Could also RNA and protein methylation of RNA be involved with the expression of molecular emotions?

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Abstract

The recent finding that synaptic connections involve more methyl marks of RNA than other parts of neurons and that the RNA marks tend associated with genes coding for proteins associated with synapses provides support for TGD based view that emotions are realized in terms of what I call bio-harmony for the dark analogs of basic biomolecules (DNA, RNA, tRNA, amino-acids) and that these these emotions are expressed as modifications of the basic biomolecules. The emotional states would have epigenetic effects changing the gene expression and inducing learning as modification of synapses in turn modifying the behavior. This picture provides also a mechanism for the inheritance of epigenetic modifications: what would be inherited would be emotional states represented in terms of bio-harmonies the level of magnetic body carrying dark protons.

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1 Introduction

Some time ago I wrote an piece of text) [L2] (see http://tinyurl.com/ydhxen4g) about learning of slime molds [?, ?]. The proposal was based on the vision inspired by the model of bio-harmony [L1, L3] and stating that harmony of music of light (and maybe of also sound) realized as 3-chords of dark photons with frequencies of 12-note scale expresses and creates emotions and that each harmony corresponds to a particular mood. The painful conditioning of the slime mold would generate a negative mood which would infect DNA and induce epigenetic change. This picture conforms also with the finding that RNA can induce learning of conditionings in snails [J1] (see http://tinyurl.com/ycqxyeqk) [L2]. Slime mold does not have central nervous system but a natural guess would be that also synaptic learning involves similar mechanism.

One can ask whether also RNA and protein methylation could be involved with learning. If molecular moods correspond to bio-harmonies and if the conditioning by say painful stimulus involves a change of the emotional state of RNA inducing that of DNA, it must change some of the chords of the bio-harmony. Since bio-harmony is essential for communications by dark photons between dark proton triplets representing dark variants of the basic biomolecules and also between communications between bio-molecules and their dark variants, one expects that the change of the harmony occurs for all dark analogs of biomolecules and also for their ordinary biomolecules. Some chords represented by DNA-, RNA-, and tRNA codons, and amino-acids - briefly basic bio-molecules - would be affected in the change of mood.

The recent finding (see http://tinyurl.com/y9qsnfeo) that synaptic connections involve more methyl marks of RNA than other parts of neurons and that the RNA marks tend associated with genes coding for proteins associated with synapses provides support for this view that emotions expressed as modifications of the basic biomolecules. The emotional states would have epigenetic effects changing the gene expression and inducing learning as modification of synapses in turn modifying the behavior. This picture provides also a mechanism for the inheritance of epigenetic modifications: what would be inherited would be emotional states represented in terms of bio-harmonies the level of magnetic body carrying dark protons.

2 Some background about modifications of the basic biomolecules

To get a some perspective consider first some background about the modifications of the basic bio-molecules.

1. In the case of DNA epigenetic modifications (see http://tinyurl.com/kdd3qmp) affect mRNA and thus also protein expression. There are two basic mechanisms involved. Methylation of C nucleotide of DNA and protein modification for histone.

   Methylation (addition of CH_3 to N) of C nucleotide leads to a silencing of gene expression. Methylation occurs typically for CpG pairs and for both strands. Before embryogenesis demethylation occurs for the entire DNA (stem cell state) but cell differentiation means methylation of genes not expressed. In vertebrates 60-80 percent of CpG is methylated in somatic cells. CpG islands form an exception involving no methylation. Demethylation (see http://tinyurl.com/ybg3mz6v) as the reversal of methylation occurs either spontaneously or actively.

   The effects on gene expression can be also inherited to next generations. The mechanism of inheritance is poorly understood. The epigenetic change should be also somehow communicated to the DNA of germ cells but this seems impossible. The mystery is deepened because before embryogenesis demethylation occurs for the entire genome. It is difficult to understand how the chemical storage of the information about methylation patterns to be transferred to the next generation is possible at all.

   The TGD view about emotional expression inducing epigenesis by communications via dark photons between basic biomolecules and their dark variants suggests an elegant mechanism. What would be inherited would be the emotional states represented by bio-harmonies assignable to the dark variants of biomolecules.

2. In the case of pre-RNA post-transcriptional chemical modifications (see http://tinyurl.com/y8c4w4mp) - in particular methylation, are known to occur, and they affect RNA splicing rates and change the distribution of mRNAs and thus of proteins. The modifications affect also un-translated RNA (UTR) but not the protein translation from mRNA.

3. Protein modifications (see http://tinyurl.com/jtczea5) in turn affect the dynamics of proteins - in particular their properties as enzymes by affecting therefore the rates for various basic processes.

   As already noticed, protein modifications are important in epigenesis by histone modification. Wikipedia article mentions lys acetylization by adding CH_3=O group (see http://tinyurl.com/yd2y7s2m), lys and arg methylation (see http://tinyurl.com/ybxgdwhz), ser and thr phosphorylation, lys ubiquintination and sumoylation. For N-terminus (H_2 group in the start of protein) the process is irreversible and new amino acid residues emerge. Methylation in C terminus (O=C-OH end of protein) can increase chemical repertoire. Note that the methylation occurs at the ends of the protein just like it tends to occur in the case of RNA as will be found.

RNA modifications deserve to be discussed in more detail. This field of study is known as epitranscriptomics (see http://tinyurl.com/y8c4w4mp) . These chemical modifications does not affect protein expression except in the case that they affect the rates of various alternative pre-RNA splicing so that the distribution of alternative protein outcomes changes. Clearly, the effect

is somewhat like the effect of mood on overall activity. There are also many other modifications of RNA (see http://tinyurl.com/y8c4w4mp). One of them is A-I de-amination which changes in RNA but does not affect protein expression.

The methylation of RNA is the most common and best understood modification of RNA.

1. The modelling of the methylation of both DNA and RNA is based on writer-reader-eraser model. Writing corresponds to methylation. Reading corresponds to attachment of enzymes involved in the splicing or protein synthesis with higher rate to methylated sites. Demethylation is example of erasing.

2. Methylation is known to occur for various variants of RNA (ribosomal rRNA, tRNA, mRNA, and small nuclear RNA snRNA related to metabolic machinery) after transcription. The biochemical modifications of RNA are called epitranscriptomes (see http://tinyurl.com/y8c4w4mp). N^6-Methyladenosine (m^6A) is the most common and best understood modification of RNA. m^6A tells that nitrogen in position 6 of adenosine (A) is methylated by adding group CH_3. m^6A sites are often located in the last exon near the end of mRNA, in untranslated RNA (UTR) at 3' end, and inside long exons.

   It has been found that 3 members of so called YTH domain protein family acting as readers have larger affinity to bind to methylated sites. One of them shortens the lifetime of mRNA after translation.

3. Methylation in general shortens the UTR (un-translated regions) of mRNA in its 5' and 3' ends (head and tail of mRNA)). One speaks of alternative poly-adenylation (APA, see http://tinyurl.com/y7aratpv) of the tail of the mRNA: poly-adenylation (PA) adds A-sequences to the end of mRNA affecting its dynamics: shortening of UTRs means shortening of PAs.

4. Methylation affects the rates in the dynamics of translation but does not affect the product of translation itself. A-sequences shields mRNA and during its life cycle its length is reduced somewhat like telomere (see http://tinyurl.com/jpbkzzc) consisting of a repeated sequence TTAGGG and also shortening during the life cycle of DNA. APA affects rates for the dynamics of translation. Also stem loops of pre-RNA can be methylated and this can increase the rate of an alternative splicing and thus change relative rates of alternative gene expressions.

3 Methyl marks in synaptic connections from the TGD point of view

What inspired this piece of text was a highly interesting popular article "Methyl marks on RNA discovered to be key to brain cell connections" about methylation of RNA in brain (see http://tinyurl.com/y9qsnfeo). The research article [J2] (see http://tinyurl.com/ybg92nyd) by Daria Merkuvjev et al has title "Synaptic N6-methyladenosine (m6A) epitranscriptome reveals functional partitioning of localized transcripts". The researchers isolated brain cells from adult mice and compared epitranscriptomes found at synapses to those elsewhere in the cells. At more than 4,000 spots on the genome, the mRNA at the synapse was methylated more often. In more than half of genes the epitranscriptomes were found in genes coding for proteins found mostly in synapses. If the methylation was disrupted, the brain cells did not function normally. It was concluded that the methylation probably makes signalling faster.

These findings conform with the idea about representation of molecular emotions as bio-harmony. Synaptic contacts are the places where emotions should be expressed to give rise to learning by conditioning realized in terms of changed synaptic strengths. If the communication between dark and ordinary biomolecules relies on resonance frequencies, it is is preserved only if the resonance frequencies for ordinary biomolecules are modified. Methylation would be one particular mechanism for changing some 3-chords of the harmony (in the simplest model only one of the 3 notes of 3-chord corresponding to A in various position). The methylations of DNA, RNA and proteins should also correlate if they are in common mood dictated by the bio-harmony.

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