

Protein Multifunctionality: Principles and Mechanisms

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Abstract: In the review, the nature of protein multifunctionality is analyzed. In the first part of the review the principles of structural/functional organization of protein are discussed. In the second part, the main mechanisms involved in development of multiple functions on a single gene product(s) are analyzed. The last part represents a number of examples showing that multifunctionality is a basic feature of biologically active proteins.

Keywords: protein, structure, function, multifunctionality

I. Main Principles of Protein Organization: Structural Compactness and Functional Variability

1. General consideration on the factors determining protein multifunctionality

The cell fulfills two main functions: (1) storage of genetic information and transfer it to the next cell generation; (2) synthesis of different molecules, protein molecules in particular, for fulfillment of numerous cell processes.

The compactness (maximum information packed in minimum DNA space) is one of the main principles of genetic information storage. The fulfillment of the first cell function is based on this principle. On the contrary, the abundance, variability and diversity of the protein molecules are necessary for realization of the second function. In contrast to DNA, proteins exhibit an apparently unlimited variety of structure. This is a necessary requirement of the vast array of different functions that they perform in maintenance of life “in contrast to the relatively static archival function of DNA” (Lesk, 2001). In the protein world, not only “a bewildering variety of form is observed but even within a common structure, there is variation in the lengths and orientation of substructures. Such variation is both a reflection of the very long evolution of protein structures and also a consequence of the fact that proteins cannot be completely rigid bodies but must have flexibility to accommodate the structural changes that are almost always necessary for them to perform their functions” (Lesk, 2001).

All multiple variations in protein structures and functions are genetically determined by DNA sequence fixed in amino acid primary structure of a protein and can be achieved by different mechanisms operating at different levels.

At the level of *genome*, a single gene may undergo duplication followed by rearrangement and/or mutations thus leading to appearance of homologous proteins possessing partially similar and/or different functions (Fig. 1, A).

At the next level of variability and complexity, *transcriptome* level, the gene transcription can be altered by several mechanisms including usage of alternative promoters, different transcription initiation sites, mRNA splicing and mRNA stability (Fig. 1, B). The extent of variability that may be obtained by mRNA alternative splicing is almost unlimited. An excellent example of this statement is the *Drosophila* gene *Dscam*, encoding Down syndrome cell-adhesion protein. Alternative splicing of *Dscam* pre-mRNA potentially generates 38 016 isoforms of a cell-surface recognition protein (Schmucker et al. 2000; Zipursky et al. 2006).

Further complexity is observed at the *proteome* level. A variety of the protein products encoded by the same gene can be achieved by three groups of specific mechanisms: those operating at the translational

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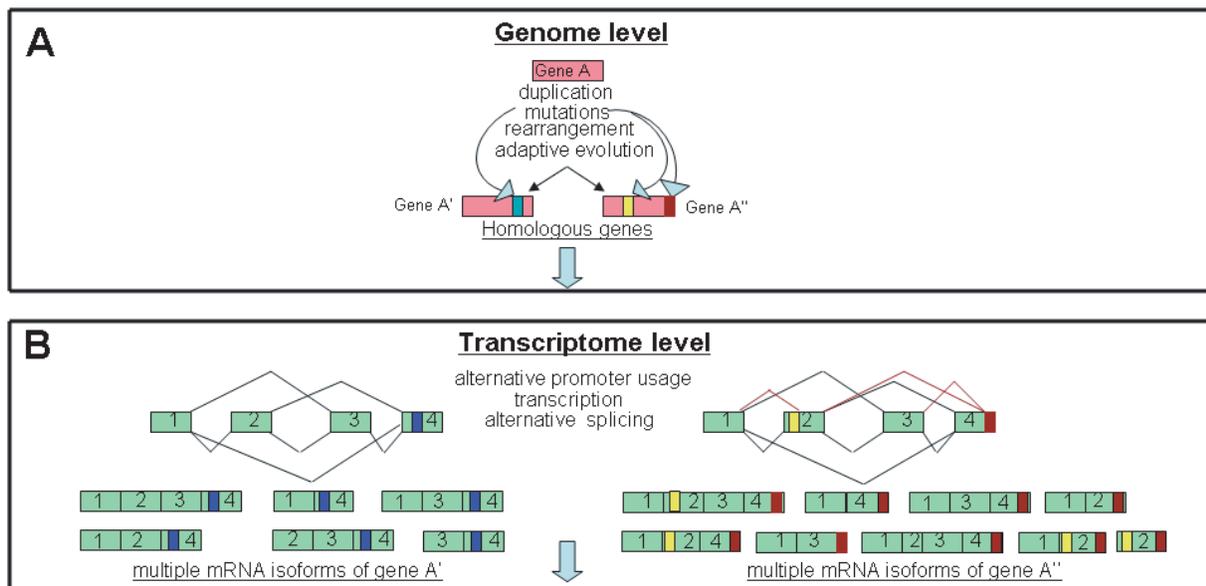
level; the mechanisms that determine post-translational modifications and mechanisms controlling the intermolecular interactions. Multiple translation products can be synthesized by usage of different cap-dependent and cap-independent internal ribosome entry site (IRES) determined initiation mechanisms (Fig. 1, C) including leaky scanning, ribosome-shunting, termination-initiation and mix (or alternative) initiation (Cai et al. 2006; Candeias et al. 2006; Holcik et al. 2000; Huez et al. 1998; Kochetov, 2006; Kozak, 2002; Lu et al. 2004; Yueh and Schneider, 1996). At elongation stage of protein synthesis, frameshifting and “hopping” (Fig. 1, D) also make substantial impact in protein diversity (Atkins et al. 2001; Herr et al. 2000b; Namy et al. 2004). Stop codon readthrough (Fig. 1, E) is the main mechanism that determines appearance of new protein isoforms at the last stage of translation (Keeling et al. 2004; Namy et al. 2002).

Post-translation modifications of the primary polypeptide molecule (Fig. 1, F) include such mechanisms as different types of glycosylation, phosphorylation, acylation, specific restricted proteolysis, protein splicing and many others (Hanada et al. 2004; Rehfeld and Goetze, 2003). The intermolecular interactions that modify protein properties and functions occur between protein and metal, protein and carbohydrate, protein and lipid and protein and protein. These interactions lead to multiple folding variants which in their turns determine topology and functions of multiple products encoded by one and the same gene.

It is important to underline once again that all possible modifications and interactions of a given gene product(s) are encoded in its nucleotide sequence and, as a consequence, in amino acid structure of polypeptide molecule(s). The reactions described above are based on the natural mechanisms by which condensed genetic information can be transformed into variable and multiple protein structures and functions.

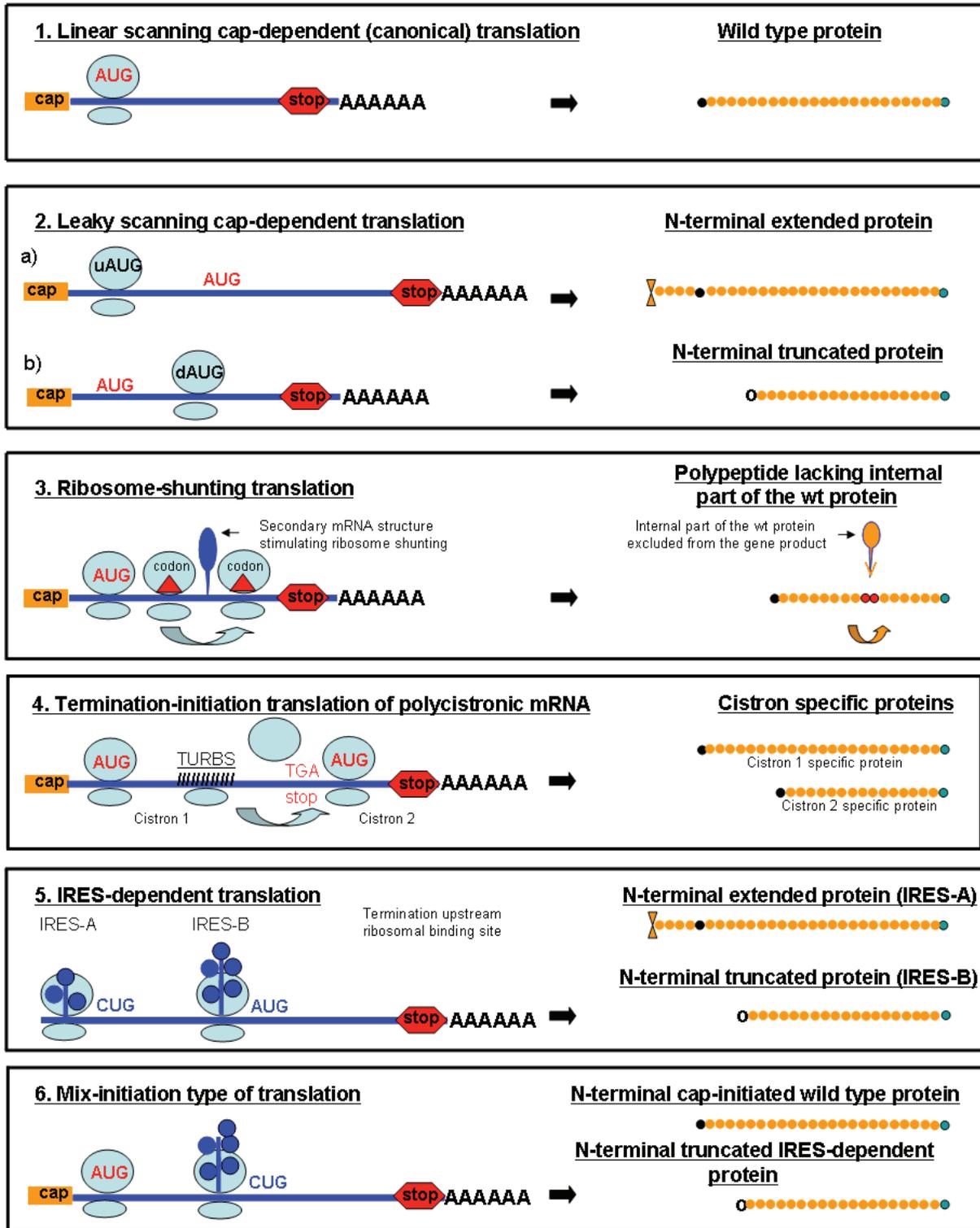
The wisdom of Nature [G-d] is that it does not create anything without specific purpose. There is nothing in nature what is superfluous or unnecessary. This is the main principle of nature. If amino acid sequence of a protein contains genetically determined possibilities for any type of modifications (by proteolysis, folding, glycosylation, phosphorylation etc), there should be definite conditions in a definite cell or tissue in an appropriate point of time which would allow realization of the encoded modifications.

Although the principle of structural and functional compactness is the most evident in nucleic acids, it would be mistake to think that this principle does not work in protein molecules. Actually, the genetic information contained in the DNA sequence is realized in two ways: each protein molecule produced by a gene contains maximum of functional possibilities, and each gene produces as much protein molecules as necessary for performing all functions encoded by the gene. These principles lead to multifunctionality of protein molecules. The following example from the virus



C

Proteome level
Initiation stage

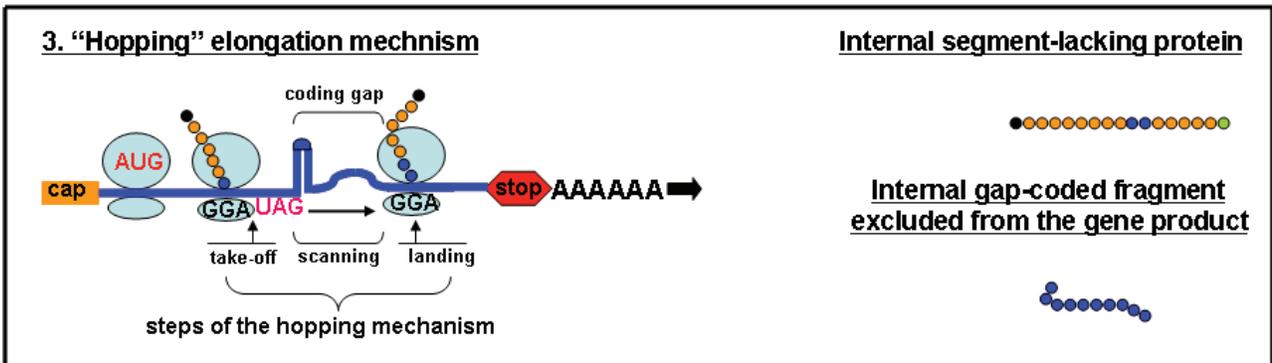
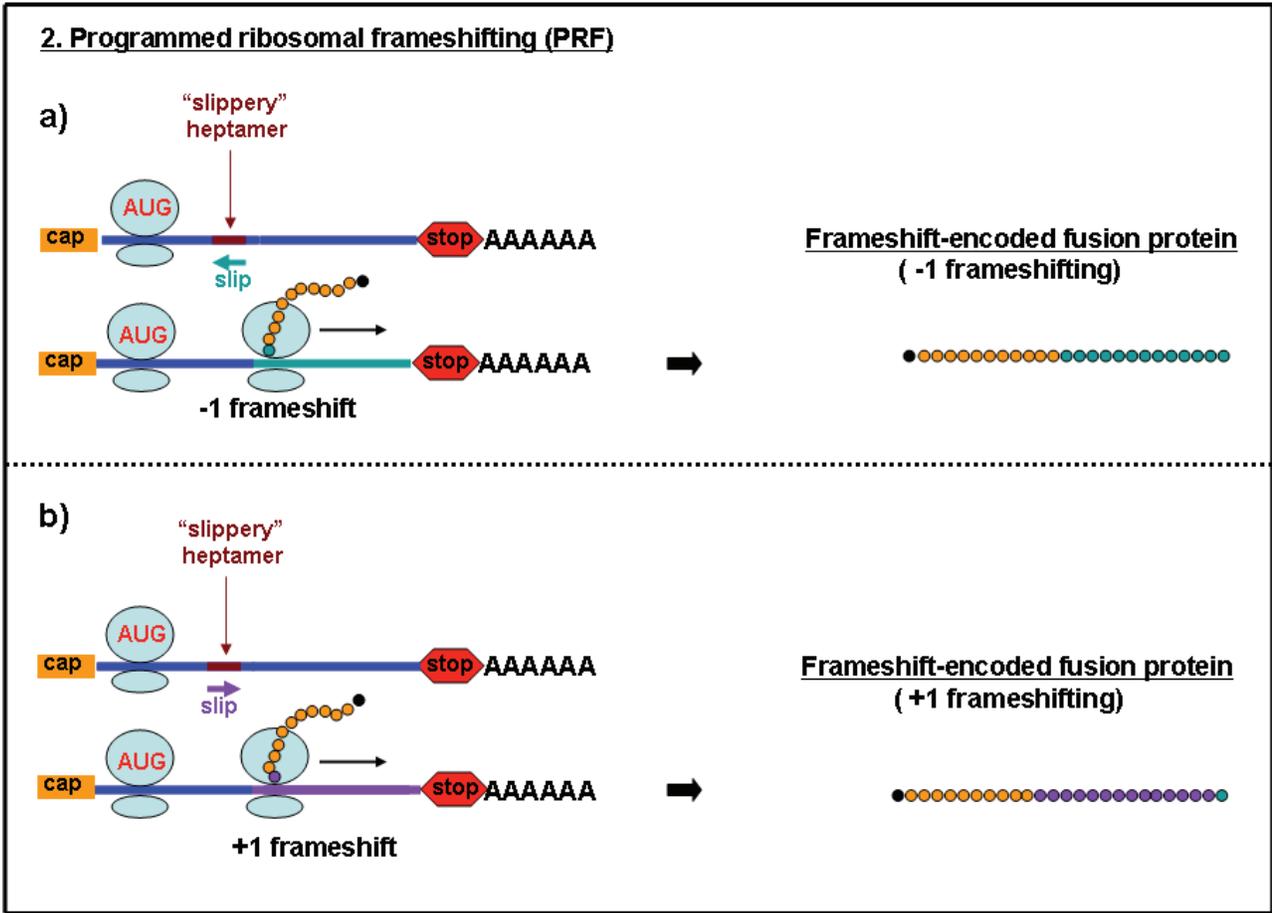




D

Proteome level

Elongation stage



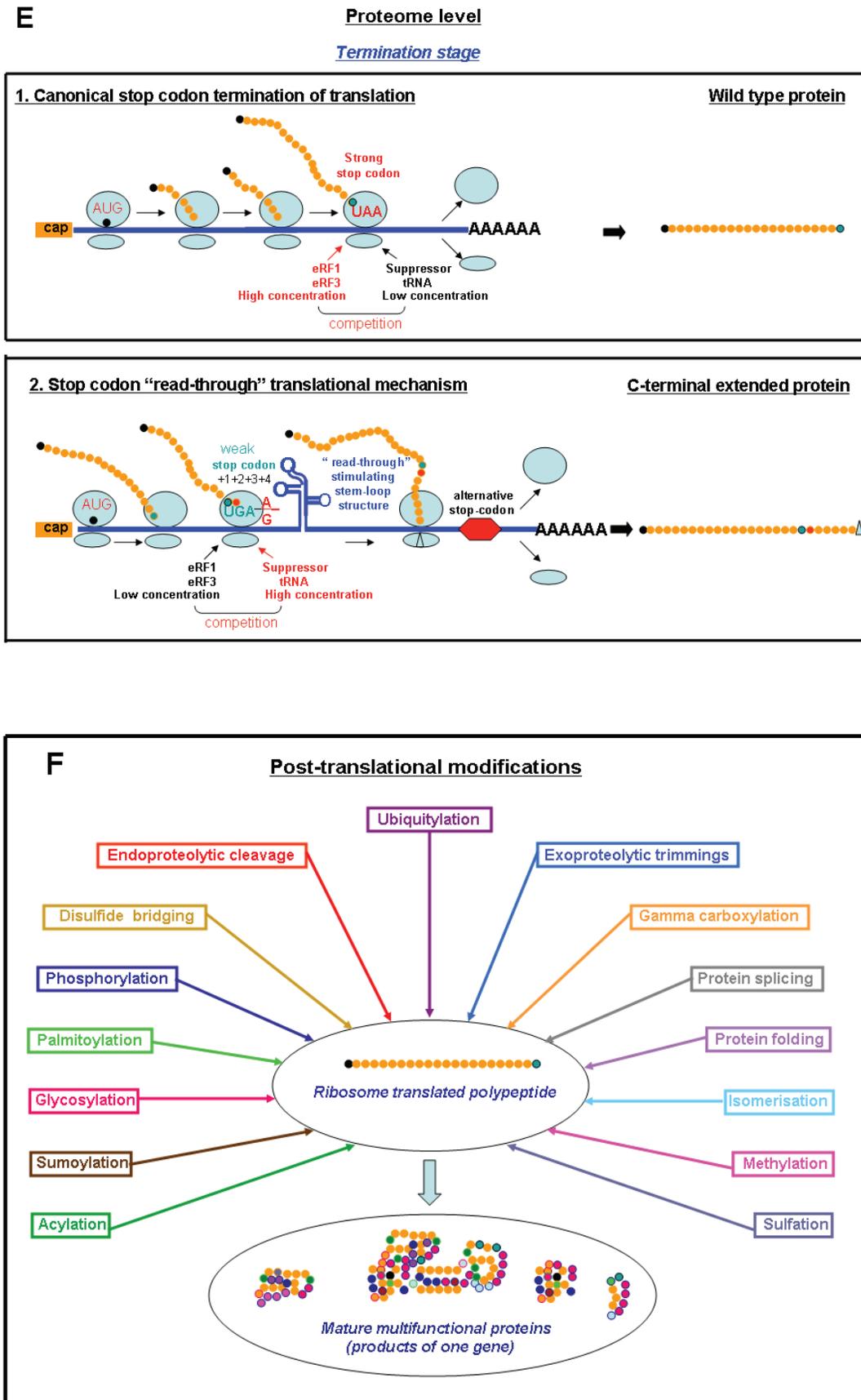


Figure 1. Mechanisms involved in development of protein multifunctionality. Mechanisms operating at genome (A), transcriptome (B), proteome (C-E) and post-translational (F) levels.

world may illustrate this idea. Owing to the small size of their genome, viruses have evolved by packing a maximum of genetic information in a minimum of polypeptide sequence. As a consequence, many of the proteins or protein domains encoded by viruses are multifunctional. The transmembrane (TM) domains of Hepatitis C Virus envelope glycoprotein are extreme examples of such multifunctionality. Indeed, these TM domains bear ER retention signals, demonstrate signal function and are involved in E1:E2 heterodimerization (Cocquerel et al. 1999; Cocquerel et al. 1998; Cocquerel et al. 2000). All these functions are partially overlapped and present in the sequence of <30 amino acids thus evidently demonstrating the principle of structure/functional compactness reflected in protein structure as well as in its functional map (Cocquerel et al. 2002).

2. Hierarchical nature of protein architecture

For better understanding ability of a protein to develop multiple functions and to discover potentials hidden in protein molecule, one should get insight the hierarchical nature of protein architecture. As pointed out by A. Lesk, several hierarchical levels of structural complexity can be observed in protein molecules (Lesk, 2001):

1. The first level is the sequence of amino acids in a polypeptide (*primary structure*).
2. The assignment of α -helices and β -sheets is the hydrogen-bonding pattern of the main polypeptide chain (*secondary structure*). This is the second level of complexity. Many proteins demonstrate recurrent patterns of interaction between helices and sheets present in one polypeptide molecule. These interactions form *supersecondary structure*.
3. The most of the protein molecules contain compact units within the folding patterns of a single chain, *domains*, that demonstrate definite structural stability and functional independence. Protein domains can be defined as segmented portions of a polypeptide sequence that assume stable three-dimensional structure (Richardson, 1981; Wriggers et al. 2005). A domain usually fulfills specific function(s). Assembly of domains and intervening flexible stretches of short peptide chains develops multidomain protein molecule characterized by *the tertiary structure* (the third level of structural complexity).

4. Within multidomain proteins, each domain is capable of autonomous function, however, some of them also mediate the formation of complexes with partner proteins (intermolecular interactions) giving rise for new functions and forming so called a domain network (Santonico et al. 2005). The multidomain proteins containing more than one polypeptide chain compose the assembly of the monomers that represents the fourth level of complexity—*the quaternary structure*.

Multidomain proteins containing several copies of closely related domains are so called *modular proteins*. The modular protein can “mix and match” sets of domains. For example, fibronectin, a large extracellular protein, contains 29 domains including multiple tandem repeats of three types of domains, F1, F2 and F3 (Lesk, 2001). These and many other domains such as EGF, Ig, PZS etc are integral parts of the multiple modular proteins. Such recurring protein motifs, domains, are significant because it is increasingly recognized that “there are only a limited number of domain families in nature” (Wriggers et al. 2005). These domains are duplicated and combined in different ways to form the set of proteins (Apic et al. 2003).

Most of the known proteins are multifunctional molecules. The presence in a protein molecule of several domains that possess different functions indicates on its multifunctionality. At the beginning of the 1990s, K. Mizejewsky proposed the hypothesis of the “modular cassette” (Dauphinee and Mizejewski, 2002; Mizejewski, 1993). According to this hypothesis, the presence of amino acid stretches (domains) in a protein that are similar to those in physiologically active proteins implies that they may have similar functions. This hypothesis allows prediction of functional activities of newly discovered proteins or proteins which function have not yet been well studied. For example, more than 20 types of functionally important sites (domains) have been predicted and later on identified in α -fetoprotein (Terentiev and Moldogazieva, 2006). Among these sites, there are sites responsible for binding of hydrophobic ligands (metal ions, estrogens, bilirubin, retinoids, flavonoids, exotoxins, various dyes and drugs (Aoyagi et al. 1979; Aussel and Negrel, 1986; Birkenmeier et al. 1983; Iturralde et al. 1991; Milligan et al. 1998; Nagai et al. 1982; Nishi et al. 1991; Ruiz-Gutierrez

et al. 2001; Ruoslahti et al. 1979; Tatarinov et al. 1991), sites that demonstrate immunosuppressive activity (Naval et al. 1985; Suzuki et al. 1992; Torres et al. 1992; Torres et al. 1989) and sites that regulate cell proliferation and tumor growth (Allen et al. 1993; Jacobson et al. 1990; Leffert and Sell, 1974; Li et al. 2002; Mizejewski et al. 1983).

It has become clear over the past decade that unrelated modular proteins frequently share significant portions of sequence similarity (Bork et al. 1997; Cesareni, 2004; Pawson and Nash, 2003; Santonico et al. 2005). Thus, a large number of functionally diverse proteins can be thought of as molecules built by combining a limited number of structurally stable folded domains. A good example of such “building bricks” is the *SAM* domains. The SMART database identifies more than 1300 *SAM*-containing proteins in genomes of all organisms from yeast to humans. They present in such different proteins as protein-kinases, lipid-kinases, scaffolding proteins, RNA-binding proteins and transcription factors. Although *SAM* domains adopt similar folds, they are remarkably versatile in their binding properties. Some identical *SAM* domains can interact with each other to form homodimers or polymers. In other cases, *SAM* domains can bind to other related *SAM* domains, to non-*SAM* domain-containing proteins, and even to RNA. Such versatility earns them multiple functional roles in different biological processes such as signal transduction, transcriptional regulation and translational control (Qiao and Bowie, 2005).

Speaking about protein architecture and function, it is important to underline the role which flexible linkers play in interconnection of the various domains in multidomain proteins. These linkers are stretches of amino acid residues that establish communication between different domains and functional modules (Gokhale and Khosla, 2000). A number of examples (e.g. immunoglobulin, diphtheria toxin, tomato bushy stunt virus protein) established a clear relationship between linker peptides and the functional dynamics they enable. Conformational transitions in multiple identical or homologous proteins have been observed. This gained widespread acceptance to the concept of hinge-bending (Dobson, 1990), whereby the relative flexibility of short regions of the polypeptide chain allow significant movement of structural domains.

One important consequence of the flexibility afforded by soft peptide linkers is the ability of

linked domains to move to and from close spatial proximity. The flexibility and hydrophilicity of the linker are important factors in preventing the disturbance of the domain functions, thereby imparting stability to the domains (Arai et al. 2004). A range of stability occurs depending on rigidity of the linker peptides. Soft linkers confer flexibility, whereas more rigid peptides may act to keep domains apart (Wilchek and Miron, 1974).

Due to their ability to break or form contacts among adjacent domains, soft linkers often facilitate essential catalytic events in the overall function of a protein, as seen, for instance, in the tomato bushy stunt virus proteins (Harrison, 1981) or in the NF κ B (Henkel et al. 1992). The hinge region of the NF κ B is flexible enough to bring “p50” and “SW16/ANK” repeat domains into contact to regulate intracellular transport of the transcription factor (Henkel et al. 1992).

The classical example of the flexible linker power to produce large number of diverse functional interactions using limited number of structural domains is calmodulin. Calmodulin contains four Ca²⁺-binding domains known as the EF-hand with highly conserved amino acid sequences in all eukaryotes (Ikura and Ames, 2006; Kretsinger and Nockolds, 1973). Calmodulin regulates numerous target proteins that are functionally and structurally diverse. It activates cyclic nucleotide phosphodiesterase (Cheung, 1970; Gopinath and Vincenzi, 1977; Kakiuchi and Yamazaki, 1970), Ca²⁺-transporting ATPase (Gopinath and Vincenzi, 1977; Jarrett and Penniston, 1977), phosphorylase kinase (Cohen et al. 1978), nitric oxide synthetase (Stuehr et al. 1991) and many others. The list of known calmodulin dependent proteins exceeds 300 in number (Yap et al. 2000).

How calmodulin could bind and regulate all these different proteins? The structure determined for calmodulin in the complex with a target protein by NMR showed remarkable conformational change in calmodulin’s two EF-hand domains upon binding to the target protein (Ikura et al. 1992; Meador et al. 1992; Yap et al. 2000). This structure revealed that central domain linker is magically flexible and can be bent dramatically upon binding to the target protein (Barbato et al. 1992; Persechini and Kretsinger, 1988; Trehwella, 1992). The flexibility of the linker enables calmodulin to change its conformation as needed depending on the structure of target protein. Such conformational plasticity of calmodulin protein allows it to gain

multifunctionality: by simply connecting two EF-hand modules via a flexible linker, an exponential increase in the number of target interactions is achieved (Ikura and Ames, 2006).

II. The Basic Mechanisms Ensuring Transformation of Protein Structural Peculiarities into Functional Multiplicity

Protein structural complexity and compactness may be achieved by different mechanisms operating at genome, transcriptome and proteome levels (Fig. 1, A-E). Several examples of multifunctional proteins described below may demonstrate how multifunctionality may be developed by these mechanisms.

Genome level

The main tools in generation of biological diversity at the genome level are mutations (insertion or deletion of nucleotides in DNA sequences), transposition of pieces of DNA and gene duplication followed by genetic divergencies in each duplicated genes. If these changes in genetic information induce changes in protein structure and function, they undergo evolutionary selection and can be traced phylogenically (Fig. 1, A).

1. Mutations as sources for multifunctionality

The product of the mutated gene can be “either an alternative protein of equivalent function -a *neutral mutation*- or a protein that carries out the same function but with an altered rate or specificity profile. It can be a protein with an altered function, or a protein that does not function—or even fold-at all” (Lesk, 2001). For instance, human adult and foetal haemoglobins differ by substitution of Ser (143 β) for His. Primarily, as a result of this mutation, foetal haemoglobin demonstrates lower affinity than adult homologue for the regulatory ligand diphosphoglycerate. This promotes the transfer of oxygen across the placenta to the foetus (Lesk, 2001).

Another example demonstrates role of minor genetic alterations in induction of fundamental functional changes in the homologous proteins. Haptoglobin is a chymotrypsin homologue. As a result of homologous gene mutations, it lost proteolytic activity characteristic for chymotrypsin but obtained several other functions: haptoglobin

may function as chaperon as well as factor preventing the loss of iron from erythrocytes and as protein mediating immune responses (Lesk, 2001).

2. Gene duplication as the origin of genetic novelties

It has been proposed that gene duplication is one of the important step for the origin of genetic novelties (Gu et al. 2002; Ohno, 1970). The following examples can confirm this proposition. GroEL is a 60 Kda heat-shock protein ubiquitous in bacteria. Interestingly, the GroEL in *Chlamydiae* became duplicated at the origin of the *Chlamydiae* lineage presenting three distinct molecular chaperones, namely the original protein GroEL1, and its paralogous proteins GroEL2 and GroEL3 (Karunakaran et al. 2003; McNally and Fares, 2007). GroEL protein copies species have diverged functionally after the gene duplication events. The functional divergence has occurred in important functional regions of these proteins. Even though the three *Chlamydiae* GroEL proteins present substantial amino acid sequence conservation in important regions involved in polypeptide binding when compared to GroEL from the *Escherichia coli*, significant differences have been spotted in GroEL binding regions and at regions involved in ATP binding and hydrolysis. Most of the amino acid replacements that have affected interaction with protein partners and were responsible for the functional divergence between GroEL paralogs were fixed by adaptive evolution after the groEL gene duplication events (McNally and Fares, 2007).

Stromal interaction molecules (STIMs) represent another example demonstrating the role of gene duplication in functional divergence of homologous proteins. STIMs function as the Ca²⁺ sensor to detect changes of Ca²⁺ content in the intracellular stores. STIMs are single-span membrane proteins with unpaired N-terminal EF-hand Ca²⁺ binding domain critical for Ca²⁺ sensor function. In addition, STIMs contain an N-terminal sterile α motif (SAM) domain and a C-terminal (cytoplasmic) coiled-coil ERM domain (Liou et al. 2005; Roos et al. 2005; Williams et al. 2001; Zhang et al. 2005). Human STIMs and invertebrate STIM share several functionally important protein domains, but diverge significantly in the C-terminus.

The phylogeny and sequence analysis revealed early adaptation of the C-terminal divergent domain in Urochordata, before the expansion of STIMs in Vertebrata. STIMs were subsequently subjected to one round of gene duplication as early as in the Euteleostomi lineage in vertebrates, with a second round of fish-specific gene duplication. After duplication, STIM-1 and STIM-2 molecules appeared to have undergone purifying selection. Furthermore, sequence analysis of the EF-hand Ca^{2+} binding domain and the SAM domain, together with functional studies, identified critical regions/residues likely underlying functional changes and proved evidence for the hypothesis that STIM-1 and STIM-2 might have developed distinct functional properties after gene duplication (Cai, 2007).

Transcriptome level

Alternative splicing is a common post-transcriptional process in eukaryotic organisms to produce multiple transcript isoforms from a single gene (Black, 2003). Alternative splicing and gene duplication are two sources of proteomic functional diversity (Fig. 1, A, B). According to the “independent model” alternative splicing and gene duplication are two independent mechanisms for increasing the proteomic complexity. Alternatively, the “function-sharing model” claims that some proteomic components can be performed either by alternatively spliced genes or duplicate genes [cited by (Su et al. 2006)].

Alternative splicing can generate multiple transcripts encoding proteins with subtle or opposing functional differences that may have profound biological consequences. Recent estimates, based on analyses of expressed sequence tags (ESTs), suggest that the transcripts from 35% of human genes are alternatively spliced (Hanke et al. 1999; Mironov et al. 1999). However, as pointed out by B. Graveley, “this number is likely to be an underestimate” (Graveley, 2001). First, the human EST collection does not represent all protein coding sequences and for most genes, ESTs cover only a portion of the transcript. Because much of the functionally significant alternative splicing occurs in the coding region of the transcript, many alternative splicing events might be overlooked by EST comparisons. Second, and perhaps more important, many alternative splicing events are very rare and occur only in a specific tissue at a specific time in development and/or under certain physiological

conditions. These types of splicing events will probably not be represented in EST collections (Graveley, 2001). Some genes produce several spliced mRNAs while it turns out that some other genes, in fact, encode transcripts that are alternatively spliced to produce tens of thousands of different mRNAs (Schmucker et al. 2000).

The neurexin proteins represent an example which demonstrates the role of alternative splicing in obtaining different functions by one gene products. The neurexins are a family of neural proteins present in vertebrates that have important functions as receptors for neuropeptides (Missler and Sudhof, 1998) and as adhesion molecules that participate in synaptogenesis (Scheiffele et al. 2000). It has been shown that more than 1000 different neurexin mRNA isoforms could potentially be synthesized virtue of alternative promoter usage and alternative splicing (Ullrich et al. 1995). The proteins encoded by these alternative spliced mRNA have altered specificities for their ligands (Ichtchenko et al. 1995; Sugita et al. 1999). Beside that, the diversity of neuroxin proteins might specify neural connectivity (Missler et al. 1998). It has been shown that interaction of β -neurexins present in pre-synaptic cells with neuroligins on the surface of post-synaptic cells is sufficient to trigger synapse formation (Scheiffele et al. 2000). Importantly, this interaction only occurs if the β -neurexin is encoded by an mRNA lacking an alternative exon 20. Proteins synthesized from exon 20-containing transcripts do not interact with neuroligins (Ichtchenko et al. 1995). Thus, alternative splicing of the neurexin transcripts might have a direct role in controlling the formation and maintenance of synapses.

Proteome level

Proteome is a set of proteins obtained by translation of mRNAs exported from nucleus to cytoplasm. Translation of mRNA into protein represents the final step in the gene-expression pathway, which mediates the formation of the proteome from genomic information (Gebauer and Hentze, 2004). As we have already underlined, at the genome level, the maximal volume of genetic information has to be encoded in minimal DNA space. At transcriptome level, the concealed diversity of future proteins encoded in DNA and mRNA is revealed by shuffling of different fragments of the primary transcript during the alternative splicing process. The alternative promoter usage in its turn discloses

the diversity of genetic information contained in mRNA and destined for translation. At the proteome level, the maximum of structural and functional potentials contained in the genetic information embedded in mRNA can be elicited by translational mechanisms. Recent data obtained by sequencing of the human genome showed that the human genome composed of about 35 000 genes which may express about 100 000 proteins. Such protein outburst is possible only because numerous mechanisms exist by which functionally diverse polypeptides are produced from a single gene (Touriol et al. 2003).

The ability to produce different polypeptides by translation of one and the same mRNA molecule is installed in the translation mechanism by itself. Conceptually, the translation process can be divided into three stages—initiation, elongation and termination. During initiation the ribosome is reassembled on mRNA, with initiator tRNA bound in the ribosomal P site and base paired with the start codon of the mRNA. Elongation refers to the polymerization of the peptide, the main function of the ribosome, while termination includes the sequence of events following recognition of the stop codon up to the disassembly of the ribosome into subunits and subsequent dissociation of the factors, tRNA, and mRNA (Touriol et al. 2003). The mechanisms operating at each stage determine the appearance of different isoforms of one and the same gene product (Fig. 1, C-E).

A. Initiation stage

1. Cap-dependent initiation

Translation initiation of eukaryotic mRNAs in general occurs by a scanning mechanism (Kozak, 2002). According to the linear scanning model, 40S ribosomal subunit binds to the cap structure (m⁷GpppN) at the 5' end of mRNA and scanning downstream to the first in frame AUG initiation codon (Pestova and Hellen, 1999). The canonical scanning mechanisms (Fig. 1, C1) rules initiation of most mRNAs, but three non-classical cap-dependent initiation mechanisms have been also described: leaky scanning, ribosomal shunting and termination initiation (Lopez-Lastra et al. 2005).

a) Leaky scanning

It has been shown that the nucleotide context in the vicinity of the start codon is important for its

interaction with the ribosome. If the context is not optimal, some ribosomes do not recognize the 5' end proximal AUG codon as starting, skip it, and begin translation at the next AUG by mechanisms known as “leaky scanning” (Kochetov, 2006; Kozak, 2002). This leaky scanning mechanism (Fig. 1, C2) produces protein isoforms with alternative amino initiation sites. Hence, the genes may produce several versions of the encoded proteins, and the shorter versions, initiated from a downstream in-frame start codons, lack the N-terminal amino acids of the full-length isoform version (N-terminal truncated version) (Touriol et al. 2003).

Besides additional AUG codons located downstream to the main start codon, many mRNAs contain upstream located AUG (uAUG) which also may be chosen by translational mechanisms for synthesis of new isofunctional protein variants. Kochetov et al. (Kochetov et al. 2005) had analyzed more than 12000 of human mRNAs bearing uAUGs and found that 3% of mRNAs contained uAUGs in the same reading frame as the coding sequences without stop codons in between. It means that such mRNAs can code for additional protein variants extended at the N ends. A comparison of their predicted subcellular locations showed that 31% of such N-extended proteins had a different location, and in 19% of the cases they had secretion signals absent from the annotated variants (Kochetov et al. 2005).

As the sequences that determine cell compartment targeting are located usually at the N-terminal region of a protein, the selection of alternative translation initiation codons may be used by cell to control cellular localization of the isoforms (Cai et al. 2006; Gandre et al. 2003; Packham et al. 1997). Cai et al. (Cai et al. 2006) showed that 85.7% of alternative translation events generated biological diversity, attributed to different subcellular localizations and distinct domain contents in alternative isoforms. Several examples presented below may illustrate how the leaky scanning mechanism is used by a cell for increasing diversity of protein isoforms produced by a single gene.

The Arabidopsis DNA ligase 1 gene (AtLIG1) is indispensable for cell viability. AtLIG1 expresses one major and two minor mRNA transcripts differing only in the length of the 5' untranslated leader sequences preceding a common open reading frame (ORF) (Sunderland et al. 2006). Control of AtLIG1 isoform production and intracellular targeting depends upon mechanisms

controlling the choice of translation initiation site within the AtLIG1 ORF. Translation of AtLIG1 mRNA transcripts from the first in-frame start codon produces an AtLIG1 isoform that is targeted exclusively to the mitochondria. Translation initiation from the second in-frame start codon produces an AtLIG1 isoform targeted only to the nucleus. The length of the 5'-UTR and more significantly the nucleotide context around alternative start codons in the AtLIG1 transcripts affect translation initiation to ensure a balanced synthesis of both nuclear and mitochondrial AtLIG1 isoforms via a context-dependent leaky ribosome scanning mechanism (Sunderland et al. 2006). Instead of having distinct genes to code the different compartment-specific isoforms of DNA ligase proteins, eukaryotic species from yeast to humans appear utilize an evolutionarily conserved mechanism that relies upon choice of in-frame translation initiation start codons within the ORF of a ligase mRNA transcript to regulate the synthesis of the appropriate DNA ligase isoform destined for the nucleus or mitochondria. As the control of subcellular localization of proteins and their interaction with specific protein partners *in vivo* are crucial for cell physiology, the importance of the mechanisms controlling production of different forms of protein and their intracellular topology is difficult to overestimate (Sunderland et al. 2006).

Ion channels are composed of membrane-spanning proteins that allow ions to permeate at high rates. Voltage-gate K⁺ (Kv) channels are indispensable for the electrical excitability of nerve and muscle fibers (Finol-Urdaneta et al. 2006). The N-terminal region of the Kv channels plays important regulatory roles, including inactivation kinetics, subunits recognition and redox modulation of the currents flowing through those channels. Thus, the differences among N-terminal regions of Kv channels can result in important functional differences between molecular forms of Kv channels. The Kv 1.7 channels from mouse heart muscle are encoded by *Kcna7* gene. Its mRNA transcript has two putative translation initiation start sites that generate two channel isoforms, mKv1.7L (489 aa) and mKv1.7S (457 aa), with different electrophysiological characteristics. The presence of both of these isoforms is very important for normal functioning myocard as absence of one of them leads to different types of heart pathology (Finol-Urdaneta et al. 2006).

Insulin-degrading enzyme (IDE) is expressed in both insulin-sensitive and insulin-insensitive tissues. Within the cell, IDE is targeted predominantly to cytoplasm, however, in some cells it presents also in several subcellular compartments. The mechanisms responsible for the targeting of IDE to different cell compartments are not well understood. Studying this issue, Leissring et al. (Leissring et al. 2004) showed that alternative translation beginning at an in-frame initiation codon located upstream of the canonical start site generates earlier nonrecognized isoform of insulin-degrading enzyme that in contrast to cytoplasm locating isoform is targeted to mitochondria. This example shows that N-terminal extension achieved by usage of alternative initiation codon can produce new protein isoform possessing new function.

These and many other examples (Porras et al. 2006; Sass et al. 2001) demonstrate the power of leaky scanning mechanisms in generating multiple functionally different protein isoforms from single mRNA transcript.

b) Ribosome-shunting

The next translation mechanism that also makes impact in diversity of protein product coding for by a single gene is ribosome shunting. The scanning model postulates that when a scanning 40S ribosomal subunit encounters a hairpin loop in the 5' UTR, it does not skip over the loop but unwinds it (Kozak, 1980; Lopez-Lastra et al. 2005). Nevertheless, there are some cases when a scanning 40S ribosomal subunit encounters the structures present in the 5'UTR and skips or shunts over a large segment, bypassing intervening segments including AUG codons and strong secondary structures that normally would block the scanning process (Fig. 1, C3). The selective translation initiation in adenovirus-infected cells under heat shock is an example of ribosome jumping mechanism (Yueh and Schneider, 1996).

c) Termination-initiation

The third non-classical cap-dependent initiation mechanism, as it has already mentioned above, is termination-initiation. In the reinitiation mechanism, a second ORF located in the same mRNAs can be translated without the 40S ribosome subunit becoming disengaged from the mRNA after reaching the first ORF stop codon (Fig. 1, C4). Strictly speaking this mechanism is more related to the

elongation stage than to initiation one although the continuation of translation needs the reinitiation step at a downstream AUG triplet.

The exploration of the termination reinitiation mechanism for regulation of protein translation is observed in different cells and viruses. For example, stress-induced eIF2 α phosphorylation increases translation of ATF4, an activator of the integrated stress response (ISR) program, by reinitiation mechanism (Lu et al. 2004). The ATF4 mRNA has two conserved upstream ORF (uORF), uORF1 and uORF2. Scanning ribosomes initiate translation at both uORFs. After translation of the uORF, the scanning ribosome efficiently reinitiate translation at downstream AUGs. In unstressed cells, low levels of eIF2 α phosphorylation favor early capacitation of such reinitiating ribosomes directing them to the inhibitory uORF2, which precludes subsequent translation of ATF4 and repress ISR. In stressed cells high levels of eIF2 α phosphorylation delays ribosome capacitation and favors reinitiation at ATF4 over the inhibitory uORF2 (Lu et al. 2004). Analogous mechanism operates in regulated translation of Gsn4 protein in yeast (Hinnebusch and Natarajan, 2002).

Translation of human hepatitis virus polymerase is another example demonstrating involvement of different translation mechanisms participating in expression of the polycistronic mRNA. The human hepatitis B virus (HBV) has a compact genome encoding four major overlapping coding regions: the core, polymerase, surface and X. The polymerase initiation codon is preceded by the partially overlapping core and four or more upstream initiation codons. Several mechanisms are used to enable the synthesis of the polymerase protein, including leaky scanning and ribosome reinitiation. Chen et al. (Chen et al. 2005a) showed that core upstream open reading frame (CO uORF), highly conserved in all HBV subtypes, played an inhibitory role in downstream expression from the core initiation site, but also stimulated reinitiation at the polymerase start when in an optimal context. Thus, the CO uORF is a determinant in balancing the synthesis of the core and polymerase proteins.

2. Cap-independent IRES-determined initiation

The described examples demonstrate the possibilities of cap-dependent initiation mechanisms to generate multiple protein isoforms possessing new

functions. However, the possibilities of translation process to increase and diversify the potentials embedded in mRNA are not restricted only to cap-dependent mechanisms as cap-independent translation mechanisms operate also in cells. Cap-independent translation (Fig. 1, C5) is mediated by internal ribosome entry sites, IRES (Holcik et al. 2000). These are usually comprised of structured regions in the 5' untranslated region and were initially identified in viruses, but have since been reported in eukaryotic mRNAs and are believed to constitute a major form of regulation of protein synthesis in mammalian cells (Candeias et al. 2006; Holcik et al. 2000). As a rule, there are no significant structural similarities between individual IRES. At present, IRESs are defined solely by functional criteria and cannot yet be predicted by the presence of characteristic RNA sequences or structural motifs (Lopez-Lastra et al. 2005). Examination of the available RNA structure prediction software and RNA motif searching programs indicates that while these programs are useful tools to fine tune the empirically determined RNA secondary structure, the accuracy of *de novo* secondary structure prediction of large RNA molecules and subsequent identification of new IRES elements by computational approaches, is still not possible (Baird et al. 2006).

a) Mix (or alternative) initiation

It is important that, although capped, some cellular mRNAs—including those encoding translation initiation factors, transcription factors, oncogenes, growth factors, homeotic gene products and survival proteins—contain also IRES elements in their 5'UTR sequences that may allow them to be translated under conditions when cap-dependent synthesis of proteins is impaired (Lopez-Lastra et al. 2005). Moreover, in some cases mRNA molecule contains both cap-dependent start codon and IRES element and upon different cell conditions may direct synthesis of different isoforms of a single protein by using cap-dependent or IRES-mediated translation mechanisms (Fig. 1, C6). For instance, expression of two p53 isoforms, full length (FLp53) and N-terminal truncated (p53/47), is controlled by alternative cap-dependent and IRES-mediated mechanisms of initiation govern the translation of the p53 mRNA (Candeias et al. 2006). In contrast to FLp53, the p53/47 isoform does not harbour the most of N-terminal p53 transactivating domain

(aa 1–40) nor the Mdm2-binding site (aa 17–23) demonstrating different functional parameters. The p53/47 may form complexes with FLP53 thus changing its stability and ability to induce activation of other p53-dependent genes. Changes in synthesis of FLP53 or p53/47 are regulated through distinct cell stress-induced pathways acting through separate regions of the p53 mRNA. The functional differences of two isoforms are manifested also in that that some cytotoxic agents require the presence of FLP53 to induce apoptosis, whereas for others p53/47 is sufficient. This indicates that by harbouring alternative translation initiation sites, the p53 mRNA gives rise to different levels of the p53 isoforms which help to orchestrate the cell biological outcome of p53 activation in response to different types of cell stress (Candeias et al. 2006).

Another example showing the role of alternative translation initiation in synthesis of protein isoforms possessing different functions is vascular endothelial growth factor (VEGF). The unusually long (1038 nucleotides) and structured 5' untranslated region (UTR) of VEGF mRNA contains two independent IRES (IRES A and IRES B). In the human sequence, four potential CUG translation initiation codons are located in between these IRES and are in frame with the classical AUG start codon. The VEGF IRES A located within 300 nucleotides upstream from the AUG codon directs a cap-independent translation initiation, which has been shown to allow VEGF synthesis in hypoxic conditions (Huez et al. 1998; Sass et al. 2001; Stein et al. 1998). It has been shown that IRES B located in the first half of the 5'UTR between nucleotides 379 and 483 controls the translation initiation of new VEGF isoform (L-VEGF) which is N-terminal extended by 206 amino acids in comparison to the classical AUG-initiated form. Translational initiation of this isoform occurs at the first of CUG codons. Different functions of two VEGF isoforms can be evidenced by different targeting of AUG- and CUG-initiated isoforms: while the classical AUG-initiated VEGF isoform is a secreted protein, the CUG-initiated L-VEGF isoform demonstrates intracellular targeting. Besides that the L-VEGF undergoes post-translational partial cleavage into two fragments, namely a 206-a.a. N-terminal fragment that after cleavage remains in cell and a C-terminal fragment that is equal to the AUG-initiated isoform by size and by ability to be secreted out of the cell (Huez et al. 2001).

B. Elongation stage

Thus, at the initiation stage of translation process the translation apparatus has numerous possibilities for material (molecular) realization of the information potentials concealed in mRNA. At the elongation stage other mechanisms may also make their impact in structural and functional diversity of synthesized protein isoforms. In contrast to the initiation and termination stages of translation, the machinery used during the course of translational elongation has been highly conserved and less variable across the three kingdom of life (Kapp and Lorsch, 2004). As noted by Namy et al. (Namy et al. 2004), the main mechanisms by which translation machinery may uncover the hidden genetic information at the elongation stage are the frameshifting (Fig. 1, D2) and to a less degree—hopping (Fig. 1, D3).

1. Frameshifting

Prediction the protein(s) encoded by a given DNA is difficult because of the lack of knowledge of the signals embedded in the genome that are involved in the translation of the genetic information. It has been shown that in many genes the standard rules of decoding postulated by the dogma of the universal genetic code are subverted by “recoding” signals found in DNA that promote alternative decoding events like programmed ribosomal frameshifting, hopping, or termination codon reassignment (Atkins et al. 2001; Gesteland and Atkins, 1996; Gesteland et al. 1992).

As noted by Namy et al. (Namy et al. 2004) “natural frameshift errors occur very rarely, but programmed ribosomal frameshifting signals increase the probability of tRNA slippage enormously, occasionally to such an extent that up to 50% of ribosomes change frame”. Analysis of the frameshifting mechanisms is beyond this review scope. They were critically studied and described in several excellent publications (Atkins et al. 2001; Brierley and Pennell, 2001; Plant et al. 2003; Stahl et al. 2001). In principle, frameshifting is triggered by two elements—a slippery and stimulator sequences. A slippery sequence is the mRNA region where tRNA movement or misalignment is favored while a stimulator is the mRNA sequence that enhances frameshifting by induction of a ribosomal pause (Namy et al. 2004).

Different kinds of frameshifting were described both in prokaryotes and eukaryotes. For example,

programmed frameshifting was observed in translation of the prokaryotic DNA polymerase III, α -fucosidase and release factor 2 (RF2) as well as eukaryotic proteins such as antizyme-1 (AZ1), IL-10, ABP140 etc [cited by (Namy et al. 2004)]. The biological expediency and functions of such frameshifting are different in each case however it is always warranted. For instance, in the case of RF2 the recoding frameshift represents an auto-regulatory mechanism controlling the abundance of RF2. At high RF2 levels, the competition between termination and frameshifting is shifted in favor of termination, leading to a decrease of the RF2 concentration in the cell. When level of RF2 begins to decrease, frameshifting begins to predominate, raising the level of RF2 (Adamski et al. 1993).

The antizyme-1 (AZ1) is another well studied example of a protein which full length expression is regulated by programmed frameshifting. AZ1 is a protein that negatively regulates polyamine synthesis by inhibiting the key synthetic enzyme ornithine decarboxylase and targeting it for degradation by the 26S proteasome (Heller et al. 1976; Murakami et al. 1992). Like RF2, the AZ1 full length protein expression depends on frameshifting which in its turn is linked to a feedback mechanism which regulates polyamine levels in mammalian cells. For AZ1, when cellular polyamine levels are low, the polypeptide corresponding to amino acid residues 1–68 is produced and translation is terminated at the following UGA stop codon (Matsufuji et al. 1995). When cellular polyamine levels are high, +1 frameshifting occurs after the 68th codon resulting in the full-length antizyme protein containing 227 amino acid residues (1–227 a.a.) (Ichiba et al. 1994). Frameshifting is employed in the expression of all known antizymes in different species and many other proteins. The conservation of this mechanism throughout evolution highlights a crucial role for frameshifting in the regulation of gene expression.

It should be pointed out that frameshifting determines multifunctionality of AZ1 only partially. Differential usage of alternative initiation sites also makes its impact in this phenomenon. AZ1 mRNA contains two initiation AUG codons separated by 32 codons. Both AUG triplets are utilized as translation start sites (Matsufuji et al. 1995; Rom and Kahana, 1994). It has been shown that N-terminal region of AZ1 contains nuclear export and mitochondrion targeting signals

(Gandre et al. 2003; Gritli-Linde et al. 2001; Murai et al. 2003). Depending on either AUG codon is used for translation, the resulting AZ1 isoform is targeted to nucleus, mitochondria or cytoplasm (Murai et al. 2003). The multifunctionality of antizyme was evidenced not only by targeting of its isoforms to different cell compartments and serving as ornithine decarboxylase inhibitor but also by recent finding that AZ1 functions as positive transcriptional regulator of the *atoDAEB* operon genes in *E. coli* (Filippou et al. 2007).

We have described here only two proteins which synthesis are directed by frameshifting. Many other examples in which this mechanism is used for development of protein diversity may be found in very informative review written by Namy et al. (Namy et al. 2004).

2. Hopping (translational bypassing)

An unusual frameshift event that also diversifies the protein structures and functions is “hopping” where the transition from frame 0 to another frame occurs by translational bypassing of an extended region of the mRNA sequence rather than by slippage past a single nucleotide, as has been described for most examples of frameshifting. When genetic code has been discovered, its translation seemed to be rigid. However, later on the reading of the genetic text (code) has been found to be quite flexible, and several alternatives in its expression have been described (Groisman and Engelberg-Kulka, 1995).

Translational bypassing joins the information found within two disparate open reading frames into a single polypeptide chain. The underlying mechanism centers on the decoding properties of peptidyl-transfer RNA (tRNA) and involves three stages: *take-off*, in which the peptidyl-tRNA/mRNA complex in the P-site of the ribosome dissociates; *scanning*, at which the peptidyl-tRNA probes the mRNA sliding through the decoding center; and *landing*, in which the peptidyl-tRNA re-pairs with a codon with which it can form a stable interaction (Fig. 1, D3) (Herr et al. 2000a). The best characterized examples of this phenomenon are T4 gene 60 and *plaA* gene (the *Prevotella loescheii* adhesion gene). In T4 gene 60, a complex signals stimulates bypassing of 50 nucleotides between the two open reading frames (Herr et al. 2000b). In *plaA*, the translation of its mRNA requires bypassing of 29-nt of coding gap (Manch-Citron et al. 1999).

Herr et al. (Herr et al. 2000a) noted that although few examples of genes are known that rely on translational bypassing to couple ORFs, ribosomes appear to have innate capacity for bypassing. This suggests that the strategy of translational bypassing may be more common than presently appreciated.

C. Termination stage

Termination of protein synthesis involves the decoding of a stop signal through an interaction between ribosome, mRNA and release factors (RF) that facilitates the hydrolytic release of the nascent polypeptide chain from the peptidyl-transferase center of the ribosome (Cridge et al. 2006). Stop codons are used to signal the ribosome to terminate the decoding of an mRNA template. Open reading frames within an mRNA are terminated by an in-frame any one of three stop or nonsense codons (UAA, UAG or UGA) which are recognized during translation by the binding of RFs to the ribosomal A site (von der Haar and Tuite, 2007; Williams et al. 2004).

1. Stop codon readthrough

Translation termination is normally a highly efficient process. It has been shown that stop codons are normally suppressed at a frequency of only 0.001%–0.1% (Loftfield and Vanderjagt, 1972; Stansfield et al. 1998). Two competing events, termination and stop codon readthrough (or nonsense suppression), can occur when stop codon reaches the A-site of a translating ribosome. Translation termination results in hydrolysis of the final peptidyl-tRNA bond and release of the completed nascent polypeptide. Alternatively, readthrough, in which the stop codon is erroneously decoded by a suppressor or near-cognate t-RNA, results in translation past the stop codon and production of a protein with a C-terminal extension (Fig. 1, E). The relative frequency of termination versus readthrough is determined by parameters such as the upstream and downstream stop codon nucleotide contexts, the activities of termination polypeptide-chain release factors and the abundance of suppressor near-cognate t-RNAs. All these parameters modulate the balance of termination to readthrough reactions in a cell-type-specific manner (Bonetti et al. 1995; Fearon et al. 1994; Janzen and Geballe, 2004; Keeling et al. 2004; Namy et al. 2002). Williams et al. (Williams et al. 2004)

underline that “the potential for even short C-terminal extension (peptide tags) to alter the cellular localization or activity of a protein is great. Addition of even a single amino acid could complete a partial targeting signal already present at the C-terminus of a protein. All protein extensions altering targeting could potentially act as genetically dominant, gain of function events. Thus, despite the generally low efficiency of stop codon readthrough events, such events may well have phenotypic consequence for the cell”.

There are an increasing number of examples of stop codon readthrough, both in viral and cellular systems, and in many cases this readthrough has physiological consequences for the cell. It is become obviously that different cells and organisms not only accommodate stop codon as a mainstream termination signal, but also used it to provide these cells and organisms flexibility to respond physiologically to various changeable environments (Namy et al. 2002; Steneberg and Samakovlis, 2001; Tate et al. 1999; Yoshinaka et al. 1985). The alternative non-canonical usage of stop codons allows production of several polypeptides from one open reading frame thus increasing structural and functional diversity of one gene products (Doronina and Brown, 2006). The classical illustration to this statement is selenoproteins.

More than 15 animal selenoproteins have been described. Many selenoproteins, such as glutathione peroxidase (Sukenaga et al. 1987), type I iodothyronine 5'-deiodinase (5'DI) (Berry et al. 1991b) and thioredoxin reductase (Gasdaska et al. 1995) are enzymes which catalyze oxido-reduction reaction. All selenoproteins contain selenocysteine (Sec). Selenocysteine incorporation is specified by a UGA codon in the open reading frame of the mRNA that is accompanied by a “selenocysteine insertion sequence” element (SECIS) in the 3' UTR (Berry et al. 1991a; Goto et al. 2001). However, in definite conditions this UGA codon may also serve as a stop codon. The competition between UGA as a stop signal and as the code for the Sec has been observed during expression of the deiodinase gene. Both the termination product (14 kD) and the complete iodine protein (28 kD) could be detected within cells (McCaughan et al. 1995). The relative amounts of these products could vary with cell type and expression system, reflecting a competition between the two UGA decoding mechanisms (Steneberg and Samakovlis, 2001).

The selenoprotein P represents even more strong illustration of competition between UGA as a stop codon and UGA as a triplet that specifies Sec-incorporations. Selenoprotein P is an extracellular glycoprotein that has been suggested to serve in oxidant defense (Burk et al. 1995). Its mRNA contains 10 UGA codons in an open reading frame terminated by a UAA, implying 10 selenocysteines in the primary structure of the protein (Hill et al. 1991). Full-length selenoprotein P and three smaller isoforms that have identical N termini but different affinity to heparin-Sepharose have been detected in rat plasma (Chittum et al. 1996). By mass spectrometric peptide analysis it was evidenced that the full-length isoform contains predicted amino acid residues, including its C terminus and all 10 selenocysteines. The shortened isoforms terminated where the second, third and seventh selenocysteines residues were predicted to be (Ma et al. 2002). This suggests that all isoforms arise from the same mRNA and that the UGAs that specify the second, third and seventh selenocysteines in full-length selenoprotein P can alternatively serve to terminate translation, producing the shorter isoforms. As Ma et al. (Ma et al. 2002) pointed out, “it remains a theoretical possibility that the shorter isoforms are produced from the full-length protein by proteolysis”. However, the protease that could cleave the protein at specific selenocysteine residue is unknown, and this excludes the possibility of proteolytical cleavage of the full-length isoform at the specific Sec-sites.

The *Drosophila kelch* gene is another example showing that translational control of gene expression may be realized through stop codon suppression and readthrough. It has been demonstrated by Robinson and Cooley (Robinson and Cooley, 1997) that the *kelch* gene produces a single transcript with a UGA stop codon separating two open reading frames (ORF1 and ORF2). From the transcript, 76 kDa ORF1 and 160 kDa full-length (ORF1+ORF2) proteins are expressed. The expression of these two proteins is regulated in tissue-specific manner causing the ratio of two isoforms to vary in different tissues (Robinson and Cooley, 1997).

The important role of “leaky” stop codon and readthrough mechanism for cell physiology can be illustrated also by the yeast *PDE2* gene which encodes the high affinity cAMP phosphodiesterase. By synthesis the cAMP phosphodiesterase this gene may regulate the intracellular concentration

of cAMP and thus protect the cell from extracellular cAMP (Wilson et al. 1993; Wilson and Tatchell, 1988). When the translation of the *PDE2* mRNA is terminated at leaky stop codon, the *pde2* protein (active phosphodiesterase) is synthesized leading to low level of intracellular cAMP and increased stress sensitivity. On the contrary, when stop codon readthrough mechanism is switched on, the C-terminal extension of 21 amino acids occurs leading to *pde2* protein destabilization which in its turn results in high level of cAMP in the cell and resistance to stress environment (Namy et al. 2002; von der Haar and Tuite, 2007). The *PDE2* is thus an example of an individual gene product in *Saccharomyces cerevisiae* where alterations in stop-codon readthrough are directly linked to phenotypic variations that have crucial consequence for cell physiology.

When physiological roles of canonical termination signals, leaky stop-codons and readthrough mechanisms are discussed, the principle difference between normal function of termination stop codon and abnormal role of premature stop codon(s) which may appear in the mRNA as result of mutations or alternative splicing to cryptic splice sites should be underlined (Frischmeyer and Dietz, 1999; Lewis et al. 2003). The nucleotide context surrounding the classical stop codon is genetically determined and promotes translational termination of the synthesized natural protein. The upstream and downstream contexts of leaky stop signal are also genetically determined for promotion of the readthrough activity which results in appearance of new protein isoform that is necessary for fulfillment of specific physiological function. Thus, the expression of terminated or extended proteins in these cases represents realization of specific steps in the normal cell program. The random appearance of the premature termination codon (PTC), or nonsense codon, in ORF of mRNA is not correlated with the inherited surrounding nucleotide context and therefore cannot be regulated by physiological translation mechanisms (Lewis et al. 2003).

Nonsense codon-bearing transcripts typically encode C-terminally truncated proteins which could possess dominant-negative or deleterious gain-of-function effects. Usually, PTCs trigger the rapid degradation of mRNA by nonsense-mediated mRNA decay (NMD) mechanism that detects and degrades transcripts harboring nonsense codons (Frischmeyer and Dietz, 1999; Wilkinson, 2005). This downregulatory response is an important

quality-control mechanism. Its function is safeguarding cells from abnormal mRNA function (Behm-Ansmant et al. 2007; Isken and Maquat, 2007). Surprisingly, recent studies strongly evidenced that components of NMD machinery (proteins UPF1, UPF2, UPF3, RNP21, Y14 and MAGOH) also promote translation of normal mRNAs in mammalian cells (Nott et al. 2004; Wiegand et al. 2003; Wilkinson, 2005). It has been shown that the function of NMD proteins depends on their location. If located within an ORF, NMD factors stimulate translation and control high-fidelity translation termination. If located downstream of an ORF, they elicit RNA decay (Lykke-Andersen et al. 2001; Maderazo et al. 2000; Wang et al. 2001; Wiegand et al. 2003; Wilkinson, 2005). Thus, NMD proteins also demonstrate multifunctionality participating in two opposite processes. On the one hand, by taking part in NMD, they degrade mRNA and decrease the level of protein synthesis. On the other hand, by binding to mRNA within ORF, they stimulate protein synthesis and even correct naturally occurring mistakes (Wilkinson, 2005).

The described examples not only document the existence of several evolutionary conserved mechanisms of translation destined for production of multiple and functionally different isoforms of one gene product but also show that proteins involved in these mechanisms are multifunctional molecules that simultaneously may participate in opposite processes leading to decrease and to increase of protein synthesis. These mechanisms make a substantial impact in transformation of compact genetic information in diverse protein moiety.

Post-translational modifications

Although the amino acid structure of a protein is defined by the gene and mRNA encoding the protein, its final functional structure is achieved by numerous post-translational modifications. The majority of all proteins undergo co- and/or post-translational modifications (Rehfeld and Goetze, 2003). Knowledge of these modifications is extremely important, since they may alter physical and chemical properties, conformation distribution, folding, stability, activity, and, consequently, function of the proteins. The protein precursor may undergo a wide variety of proteolytic cleavages, N- and C-terminal trimmings and

amino acid derivatization in cells that express the protein. Occasionally, the same precursor is differently processed in different cell types (Rehfeld and Goetze, 2003). According to Rehfeld and Goetze (Rehfeld and Goetze, 2003) all post-translational modifications may be divided in three groups [Table 1 cit. from (Rehfeld and Goetze, 2003)].

Although this table contains many types of post-translational modification, it can not be considered as a complete list of possible modification. For example, it does not contain such modification as palmitoylation, ubiquitylation, methylation, protein folding and protein splicing which appear to be a powerful mechanism of protein diversity (Draper et al. 2007; Hanada et al. 2004; Mostaqul Huq et al. 2008; Nagradova, 2004; Perler, 2005; Schartner et al. 2007). The limit of the review volume does not allow discussion of all the possible post-translational modifications depicted in Fig. 1, F. Therefore, we will concentrate just on some of them—phosphorylation, glycosylation, palmitoylation, protein folding and protein splicing.

1. Protein phosphorylation

Protein phosphorylation is one of the most widespread type of post-translational modification of protein that allows the cell to control various cellular processes, including signal transduction, transcriptional and translational mechanisms,

Table 1. Post-translational modifications.

Endoproteolytic cleavages:

1. Dibasic sites
2. Monobasic sites
3. Post(poly) Clu/Asp sites
4. Post Phe-sites
5. Tri and tetrabasic sites

Exoproteolytic trimmings:

1. Carboxyamidation
2. Glutaminy cyclation
3. N-terminal dipeptidyl cleavage

Amino acid derivatizations:

1. Acylations
 2. Disulfide bridgings
 3. Gamma carboxylation
 4. Glycosylations
 5. Isomerisations
 6. Phosphorylations
 7. Sulfations
-

metabolism, growth, division, differentiation, motility, organelle trafficking, membrane transport, immunity, learning and memory (Manning et al. 2002a; Manning et al. 2002b). In eukaryotic cells, most phosphorylation occurs on Ser, Thr and Tyr residues (Ubersax and Ferrell, 2007). The phosphorylation state of phosphoproteins is controlled by the activity of protein kinases and phosphatases (Urner and Sakkas, 2003). According to calculation performed by Ubersax and Ferrell (Ubersax and Ferrell, 2007), a typical protein kinase must recognize between one and a few hundred *bona fide* phosphorylation sites in a background of about 700,000 potentially phosphorylatable residues in typical eukaryotic cell. Multiple mechanisms have evolved that contribute to this exquisite specificity, including the structure of the catalytic site, local and distant interactions between the kinase and substrate, the formation of complexes with scaffolding and adaptor proteins that spatially regulate the kinase etc (Ubersax and Ferrell, 2007).

Although different kinases demonstrate their individual specificities and peculiarities in phosphorylation processes, the main results of this post-translational modification are structural and functional changes of the substrate protein. Several examples can illustrate this statement.

Many nuclear receptors have been found to be modified by phosphorylation (Rochette-Egly, 2003). Testicular receptor 4 (TR4) is an orphan member of the nuclear receptor superfamily. In the absence of specific ligands the activity of TR4 can be modulated by mitogen-activated protein kinase (MAPK)-mediated phosphorylation of its AF-1 domain (activation function 1). MAPK-mediated phosphorylation of the AF-1 domain renders TR4 a repressor while dephosphorylation of the AF-1 domain makes TR4 an activator (Huq et al. 2006). Reversible protein phosphorylation, like bidirectional regulation of TR4, is known to control a wide range of biological activities (Chen et al. 2005b; Collins et al. 2004; Kim et al. 2003; Koritschoner et al. 2001; Shyr et al. 2002; Tanabe et al. 2002).

Another example also may show the power of post-translational phosphorylation in determining the protein function. Glucose-mediated phosphorylation converts the transcription factor Rgt1 from a repressor to an activator (Mosley et al. 2003). In the yeast *Saccharomyces cerevisiae*, glucose induces the expression of the hexose transported *HXT* genes by modulation the activity of

transcription factor Rgt1 that functions as a repressor when glucose is absent. However, in the presence of high concentration of glucose, Rgt1 is converted from a repressor to an activator by glucose-mediated phosphorylation. Rgt1 activator is required for maximal induction of *HXT1* gene expression (Mosley et al. 2003).

Several transcription factors, as well as other proteins, have been shown to change their subcellular localization in response to external stimuli (De Vit et al. 1997; Komeili and O'Shea, 1999). Yeast protein Mig1 is phosphorylated by the Snf1 kinase in the absence of glucose and is trapped in the cytoplasm. High concentrations of glucose cause dephosphorylation of Mig1 and translocation into the nucleus (Komeili and O'Shea, 1999; Treitel et al. 1998). The subcellular localization of the other yeast protein, Pho4, is regulated in response to another agent, phosphate. At high concentrations of phosphate, Pho4 is phosphorylated and exported into cytoplasm, whereas starvation for phosphate causes dephosphorylation of Pho4 and translocation into the nucleus (Komeili and O'Shea, 1999).

These examples clearly demonstrate that definite functional potentials encoded in the primary protein structure by specific topology of Ser, Thr and Tyr residues may be uncovered and realized by specific phosphorylation events.

2. Glycosylation

Glycosylation is another widely observed post-translational modification of proteins. Proteins can be glycosylated on certain amino acid side-chains, and these modifications are designated as N- and O-glycosylation (Medzihradszky, 2002). N-glycosylated species are modified at Asn residues. O-glycosylation occurs at Ser or Thr-residues. It should be noted that characterization of both types of glycosylation is complicated by the fact that in some cases the same amino acids within a population of protein molecules may be derivatized with an array of different carbohydrate structures while in other cases they may remain unmodified. This site-specific heterogeneity may vary by species, tissue and may be affected by physiological changes (Medzihradszky, 2002). Thus, the same protein may be glycosylated in one type of cells and unmodified in another type of cell and the difference in glycosylation status will be reflected by different functions of a given protein in different

cells (Bloom et al. 1996; Hironaka et al. 1993). The analogous situation can be observed even in the same cells, however, at different physiological conditions (Nemansky et al. 1998).

The purpose of glycosylation, as any other post-translational modification, is to uncover functional activities hidden in the protein structure. By adding sugars to polypeptide molecule, glycosylation changes its structure in such a way that new function(s) may occur. For instance, Miranda et al. (Miranda et al. 2007) showed that neutralization properties of the HIV-specific antibody F240 were dramatically altered by glycosylation. This Ab, when produced in a hybridoma, is nonneutralizing. However, F240 IgG1 Ab expressed in CHO cells acquired a strong neutralization activity without a change in immunoreactivity. Sequencing of the F240 mRNA produced in the parental hybridoma and CHO cells revealed identical sequences, suggesting that acquired neutralization resulted from cell-specific post-translational modifications. Among different types of post-translational modification which the Abs may undergo during their intracellular maturation process, N-linked glycosylation is one of the best characterized. It is widely acknowledged that an Ab expressed in CHO cells is differentially glycosylated as compared with an Ab produced in other mammalian cells (Routier et al. 1997; Sheeley et al. 1997). Miranda et al. (Miranda et al. 2007) showed that the Ab produced by CHO cells is glycosylated to a greater extent than parental Ab produced by the hybridoma. It was found that the F240 Ab produced in CHO cell had significantly more terminal glycans and core fucose when compared with the F240 Ab from hybridoma. Moreover, treatment with peptide N-glycosidase F abrogated F240 neutralization. This study showed that structural changes induced by additional N-glycosylation in the F240 Ab determined functional changes in its neutralizing activity.

Two other examples show the effect of O-glycosylation on the conformation and biological activities of two other proteins, calcitonin and prion protein. Using different O-glycosylated calcitonin derivatives, each with a single GalNAc residue attached to either Ser or Thr, Tagashira et al. (Tagashira et al. 2001) have demonstrated that calcitonin conformation and its hypocalcemic activity were strongly dependent on O-glycosylation. Moreover, these authors evidenced that effect of glycosylation was clearly site-specific:

glycosylation at Thr-6 affected both the structure and activity, at Ser-5 only activity and at Ser2 none, indicating that the site dependence was very strict. The drastic difference in the hypocalcemic activity observed in this study could be explained by the steric inhibition of the interaction with the receptor (Tagashira et al. 2001).

It has been known for a long time that the structural transition from PrP-c, the normal product of the prion gene, to PrP-sc, the pathological form of the protein, leads to the prion formation and to disease, however, the mechanism of this transition was obscured. Based on prion peptide studies, Chen et al. (Chen et al. 2002) provided evidence for linking of O-glycosylation to the structural transition of PrP-c to PrP-sc. They found that O-linked α -GalNAc at Ser-135 suppressed the development of the amyloid fibril formation of the prion peptide at physiological salt concentration, whereas the peptide with the same sugar but at different location, at Ser-132, showed the opposite effect. Moreover, this effect was sugar specific: replacing α -GalNAc with β -GalNAc did not yield the same effect (Chen et al. 2002).

As we have already noted, many types of post-translational protein modifications have been described (Rehfeld and Goetze, 2003). They all are directed to modify structure of the parental polypeptide chain thus increasing number of protein's functions. It is *a priori* obviously, that for achieving maximal functional variability and adaptivity to environment by post-translational modification, the compact polypeptide structure must contain sites that might be sensitive to different type of modification. Moreover, the same site could be sensitive to different modifying reactions, so the different modifying agents could compete for these sites (competitive modification). The correctness of such suggestion was confirmed by the discovery that phosphorylation and glycosylation may compete for and modify the same amino acid residues in targeted proteins (Kelly et al. 1993).

The O-linked β -N-acetylglucosamine (O-GlcNAc) is a monosaccharide modification abundant on serine and threonine residues of a multitude of nucleo-cytoplasmic proteins in virtually all higher eukaryotes, including plants and fungi (Comer and Hart, 2000; Hart, 1997; Hart et al. 2007; Torres and Hart, 1984; Wells and Hart, 2003). The attachment and removal of O-GlcNAc by O-GlcNAc-transferase and O-GlcNAcase, respectively, is rapid reactions analogous to

dynamics of O-phosphate adding or removing controlled by kinases and phosphatases (Dong and Hart, 1994; Haltiwanger et al. 1992; Haltiwanger et al. 1990; Krebs, 1993; Kreppel et al. 1997; Kreppel and Hart, 1999; Lubas et al. 1997). It has been shown that O-GlcNAc sites resemble phosphorylation sites, and in many cases the two modifications are mutually exclusive (Kelly et al. 1993). Reversible phosphorylation and alternative glycosylation induce changes in secondary and tertiary structures and control the functional behaviour and modular interactions of proteins (Ahmad et al. 2007; Cheng and Hart, 2001; Pawson and Gish, 1992). For example, in case of estrogen receptor β (Cheng et al. 2000), SV-40 large T antigen (Medina et al. 1998) and the c-Myc oncogen (Chou et al. 1995a; Chou et al. 1995b), O-GlcNAc and O-phosphate compete for the same hydroxyl moiety. Like phosphorylation, O-GlcNAcylation is responsive to the cell cycle, extracellular signals, glucose metabolism, cell growth and regulation of transcription and translation (Chou and Omary, 1994; Datta et al. 1989; Du et al. 2000; Han et al. 2000; Kears and Hart, 1991; Roos et al. 1997; Roquemore et al. 1996).

The examples described above show once again that primary protein has many possibilities to be modified. What type of modification it will undergo depends on many factors such as cell type, cell cycle, extracellular and intracellular signals, pH gradient, local concentrations of specific modifying molecules etc. As a result, the protein will possess a specific function in an appropriate cell, at definite cell compartment and at the precise time.

3. Protein palmitoylation

The next type of protein modification that we would like to discuss is S-palmitoylation. A major mechanism by which cells regulate the subcellular localization of proteins is post-translational lipidation (Draper et al. 2007). S-palmitoylation is one of lipid modifications that is reversible thioester linkage of palmitate, a 16 carbon saturated fatty acid, to cystein residues (S-palmitoylation) catalyzed by membrane-bound palmitoyl-transferases (PATs). Palmitoylation increases the hydrophobicity of the modified molecules (Greaves and Chamberlain, 2007).

It is *apriori* obviously, that simultaneous display of the principles of structural compactness with maximal functional variability demands that sites on the polypeptide molecule that may undergo

different types of modification should be overlapped or even be the same, and different modifying agents should compete for these sites of proteins by altering their conformation. The changes in structure of proteins promotes their localization to specific cellular compartments, contributes to their membrane association and control protein-protein interactions. They also regulate subcellular trafficking of proteins between membrane organelles and within microdomains of the same membrane compartments and modulate their functions (Bijlmakers and Marsh, 2003; Casey and Seabra, 1996; Dunphy and Linder, 1998; el-Husseini Ael and Bredt, 2002; Milligan et al. 1995; Nadolski and Linder, 2007; Resh, 1999; Silvius, 2002).

For many palmitoylated proteins, the half life of the palmitate moieties is significantly shorter than that of the substrate proteins, indicating that the complex goes through cycles of depalmitoylation and repalmitoylation. The reversibility of palmitoylation suggests that it is a regulated modification much like protein phosphorylation. Depalmitoylation and repalmitoylation could provide a mechanism to regulate such processes as binding cytosolic proteins to membranes, segregating proteins to microdomains and mediating protein-protein interaction. For proteins involved in signal transduction, these cycles could be induced by activation and by controlling access to specific substrates (Bijlmakers and Marsh, 2003; Casey and Seabra, 1996; Dunphy and Linder, 1998; el-Husseini Ael and Bredt, 2002; Milligan et al. 1995; Nadolski and Linder, 2007; Resh, 1999; Silvius, 2002). Palmitate cycling on the scaffolding protein PSD-95 may illustrate this mechanism. Palmitoylation allows PSD-95 to cluster in the postsynaptic membrane. Blocking of PSD-95 palmitoylation leads to a loss of AMPA receptors from these domains by the rapid endocytosis of AMPA receptors which requires depalmitoylation of PSD-95 (el-Husseini Ael and Bredt, 2002; Nadolski and Linder, 2007).

Several other examples can additionally illustrate the roles of palmitoylation in protein functioning. It has been shown that palmitoylation controls the regulator of G-protein signaling (RGS). Palmitoylation of the Cys residue in the RGS box is essential for RGS16 GAP activity and their ability to regulate G-coupled signaling in mammalian cells. Enzymatic palmitoylation of RGS16 results in internal palmitoylation on residue Cys-98.

Mutation of this residue to alanine reduces GAP activity of the 5-HT-1A/G α fusion protein (Osterhout et al. 2003).

S-palmitoylation, as shown by study of Marino et al. (Marino et al. 2006), can modulate estrogen receptor α (ER α) localization and functions. In cells expressing wild-type of ER α , a major population of estrogen receptor was membrane-associated whereas in cells expressing the ER α Cys447->Ala mutant no membrane-bound receptor has been detected. Moreover, ER α Cys447->Ala mutation does not allow E2-induced proliferative signaling via ERK/MAPK and P13K/AKT pathways in human cancer cells (Acconcia et al. 2005). As a whole, S-palmitoylation allows the extra-nuclear localization of ER α and promotion downstream of signaling for E2-mediated proliferation (Marino et al. 2006).

S-palmitoylation, like phosphorylation and glycosylation, is important post-translational modification that provides proteins with many important functions and controls cell processes dependent on these functions. Thus, as other post-translational modifications, palmitoylation fulfills the main principle of protein structural/functional relationship: gaining maximal functional activities by introducing minimal but specific changings in the protein structure.

4. Protein folding

The protein architecture opens many ways for proteins to obtain multiple functions. Evolution gives many examples confirming this statement. In some cases, evolution can merge proteins by changing tertiary to quaternary structure. For instance, five separate enzymes in the bacterium *E. coli* that catalyze successive steps in the pathway of biosynthesis of aromatic amino acids, correspond to five regions of a single protein in the fungus *Aspergillus nidulans* (Lesk, 2001).

To become functionally active, a newly synthesized polypeptide chain must fold a unique three-dimensional structure. Although experiments *in vitro* have firmly established that the information on the three-dimensional structure of a protein is genetically determined and contained in its amino acid sequence (Anfinsen, 1973; Dobson and Karplus, 1999; Nagradova, 2004), protein folding in the cell cannot be regarded as occurring spontaneously (Nagradova, 2004). It has become clear that many proteins require assistance to fold in the

cell and that this is provided by helper proteins (molecular chaperones) (Bukau and Horwich, 1998; Coyle et al. 1997; Fewell et al. 2001; Gutsche et al. 1999; Hartl and Hayer-Hartl, 2002).

The action of chaperones is based on two different mechanisms. The first mechanism consists of maintaining the polypeptide chain in a state capable of productive folding, which occurs spontaneously after release of unfolded chains into solution. Thus, interaction with the chaperone has no effect on the folding *per se* (Nagradova, 2004).

The second mechanism is used by chaperons, whose large cylindrical complexes create physically isolated compartments destined for the folding of polypeptides, partially folded or misfolded proteins, which become encapsulated inside the central cavity. Since only one molecule of the substrate protein can fit inside the cavity, its folding takes place under conditions, which completely exclude aggregation (Nagradova, 2004). However, the role of chaperons clearly is not limited to their ability to create isolated compartments where protein can fold spontaneously under condition simulating infinite dilution (the "Anfinsen cage" model) (Ellis and Hartl, 1996). A large body of information accumulated to date supports the notion that chaperons can play an active role in protein folding, accelerating this process and considerably increasing its efficiency (Nagradova, 2004). A special group of helper proteins so called foldases (Balbach, 2000; Wu and Matthews, 2002) and protein disulfide isomerases (Creighton, 2002; Frand et al. 2000) assist protein folding by catalyzing the rate-limiting isomerization reactions.

5. Protein splicing

A simple view of protein expression is continually challenged by new examples of post-translational processing. These examples include non-ribosomal addition of moieties and proteolytic cleavage of polyprotein as well as excision and rearrangements such as intein-mediated protein splicing, splicing by reverse proteolysis, protein auto-processing and proteasome-mediated peptide ligation (David et al. 2004; Hanada et al. 2004; Noren et al. 2000; Paulus, 2001; Perler, 2005; Perler et al. 1994; Vigneron et al. 2004).

a) Intein-mediated protein splicing

Inteins are internal segments of precursor proteins that catalyze their *ipso* excision by an

intramolecular process called protein splicing, with the concurrent ligation of the two flanking external regions (N- and C-exteins) through a native peptide bond (David et al. 2004; Perler, 2005). Inteins are found in proteins of unicellular organisms belonging to all three domains of life Archaea, Bacteria and Eukarya as well as in viral and phage proteins but have not yet been detected in higher organisms such as Vertebrata (Hanada and Yang, 2005). More than 100 inteins are known. Intein host proteins are very diverse, including DNA and RNA polymerases, ribonucleotide reductases, ATPases, proteases, metabolic enzymes, transcription and translation factors (Petrokovski, 2001). The following properties differentiate intein-mediated protein splicing from other types of protein rearrangements: (a) intein signature sequence, (b) a self-catalytic reaction in the absence of exogenous proteins, cofactors or energy sources, and (c) the formation of a native peptide bond between the ligated exteins (Perler, 2005).

Inteins can be divided into four classes: the maxi inteins (with integrated endonuclease domain), mini inteins (lacking the endonuclease domain), trans-splicing inteins (where the splicing junctions are not covalently linked) and Ala inteins (Ala as the N-terminal amino acid) (Evans and Xu, 2002). The intein specific sequences have some characteristics in common. They appear in conserved regions of the host protein. All intein sequences harbor different blocks termed A and B at the N-terminal splicing domain and F and G at the C-terminal splicing domain.

Inteins typically have N-terminal Cys, Ser or Ala residues and C-terminal His or Asn and inserted into host proteins next to Cys, Ser or Thr (Hanada et al. 2004). Although amino acids indicated above are typical for inteins, many inteins have other amino acids at specific blocks. It is likely that each intein has specific combination of nucleophiles and assisting groups honed during evolution for optimal function. Structural studies have not identified more consensus facilitating residues because each intein has different residues with similar chemical functionalities at or near its active site (Perler, 2005). The smallest known intein consists of 134 amino acids (Evans et al. 1999), and most are much larger.

The role of inteins in the cell is as yet unclear, however, one can assume that because inteins are integrated in highly conserved protein regions, the

function(s) of host protein before and after excision of intein might be different. If intein has to excise itself for activation the host protein function, it has to be sensitive to specific signals. There are some indications that this is the case (Chong et al. 1998; Southworth et al. 1999). It has been established that intein regulates activity of *Synechocystis* sp.PCC6803 DnaE functioning as internal regulator (Ghosh et al. 2001). Free inteins (after splicing) may perform regulatory as well as enzymatic function by itself (Klabunde et al. 1998; Starokadomskyy, 2007). Thus, although it has been evidenced only in limited number of proteins, inteins may determine different functions of host protein before and after splicing and to obtain new function(s) after self-excision.

b) Post-translational splicing by reverse proteolysis

Another example of post-translational modification, protein splicing by reverse proteolysis, is a protein splicing discovered in plants. It was observed with the lectin concanavalin A (Con A) (Carrington et al. 1985). The following steps of this kind of protein splicing were described. The initial precursor of Con A (glyco-pro-Con A) is first activated by deglycosylation to pro-Con A. Pro-Con A is then cleaved to produce two distinct proteins that are transposed and relegated to become mature Con A. Although the exact mechanism of this splicing in plants is still not clear, *in vitro* study showed that asparaginyl endopeptidase can digest Con A and then re-ligate the digested fragments by its reverse proteolytic activity (Min and Jones, 1994).

c) Proteasome-mediated protein splicing

Recently it has been shown that proteasomes are cell compartments where not only protein degradation but also post-translational protein modifications occur (Hanada and Yang, 2005; Hanada et al. 2004; Vigneron et al. 2004). Hanada et al. (Hanada et al. 2004) discovered that antigen maturation and presentation may be performed in proteasome by protein splicing involving peptide excision and re-ligation. They showed that in contrast to intein splicing that usually excised polypeptide of not less than 134 amino acids in length (the smallest known intein is consist of 134 amino acids) the excised polypeptides in their system were as short as 18–40 amino acids. Using the proteasome inhibitor, clasto-lactacystin β -lactone, the authors

evidenced that FGF-5 protein splicing observed in their system was proteasome-mediated (Hanada and Yang, 2005). Moreover, these authors showed for the first time that protein splicing may occur in human cells.

Another group also described an antigen production from a protein by splicing of noncontiguous peptides in the reverse order (Vigneron et al. 2004). This splicing was conducted by 20S proteasome *in vitro* and *in vivo*. In the described systems the length of excised intervening region was only four amino acids (Noren et al. 2000; Vigneron et al. 2004). Thus, the proteasome-mediated splicing overcomes the limitation associated with the length of intervening sequences which is crucial for intein-mediated protein modification.

What are the implications of these findings? As Hanada et al. underlined these findings show that “immune system monitors non-contiguous peptide sequence generated post-translationally. This capability represents an enormous increase in the ability of CTLs to recognize self and foreign proteins... In a broader context, the existence of protein splicing in vertebrates greatly increases the cell's options for converting genetic information into proteins” (Hanada et al. 2004). These results also show that protein splicing is a powerful mechanism allowing realization of the main principle of protein multifunctionality—transformation of compact genetic information into wide diversity of protein structures and functions. “Processes such as DNA recombination and RNA splicing were already known to increase the number of different proteins produced by each of mammalian genes; the discovery of protein splicing adds to the tool kit” (Rammensee, 2004).

III. Multifunctionality as Intrinsic Feature of Different Types of Proteins

In the previous section we have described some of the mechanisms by which the Nature develops multifunctionality of the protein molecules. Below, we present examples of proteins belonging to different groups that demonstrate high extent of multifunctionality.

1. Amino-acyl tRNA synthetases

Amino-acyl tRNA synthetases, an ancient conserved family of proteins well known for its

participation in protein synthesis, are a good paradigm of protein multifunctionality. Several studies have described numerous examples of these “housekeeping” proteins taking part in extensive critical cellular activities other than protein synthesis. These are cellular fidelity, cytokine-like activity, angiogenesis, RNA splicing, RNA trafficking, apoptosis, transcriptional and translational regulation. Amino-acyl tRNA synthetases can even block protein synthesis as established by the recent studies performed with glutamyl-prolyl-tRNA synthetase (Glu-ProRS) (Otani et al. 2002; Sampath et al. 2004; Wakasugi and Schimmel, 1999).

The lysyl-tRNA synthetase (LysRS) has been shown to have a dual functionality. In addition to its contribution to the translation process, LysRS also function as a positive regulator of MITF and USF2 transcription factors via the synthesis of Ap4A (Lee et al. 2004; Lee and Razin, 2005; Plateau and Blanquet, 1982; Yannay-Cohen and Razin, 2006; Zamecnik et al. 1966).

Tyrosyl-tRNA synthetase and tryptophanyl-tRNA synthetase upon their release in intracellular environment become proinflammatory cytokines with multiple activities during apoptosis, angiogenesis and inflammation. In addition, these proteins play important role in cancer progression, modulation tumor angiogenesis and its escape from surveillance by immune system (Ivakhno and Kornelyuk, 2004).

2. Cell-surface receptors

a) MUC1 protein

The MUC1 is a mucin-like type I transmembrane glycoprotein normally expressed on the surface of epithelial, hematopoietic and some other cells (Baruch et al. 1997; Weiss et al. 1991; Zaretsky et al. 1990). It is generally accepted that MUC1 gene is transcriptionally regulated (Zaretsky et al. 2006; Zaretsky et al. 1999). It is transcribed as a single pre-mRNA followed by alternative splicing leading to synthesis of isoform specific polypeptide chains. Several MUC1 isoforms, MUC1/TM, MUC1/X, MUC1/Y, MUC1/Z and MUC1/SEC, have been identified (Tsarfaty et al. 1990; Williams et al. 1990; Wreschner et al. 1990; Zrihan-Licht et al. 1994). MUC1/TM and MUC1/X are synthesized by translation of alternatively spliced mRNAs as single polypeptides that undergo auto-cleavage while in the endoplasmic reticulum to yield the

amino-terminal extracellular α -subunit, which in case of MUC1/TM contains O-glycosylated tandem repeats of 20 amino acids, and the carboxyl-terminal β -subunit, containing the membrane anchor (transmembrane domain) and cytoplasmic tail (Altschuler et al. 2000; Hilkens and Buijs, 1988; Kinlough et al. 2004; Ligtenberg et al. 1992; Linsley et al. 1988; Litvinov and Hilkens, 1993; Zrihan-Licht et al. 1994). The resulting subunits remain tightly associated with each other composing the MUC1/TM and MUC1/X isoforms, respectively.

The MUC1/TM and MUC1/X contain the SEA domain which is responsible for the self-cleavage of the precursor protein molecules leading to development of α and β subunits. The MUC1/Y isoform also contains SEA domain, however, it lacks of 18 amino acids present in SEA domain of the MUC1/X isoform. In contrast to MUC1/X, the MUC1/Y is expressed as a single non-cleaved nascent polypeptide chain (Levitin et al. 2005b; Wreschner et al. 2002).

Translation of the MUC1/Z isoform is associated with frame shifting (Levitin et al. 2005a). The translation initiation of the MUC1 secreted form, MUC1/SEC, begins with the same AUG codon as other MUC1 isoforms, however, its termination stop codon is located in the first intron (Smorodinsky et al. 1996; Wreschner et al. 1990). The described structural peculiarities of MUC1 show its structural diversity which supposes also multiple different functions. Indeed, MUC1/TM, MUC1/X and MUC1/Y are expressed in plasma membrane and suppose to function as membrane receptors which cytoplasmic domains participate in different signal transduction pathways by interaction with the pathway specific transducer molecules (Li et al. 1998; Li et al. 2003a; Li et al. 2001a; Li et al. 2001b; Li et al. 2003b; Ren et al. 2002; Singh and Hollingsworth, 2006; Wen et al. 2003; Wreschner et al. 1994). It has been shown that besides participating in mucin forming layer, MUC1/SEC functions as ligand for MUC1/Y (Baruch et al. 1999). MUC1/Z demonstrates structural homology with some cytokins suggesting participation in defense inflammation reactions. Recently, it has been established that Hkr1 and Msb2, the yeast analogs of human transmembrane mucins, are putative osmosensors (Tatebayashi et al. 2007). These results indicate on possible new function of the MUC1.

b) LDL

The members of the low-density lipoprotein (LDL) receptor family are evolutionary conserved cell-surface receptors produced by mammals and other organisms (Nykjaer and Willnow, 2002). Initially thought to be endocytic receptors that exclusively mediate the uptake of lipoproteins (Goldstein, 2001; Willnow et al. 1994), recent studies in various experimental systems including knockout mice and patients with receptor gene defects uncovered a plethora of additional activities performed by these receptors (Gliemann, 1998; Gotthardt et al. 2000; Herz and Strickland, 2001). The prototype of the gene family is the LDL receptor, an endocytic receptor that mediates cellular uptake of cholesterol-rich lipoproteins. The LDL receptor like other members of this family is built by several functionally different domains which may interact with numerous of cellular proteins. These domains are represented by EGF precursor homology domain, complement-type repeat domain, O-linked sugar domain and NPxY motif. Among other molecules, these domains bind to proteases, protease inhibitors, signaling molecules, heat-shock proteins, vitamin carriers, toxins and antibiotics (Basu et al. 2001; Gliemann, 1998; Herz and Strickland, 2001; Howell and Herz, 2001). These receptors physically or functionally interact with other classes of cell-surface proteins such as seven-transmembrane-span receptors, ion channels, glycosylphosphatidylinositol (GPI)-anchored proteins and adhesion molecules, thereby acquiring activities not usually observed for endocytic receptors. Binding of ligands not only results in endocytic uptake but also affects many cellular functions, including migration, Ca-influx, transcytosis, protein processing, antigen presentation, signal transduction, synaptic plasticity and cholesterol and vitamin homeostasis (Nykjaer and Willnow, 2002).

3. Proteases

Proteases compose one of the biggest groups of proteins. Approximately 2% of mammalian genes encode proteases (Kaiserman et al. 2006)[179]. Comparative genomics reveals that those involved in immunity and reproduction show the most interspecies diversity and multifunctionality selected during evolution. Granzymes, the cytotoxic serine proteases used by cytotoxic lymphocytes to destroy virus-infected and malignant cells, are the examples of this protein group.

There are 5 granzyme genes in humans and 10 in mice, and it is suggested that granzymes have evolved through gene duplication. Although high sequence homology and conserved primary cleavage specificity of human and mouse granzymes were observed, they are structurally and functionally divergent (Bell et al. 2003; Kaiserman et al. 2006).

Human granzyme B (GrB) has multiple paralogues in the mouse and rat, suggesting that the roles fulfilled by a single enzyme in humans may be split among several in rodents (Pham et al. 1996; Revell et al. 2005). Although functioning primarily as a cytotoxin, GrB has other roles also. In humans it is found in testis and has been implicated in reproduction (Hirst et al. 2001). It is also involved in extracellular matrix remodeling (Buzza et al. 2005).

4. Protein kinases

Numerous protein kinases regulate multiple pathways of signal transduction. For instance, human platelets express at least six protein kinase C (PKC) isoforms which phosphorylate multiple proteins during platelet activation (Quinton et al. 2002; Tsukuda et al. 1988). During hemostasis and thrombosis, platelets have two distinct but additive functions in thromboformation, aggregation and procoagulant activity. Recently, the stimulating and inhibitory properties of all PKC isoforms in the thrombus-forming process have been studied. It was found that platelet PKC isoforms have a dual controlling role in thrombus formation as follows: (1) by mediating secretion and integrin activation required for platelet aggregation under blood flow, and (2) by suppressing Ca^{2+} -dependent phosphatidylserine exposure, and consequently thrombin generation and coagulation. Thus, platelet PKC is the signaling protein that balances the pro-aggregatory and procoagulant functions of thrombi (Strehl et al. 2007).

5. Cholinesterases

Cholinesterases A and B, AChE and BChE, are two enzymes which classical roles are “cholinergic functions” that originate from their cholinolytic capacity (Layer et al. 2005). However, recently non-classical functions of these enzymes have been uncovered (Johnson and Moore, 2004; Layer et al. 1993; Paroanu and Layer, 2004). A high degree of sequence homology between AChE and a family

of synaptic cell adhesion proteins, e.g. neuroligins, suggested that AChE may act also as a heterophilic cell adhesion molecule. Indeed, AChE was found to bind laminin- β 1, an extracellular matrix protein involved in neuronal differentiation and adhesion. AChE binds to the laminin- β 1 chain and through it can activate integrin receptor which in its turn activates intracellular signaling pathways. Thus, the complexing of AChE with laminin-1 represents a major signaling mechanism of AChE in cell formation process and pathfinding (Layer et al. 2005).

Besides of the described functions, both types of cholinesterases exhibit also aryl acylamidase activities (called AAA-AChE and AAA-BChE, respectively), which have been suggested to be involved in developmental processes (Layer et al. 2005).

6. Deglycosylation enzymes

Deglycosylation enzymes represents of group of proteins that catalyze separation of peptide component of glycoprotein from its carbohydrate part. As a paradigm of polyfunctional member of this group we chose the peptide: N-glycanase (PNGase). PNGase releases intact N-glycans from misfolded glycopeptides or glycoproteins which undergo deglycosylation during their degradation (Suzuki et al. 2002; Suzuki et al. 2007). The PNGase is a member of the transglutaminase (TGase) superfamily (Makarova et al. 1999). The orthologues of this enzyme are widely distributed throughout eukaryotes. While the “core” TGase domain is well conserved, a key difference is that orthologues in higher eukaryotes have additional domains at both N- and C-termini of the core domain. The PNGase of *S. cerevisiae* contains only TGase/PNGase domain, while *C. elegans* enzyme in addition to TGase domain has thioredoxin domain and Man-binding domain located N- and C-terminally, respectively. *S. cerevisiae* possesses only deglycosylation activity whereas PNGase from *S. elegans* exhibits dual enzyme functions, not only as PNGase but also as an oxidoreductase (thioredoxin). Thus, structural changes associated with additional domains exhibited additional function to modified molecule.

7. Growth factors

Growth factors are typically multifunctional proteins. Two examples will illustrate this notion.

FGFs are heparin-binding multifunctional growth factors which play a crucial role in a variety of developing processes (Bohlen, 1989). FGF-2 is one of the currently known members of the fibroblast growth factor family. It has been established that FGF-2 functions as 1) a differentiation factor for sympathoadrenal progenitor cells; 2) a target-derived neurotrophic factor for the preganglionic sympathetic neurons of the spinal cord and 3) an element of the auto-/paracrine chain in the adrenal medulla (Grothe and Meisinger, 1997).

Growth-colony stimulating factor (G-CSF), named for its specific stimulation of the growth of neutrophil progenitor cells *in vitro* (Roberts, 2005), is a growth factor known as a major extracellular regulator of haemopoiesis and innate immune system. G-CSF influences the survival, proliferation and differentiation of all cells in the neutrophil lineage, from haemopoetic stem cell to mature neutrophils. Recent researches uncovered initially unsuspected polyfunctionality for G-CSF. This growth factor is well recognized now as a signaling molecule as well as mobiliser of haemopoetic stem cells from bone marrow into the blood. Beside that G-CSF influences T-cell function and dendritic cell activation (Roberts, 2005).

8. Cytokines/chemokines

Chemokines are small cytokines that function in immune responses, wound healing, inflammation and tumorigenesis (Sorg, 1989). This multifunctionality has been attributed primarily to ligand interaction with multiple receptors. Recent studies have shown that their multifunctionality could also result from interactions of the receptors with small peptides produced by processing of the chemokines. Li et al. (Li et al. 2004) have analyzed the interactions between the two forms of human interleukin 8 (hIL8), N- and C-peptides, with the chemokine receptors hCXCR1 and hCXCR2 and showed that the N and C termini of the chemokine could stimulate the respective CXCR1 to induce intracellular Ca^{2+} release and MAPK activation independent of the other regions of molecule. These peptides could also stimulate chemotaxis of several cell types and this function is specific and mediated by hCXCR1 and/or hCXCR2. These findings advance understanding of the multifunctionality exhibited by chemokines.

9. Growth hormone

The growth hormone (GH) is a large multifunctional protein. It exhibits extensive heterogeneity. Some GH molecules/fragments are generated and secreted directly from the pituitary gland without any post-translational modification, whereas other molecules or fragments do arise from post-synthetic modifications (De Palo et al. 2006; Lewis et al. 2000; Wood, 2001). The link between molecular structures (different fragments of the GH-molecule) and biological effects were studied and analysis of functional activities possessing by different fragments of the GH molecule confirmed this statement.

It has been shown that the GH1-43 a.a. fragment possesses an important insulin-like activity, but does not appear to have growth-promoting activity. The insulin-like action of this amino-terminal segment has been confirmed in a series of GH peptide fragments including GH1-20 a.a., GH1-15 a.a. and GH6-13 a.a. All these GH fragments have been demonstrated to induce hypoglycaemia *in vivo* and amplify the actions of insulin *in vitro* (Ohkura and Hori, 2000).

GH44-191 a.a. fragment demonstrates neither growth-promoting nor insulin-like activities. On the contrary, it possesses GH antagonist activity (Clerico et al. 2000; Heffernan et al. 2000). GH108-129 a.a. fragment appears to possess mitogenic activity although intact GH demonstrates anti-mitogenic activity (De Palo et al. 2006). These data evidently demonstrate that different domains of the same protein molecule possess different and sometimes opposite functions.

10. Lactoferrin

Lactoferrin, a component of mammalian milk, is a member of the transfer proteins family (Brock, 2002; Kanyshkova et al. 2001). These glycoproteins transfer Fe^{3+} ions (Brock, 2002; Suzuki and Lonnerdal, 2002). Lactoferrin is a polyfunctional protein that influences cell proliferation and differentiation (Baveye et al. 1999). It regulates also granulopoiesis and DNA synthesis. Lactoferrin inhibits prostaglandin synthesis in human milk macrophages and activates the nonspecific immune response by stimulating phagocytosis and complement (Baveye et al. 1999; Mann et al. 1994; Ward et al. 2002). It interacts with macromolecules such as DNA, RNA, proteins, polysaccharides and heparin-like polyanions (Elass-Rochard et al.

1995; He and Furmanski, 1995; Son et al. 2002). In some cells lactoferrin functions as transcription factor (He and Furmanski, 1995; Mariller et al. 2007). It was recently demonstrated that lactoferrin also possesses ribonuclease activity (Kanyshkova et al. 2001).

11. Protein synthesis regulatory proteins

Protein synthesis regulatory proteins as well as proteins of other groups demonstrate extensive polyfunctionality. Sometimes, the functions they possess are unrelated or even opposite. As a paradigm of these proteins we will discuss the iron regulatory protein 1 (IRP1). IRP1 is a cytosolic, RNA binding protein that regulates the translation and stability of mRNAs encoding proteins for iron transport, storage, and use (Walden et al. 2006). IRP1 has an alternate function as cytosolic (c)-aconitase when the iron sulfur [4Fe-4S] cluster is bound (Eisenstein, 2000; Henderson and Kuhn, 1995; Hentze and Kuhn, 1996; Hentze et al. 2004; Kennedy et al. 1992; Theil and Eisenstein, 2000). The distribution of IRP1 between these mutually exclusive functions requires no new protein synthesis; iron excess promotes (c)-aconitase activity while starvation activates RNA binding function (Henderson and Kuhn, 1995). Assembly and disassembly of the iron-sulfur cluster appears to be effective mechanism for regulation IRP1 activity, dependent on facile interchange between the two functional conformations.

The RNA-binding and enzyme active sites are extensively overlapped in IRP1, with many amino acids serving important, but different, roles in each functional state of the protein. The functional plasticity of amino acids serving both catalytic and RNA binding roles reflects the conformational flexibility of the protein, particularly in the vicinity of the Fe-S and RNA binding sites (Walden et al. 2006).

12. Transcriptional factors

Proteins regulating transcription belong to a huge group of DNA binding proteins. Zinc-finger containing proteins represent one of the subgroups of these proteins. The WT1, zinc-finger containing transcription factor, is a multifunctional protein. Two alleles of WT1 gene is described: one contains insertion of three amino acids (+KTS) immediately after the zinc-finger 3b and another which does not contain this insertion (-KTS). In its transcriptional

roles the WT1(-KTS) acts as an activator (Lee et al. 1999) while WT1(+KTS) functions as a repressor of transcription (Loeb et al. 2002). The WT1(-KTS) also binds RNA and interacts with SF1 (steroidogenic factor nuclear hormone receptor). On the contrary, the WT1(+KTS) weakly interact with SF1 but strongly binds to U2snRNP-associated splice factor (Ladomery and Delleire, 2002).

Another zinc-finger protein coding gene, ZNF74, can produce multiple protein isoforms through alternative promoter usage and splicing: these exhibit differences in their transcriptional activities and nuclear partitioning (Cote et al. 2001). The original isoform, ZNF74-I, lacks the canonical N-terminal sequences of KRAB box A, localizes to speckle domains and exhibits weak transcriptional repression. In contrast to this, the ZNF74-II isoform contains the full KRAB A and B boxes, exhibits strong transcriptional repression and localizes in a diffuse pattern throughout the nucleus (Ladomery and Delleire, 2002).

The presented data show that these and probably other Zn-finger proteins possess functional versatility of the zinc finger motif and suggest that both alternative splicing and sub-cellular compartmentalization may modulate their multifunctionality.

13. Bacterial toxins

Bacterial toxins represent interesting examples of protein multifunctionality. Many toxins that act intracellularly have multidomain organization, with each domain capable of mediating a separate step of the intoxication process. There are numerous different mechanisms by which a bacterial toxin can produce pleiotropic cellular effects. On the basis of their ability to cause pleiotropic cellular effects, bacterial toxins may be regarded as multifunctional proteins (Cover and Blanke, 2005).

Two of the most extensively studied examples of multifunctional bacterial toxins are ExoS and ExoT from *Pseudomonas aeruginosa*. These toxins have multiple effector domains, each of which is associated with a discrete activity against the host cell. The N-terminal domains of ExoS and ExoT are GTPase-activating proteins (GAPs) that target members of the Rho family of small GTPases, which regulate processes in cytoskeleton (Goehring et al. 1999). The C-terminal domains are ADP-ribosyltransferases that modify multiple host proteins, including Ras and Ras-like GTPases

(Vincent et al. 1999). The discrete effector domains of these toxins may retain functional activity if expressed as individual proteins. The RhiGAP activities of EXoS and ExoT are almost identical, whereas ExoS and ExoT ADP-ribosylation effects are directed to different substrates (Barbieri and Sun, 2004).

Another example of a multifunctional toxin is the binary toxin produced by *Bacillus anthracis*. The B subunit of this toxin (protective antigen) can translocate two different A subunits into host cells. The A subunits may function as a metalloproteinase known as lethal factor or as adenylate cyclase known as oedema factor. On entry into host cells, lethal factor can cause many different effects, including alteration of dendritic-cell functions, repression of glucocorticoid-receptor transactivation, lysis of macrophages and apoptosis (Agrawal et al. 2003; Friedlander, 1986; Kirby, 2004).

The VacA toxin of *Helicobacter pylori* also possesses multiple functions producing upon entry into the cell: alterations in late endosomes, alterations in mitochondrial membrane permeability and inhibition of T-cell proliferation (Cover and Blanke, 2005).

Thus, many bacterial toxins are multifunctional proteins. By producing toxins with multifunctional properties, bacteria are able to use a single protein to produce a range of effects at different sites in the host, depending on which cell types and tissues are targeted. Consolidating multiple functions within a single protein has several advantages to the bacteria, including conservation of genome space, conservation of energy and resources that would be needed to regulate, produce and secrete multiple gene products, and stoichiometric, special, and temporal control of multiple host-modulating activities.

14. Plant ABC transporters

The ABC-transporter superfamily is one of the largest protein families known. Its members can be found in bacteria, fungi, plants and animals (Henikoff et al. 1997; Martinoia et al. 2002). All ABC transporters consist of two pairs of basic structural elements: integral membrane-spanning domains and nucleotide-binding folds oriented towards the cytoplasm. In bacteria, most members of this family are responsible for the high-affinity uptake of small molecules (for example, maltose and histidine) (Higgins, 1992). Eukaryotic ABC

transporters mediate diverse cellular transport processes, such as excretion of potentially toxic compounds, lipid translocation, excretion of the mating factor of yeast, conferring heavy-metal tolerance, multidrug resistance, and antigen presentation, as well as exhibiting ion channel activity (Balzi and Goffeau, 1994; de Souza et al. 2000; Gottesman and Pastan, 1993; Higgins, 1995; Kelly et al. 1992; Kuchler et al. 1989; McGrath and Varshavsky, 1989; Szczypka et al. 1994). The first reports on plant ABC transporters showed that they are implicated in detoxification processes. Recent results indicate that the function of this protein family is not restricted to detoxification. Plant ABC transporters have been demonstrated to participate in chlorophyll biosynthesis, formation of Fe/S clusters, stromal movement and ion fluxes. They may also transport steroids and participate in signal transduction. Hence, plant ABC transporters play multifunctional central role in plant growth and development (Higgins, 1992).

“Hidden” protein functions

The list of the multifunctional proteins is not limited to the described examples and could be extended. The multifunctionality appears to be a general feature of proteins. It is most likely, that in cases where proteins exhibit monofunctionality, the other functions of a protein have simply not yet been identified. These are “hidden” functions.

The “hidden or eclipsed” function is not a rare phenomenon. Many causes may lead to situation when one or several protein isoforms can not be detected while they were synthesized and present in the cell. One such a cause is a very short half-life time of some mRNA and/or protein. Another cause is the efficiency of the mRNA detection methods. The generally used analysis of expressed sequence tags (ESTs) is not perfect because the EST collection does not represent all protein coding sequences and for most genes ESTs cover only a portion of the transcripts. For instance, only half of the genes located on human chromosome 22 are represented in the current EST database (Dias Neto et al. 2000). Moreover, 26% and 65% of the ESTs correspond to the extreme 5' and 3' ends, respectively, of any given transcript (Graveley, 2001; Regev-Rudzki and Pines, 2007). Because much of the functionally significant alternative splicing occurs in the coding region of the transcript, many alternative splicing

events might be overlooked by EST comparisons (Graveley, 2001).

Speaking about the causes leading to “loss of protein functions”, one should consider the phenomenon of dual- or multi-targeting of proteins and its consequence. The precise subcellular localization of a protein is critical for its function. Eukaryotic cells synthesize thousands of proteins, each having a specific function in a specific subcellular compartment. In recent years, a growing number of examples of single genes whose products are located to two (or more) separate compartments have been discovered (Huh et al. 2003; Karniely and Pines, 2005; Mackenzie, 2005).

There is a growing number of studies designed to develop a global screens of protein localization in order to characterize location-specific function (Kumar et al. 2002; Regev-Rudzki et al. 2005; Yook et al. 2004). However, these “large-scale” analyses often fail to detect one of the isoproteins in one of the locations of a dual targeted protein due to a highly uneven distribution between compartments. In frame of this phenomenon called by N. Regev-Rudzki and O. Pines ‘eclipsed distribution’ (Regev-Rudzki and Pines, 2007), the relatively large amount of an isoprotein in one subcellular compartment obscures the detection of the small amount of the other isoprotein in the other location (Levay and Viljoen, 1995).

As underlined by Regev-Rudzki and Pines (Regev-Rudzki and Pines, 2007), ‘such eclipsed distribution phenomena have a wider occurrence than recorded currently; the reason being that, in most cases, the small fraction of one of the isoproteins, in one of the locations, makes its detection very difficult. This is particularly true for the cytosol which occupies several fold larger volume than other compartments thus diluting a significant amount of a dual targeted protein, so that it is easily missed by the currently used large-scale visualization methods’.

Conclusion

The data presented in this review evidently show that genetic information embedded in nucleotide sequences of a genome contains a program of multiple structural and functional transformations of this information into real protein molecules that are involved in mirriads of reactions which ultimately determine physiology of a cell. Moreover, the encoded physico-chemical potentials of the

molecules allows intermolecular interactions in such a way that one molecules may modify the other molecules thus increasing structural and functional diversity of the proteins produced by a given gene. After all, thousands of protein molecules that build the multiple mechanisms responsible for protein synthesis and different post-translational modifications are encoded in a compact form in cell genome. Hence, the cell may be considered as a very economic self-coding and self-realizing system which effectivity is being achieved by usage of multifunctional protein molecules. Thus, the multifunctionality is not an exceptional feature of a particular protein but to the contrary it is a fundamental basic property of most or all proteins which allows the cell effective accomplishment of multiple and complex physiological processes.

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