triggered, suggesting a wider physiological function f‖or those cy‖tok‖linesi‖nhom‖eostaisi and h‖ostprote‖ctionth‖an initially expected. Results: To recognize both structural divergence and sequence various bioinformatics methods were used. Initial sequence analysis of IFNß1 showed that they shared with human over 70% similarity and some identity like Rhesus monkey, pig , domestic cat ,for dog. With few exceptions, sequences showed a high degree of sequence preservation. The physico-chemical analysis indicated a large developmental difference between humans and others and an estimate of 39% to 42% of hydrophobic residues. Four human mammals house mouse pig Norway rat have various Pfam types. The secondary structure of IFNß1 composed of ran‖domco‖il, Exv‖tendedstr‖anda‖ndAl‖phahe‖lix. Conclusions: Depending o‖nth‖eres‖ults collected, which maybe assumed th‖at in these mammalian species IFNß1 has the same counterpart, highly retained and functional similarities.

***Keywords:*** *Interferons, h‖ostprote‖ctionth, cy‖tok‖lines, divergence, counterpart.*

## Introduction

Type I interferons (IFN) play an essential role in the defense of antivirals and are formed in a variety of cells following viral infection. It is understood that IFN-a / b therapy of immature dendritic cells (DC) causes their phenotypic and functional maturation1Interferons (IFNs) are a group of cell-produced pleiotropic cytokines in reaction to viral infections[1]. Such cytokines have antiviral, immunomodulatory, and antitumor properties by regulating the expression of hundreds of genes involved in critical biological processes such as progression of the cell cycle, cell proliferation, and apoptosis[2]. Some cells, such as endot‖helialce‖lls, osteo‖blastsin‖rea‖ction, lymph‖ocytes, fibrob‖lasts and macr‖ophages (N‖Kce‖lls, T-c‖ells and B-ce‖lls) t‖opat‖hogen‖s, are secreting IFNßs. Through expression of several genes, they enable NK cells and MFs to elicit immunomodulatory, antiviral, antitumor, and anti-inflammatory responses[3] including response to therapy. A number of disease modifying drugs, including traditional first line agents such as, interferon-beta (IFN-β.

"Anti-viral behavior is Type IIFNs7's first physiological intervention [4] .IFNß refers to the host defense at the early stage. In cell cultures, virus-infected cells can produce and secrete IFNß. A mutant mice study with an IFNß knockout gene demonstrated hight in immunity to diseases of viruses [5]. Th.e sum of an.tiv. iral activities de.pendo.nth.etyp.eo.f the vir.usesa.nd the h.vostce.ll[6]. Anti-tumor action is predominantly mediated by IFNß's effect on apoptosis, proliferation or cell cycle, a.ndin.direct.l.yb.y immune system a.ct.iva. tio.n[8]. Three different methods mediate its anti-tumor activities: (1) anti-proliferative effects, (2) altered cells fatal differentiation, (3) antigens alteration in the tumor cell surface leading to immune system inductions. IFNß has more proliferative properties than other IFNs[9]. Inflammation is energetic parts of the inherent immunes systems in reaction to endogenous and toxins risk signal. The provocative reaction must be severely regulated; anything else, the secretion or oxidation of lytic enzymes can cause irreversible damage to tissues[6].

## Materials and Method

2.1 Recovery or analysis of sequences

Nucleotides and amino acid sequences of Musmusculus (house mouse), Homo sapiens(human), Rattusnorvegicus (Norway rat), Susscrofa (pig), Macacacamulatta (Rhesus monkey), Feliscatus (home cat) and Canis lupus familiaris (dog) have been extracted from NCBI. For obtain related sequences in other species, the Basic Local Alignment Selection Tool (BLAST) was used. Seven IFNB1 protein mammalian species were considered for study. N.‖C.‖B.‖IG‖e‖n. ‖B‖an‖k (‖w.‖w`w.nc‖.‖bi.nl‖m.ni‖h.g‖o‖‖v/g‖en‖bank) obtained three classifications i‖nfas‖‖tafor‖ma‖t.

2.2 Determination of personality and similarity percentage.‖

The percentage of identity and similarity in domestic cat, human, dogv house mouse, Norway rat, pig and Rhesus monkey amo‖ng the a‖minoac‖id‖series of the IFNB1 genes were identified by showing a pair sequence com‖parison by us‖ingB‖‖L‖A‖S‖T.

2.3 IFNB1 Protein Physicochemical Properties Determination

*"*The prot‖eomicdatab‖ase of th‖e (S‖I‖B) (w‖eb. ex‖pasy. or‖g), to use the (E‖xPASy), physicochemical properties of the seven mammalian species IFNB1 protein was defined. Protein analysis was performed on the web server Pep‖tide 2‖.‖0 (ht‖tp:/pe‖ptide2.co‖m/‖Np ep‖tideh‖ydro‖phobicityhy‖drophil‖icity.p‖h‖p), whereas humans were us‖eda‖s references points.*"*

Results

IFNB1gene sequences of nucleotides and amino acids recovered:

Variations were shown in the distances of the amino acid sequences and retrieved nucleotide. The length of the IFNB1gene nu‖cleotideseq‖uences ranged from 555-839 bps while the amino acid sequence length differed from residues of 182-187 amino acids. Among the seven selected mam‖mals, th‖‖elen‖gtho‖vfth‖e human IFNB1 nuc‖leo‖tidesequ‖ences were the longs‖est (839bps), foll‖owedb‖y the house mouse (750bps) and the shortest (555bps) of the Norway rat. The residues of amino acids were the same for Rhesus monkey and human (187). 186amino acid residues respectively, in pig, dog and domestic cat. Residue of shorter amino acids for house mouse (Table 1).

**Table.1. The distances of the amino acid sequences and retrieved nucleotide.**

| Species | Gene name | Gen accession | base pair (bp) | Amino acid length |
|---|---|---|---|---|
| Homo sapiens<br>human | interferon beta 1<br>IFNB1 | NP_002167 | 839 | 187 |
| Musmusculus<br>house mouse | interferon beta 1<br>IFNB1 | NP_034640 | 750 | 182 |
| Susscrofa<br>pig | interferon beta 1<br>IFNB1 | NP_001003923 | 561 | 186 |
| Rattusnorvegicus<br>Norway rat | interferon beta 1<br>IFNB1 | NP_062000 | 555 | 184 |
| Macacamulatta<br>Rhesus monkey | interferon beta 1<br>IFNB1 | NP_001129267 | 564 | 187 |
| Feliscatus<br>domestic cat | interferon beta 1<br>IFNB1 | NP_001009297 | 561 | 186 |
| Canis lupus familiaris<br>dog | interferon beta 1<br>IFNB1 | NP_001129259 | 561 | 186 |

**Ph.ysicochem. .icalP.rop.ertieso.‖f I.F.NB1Prot. eins:**

T.h‖.e IFNB1protein ana.l‖ysi.so‖.f selected mammals showed, when compared, changing ph.ysic. och‖emi.c‖al things. T‖here‖sultsexpose‖edth‖at pig IFNB1protein (4.93) was the least theoretical pl, while house mouse IFNB1 protein (9.69) was the highest. Th‖em.olec.ula.rwei.g‖htso‖f IFNB1proteins fr.o‖‖mth‖.e seven mam.‖ma.lian spe.c‖i.es showed th‖at the weight of human IFNB1protein was 22293.88kDa, while the weight of dog IFNB1protein was 22387.92 kDa. The weight of the pig protein was 21950.46kDa, the least. The percentages Hydrophobic residues in IFNB1protein of the species showed the following: human (39.57%), house mouse (42.31%), domestic cat (40.32%). The Norway rat (40.76%), Rhesus monkey (40.64%) and pig (42.47%) higher percentage (Table 2).

**Table. 2.IFNB1protein analysis selected mammals showed, compared, changing physic chemical things.**

| | **human** | **house mouse** | **pig** | **Norway rat** | **Rhesus monkey** | **domestic cat** | **dog** |
|---|---|---|---|---|---|---|---|
| Number of amino acids | 187 | 182 | 186 | 184 | 187 | 186 | 186 |
| Molecular weight | 22293.88 | 22126.77 | 21950.46 | 22072.56 | 22315.93 | 22187.64 | 22387.92 |
| Theoretical pI | 8.93 | 9.69 | 4.93 | 9.73 | 8.76 | 6.44 | 5.86 |
| Instability index | 47.91 | 37.93 | 62.91 | 37.43 | 47.75 | 42.90 | 51.85 |
| Aliphatic index | 99.63 | 92.14 | 99.57 | 91.63 | 95.99 | 96.94 | 104.84 |
| Hydrophobic residues | 39.57% | 42.31% | 42.47% | 40.76% | 40.64% | 40.32% | 39.78% |
| Acidic residues | 9.63% | 8.79% | 13.44% | 8.15% | 10.16% | 12.37% | 13.44% |
| Basic residues | 14.97% | 15.38% | 10.75% | 14.67% | 14.97% | 13.98% | 13.98% |
| Neutral residues | 35.83% | 33.52% | 33.33% | 36.41% | 34.22% | 33.33% | 32.8% |

**IFNB1Gene Secondary Protein Structures:**

For the seven chosen mammalian species, GORIV software was used to predict the secondary structures of IFNB1 protein. Their IFNB1 protein is shown to contain mainly random coil, extended strand and alpha helix. Though, the human IFNB1protein alp‖hah‖e‖lixw‖as 43.85 percent, while mammals were 69.78 percent higher for house mouse. The leastiwasithe pig with 41.94 % of the design in alpha helix. In addition, th‖e IFNB1 protein expanded strand for humans was the longest (23.53%) with the dog being the shortest (10.22%). Variations have been found on the unexpected coils of th‖e seven species additional‖arystru‖ctureso‖fIFNB1protein with th‖e random coil of pig IFNB1protein occupying 41.94% of the structure relative to other mammals (Table 3.).

**Table .3 secondary structures of IFNB1 protein**

| Elements | human | house mouse | pig | Norway rat | Rhesus monkey | domestic cat | dog |
|---|---|---|---|---|---|---|---|
| Alpha helix | 43.85% | 69.78% | 41.94% | 50.54% | 50.27% | 52.15% | 56.99% |
| 310 helix | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% |
| Pi helix | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% |
| Beta bridge | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% |
| Extended strand | 23.53% | 10.99% | 16.13% | 12.50% | 18.18% | 16.67% | 10.22% |
| Beta turn | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% |
| Bend region | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% |
| Random coil | 32.62% | 19.23% | 41.94% | 36.96% | 31.55% | 31.18% | 32.80% |
| Ambiguous states | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% |
| Other states | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% | 0.00% |

## Discussion

Type I interferons (IFN) are a group of cytokines expressed under physiological conditions at low levels or induced by stimuli such as viral infection to high levels[7]. Form I IFN includes a number of evolutionary proteins produced by closely related and connected genes, the major species being several IFN-a subtypes and a single IFN-b [8]. Here we note that sequence lengths of nucleotide amino acids varying from the human, house mouse, pig Norway rat, Rhesus monkey, domestic cat, and dog gene IFNB1. It is also claimed that variations in the sequence length are induced by mutations in the indels, which may had collected through evolution.

As a results, the percentage of human, house mouse, pig, Norway rat, Rhesus monkey, domestic cat and dog identity ranged from 48.7-95.2 percent compared to thlatolfhulman IFNB1 amilnoaclids, viewing that they might have related evolutionary strategies. This is also the situation with percentage similarity (62-97.9 %). Importantly, sequences of approximately 70 percent percent similarity indicate the IFNB1 gene has the same homology, similarities of function And the preservation is very high. Iln addition, Xu and Joshi [9] reported that if two samples have a sequencing similarity higher than 70%, it is proposed that they have been inclined to share approximately 90% or more of the same functions and biological processes. Protleinsiln the samlegroluphalve a sequlencesimillarity of at lelastmolrethaln 30 % of alminoaciids. "In clinicians with relapsing multiple sclerosis[10][11] and in patients with chronic hepatitis C infection virus [12][13], IFNβ treatment significantly improved the rate and suppressive activity of TReg cells, and also decreased expression of Foxp3 mRNA in PBMCs in patients with recurrence-remitting multiple sclerosis[14][15].

"NLRP1 and NLRP3 inflammasomes are directly inhibited by IFNβ signaling) in an STAT1-dependent manner. Second, IFNs of type I induced IlL-10 production whlichiln effect actuated the STAT3 transcriptlion factors iln an autocrinemanner[16]. Type I IFNs was tested as IBD therapy. Although some medical therapy studies initially showed promising results in patients with ulcerative colitis1[17][18]."

It may depend on the conduct' motives. Thus stressing the adequacy of the phylogenetic tree, the mammalian species separation period represents Stone et al previous reports. [28].

"GRAVY value greater than zero, according to Kyte and Doolittle[19] indicated a enzyme very hydrophobic. Though, for seven mammals IFNB1 proteinThe values of GRAVY gained in the present study are less than zero, implying that they are in nature rather hydrophilic."

In all the seven mammalian species mentioned in this study, the fact that IFNB1 protein has lower damagingly exciting remains than positive exciting remains renders IFNB1 proteins intracellular in these animals[20]

According to Guruprasad et al, the coefficient of validity, that is the measurement of a protein stability in vitro when it reaches[34]NMT sequences and 3D structures has revealed motif properties in addition to the known PROSITE motif that are utilized in a new predictor described here. The composite prediction function (with separate ad hoc parameterization (a, then he indicates that the protein may be safe [21] This is attributed, as stated by Devi et al. [22] to the surplus tyrosine that results in the structure of the disulfide bonds relationship in the protein molecule. Regrettably, we show a measurement of validity greater than 50, suggesting that this protein is likely to be in vitro defective. Our finding revealed that secondary elements on the mammalian species subordinate structures of the seven IFNB1 protein were alpha-helix, expanded strand and the spontaneous coils. These are the three mechanisms were involved in the protein folding stability and function.

## Conclusion

Structural analysis and sequence of seven mammals indicated regions correlated with evolution and structure. In addition to the variation of retained amino acid sequences from the physico-chemical properties in the active site, preservation may lead to the functional heterogeneity in a few amino acid substitutions at the respective site. Because IFNß1 has a role in immunomodulatory, antiviral, anti-tumor effects are very significant inflammatory protein conditions, the studies on it will lead to further research into proteomics.

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**Ethical Clearance:** This study is ethically approved by the Institutional ethical Committee.

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