The problems of how genes code information about the morphology of
organism   and how this information is expressed, belong to the
great
puzzles of the   developmental biology. A closely related mystery is
the
differentiation of cells. The notion of the genetic program is far
from
precise and it is not clear how close the analogy with a computer
program
is. There are also several problems which challenge the basic
dogmas of
genetics.

\begin{enumerate} \item Only 1 per cent of DNA of human genome
actually
codes polypeptides. Eukaryote genes contain intron sequences which
are
transcribed into hnRNA but snipped of when hnRNA is transformed mRNA
in
process called slicing. The higher the evolutionary level of
organism, the
higher the fraction of introns is. Molecular Darwinists see introns
as
\blockquote{junk DNA} but there is evidence that introns are far
from junk. For
instance, the splicing of intron contribution from hnRNA to give
mRNA can
give several different outcomes depending on the stage of
development of
the organism and introns are crucial for the effectiveness of
immune
system. Hence one can wonder whether intronic mRNA and protein mRNA
could
both form the real output of gene subprograms serving in some sense
as
input for other gene subprograms. This interpretation obviously
conflicts
with \blockquote{gene-single protein} dogma in its basic form.

\item There are large amounts of highly repetitive DNA which is
silent. One
can wonder whether there is some fundamental mis-understanding
involved.
Could it be that this DNA is analogous to control DNA not
transcribed to
RNA and therefore not all useless.   There is also active repetitive
DNA.

\item There is large amount of silent DNA in control sections
between
genes. Could it be that this silent DNA expresses itself in some
nonchemical manner? Chemical expression is very slow, translation
rate

being twenty aminoacids per second, and one can wonder whether life might
have invented faster modes of gene expression and control of gene expression.

\item Plant genome is often by a factor of hundred longer than human
genome. One could argue that the complexity of organism is measured by the
length of the shortest program coding the organism. It is however not at
all obvious how the genome of plants could be more redundant than human
genome since repetitive sequences common to all animals are present.
Introns are in fact more frequent in human genome. This suggests that some
new unidentified degrees of freedom giving rise to complexity might be
present and that the chemistry of DNA in the sense of standard physics is
perhaps not all that is needed to understand genetic program.

\item Various self-organization processes such as self-assembly and
de-assembly are very frequent in living systems. The problem how genes give
rise to morphology of the organism is poorly understood.   This forces to
challenge the dogma of genetic determinism. One should be able to
understand what is determined by genes and what is determined by
self-organization and whether the genes of the   standard physics are
enough. \end{enumerate}

The reason why the above mentioned problems have turned out to be so
untractable might be due to a wrong view about space-time. Many-sheeted
space-time concept of TGD might be absolutely crucial for the expression
of genetic code. Gene itself might be many-sheeted space-time structure
coding faithfully   the topology of the expression domain of gene. This
many-sheeted structure of DNA could allow to understand the miraculous
looking features of DNA replication   and cell differentiation. TGD based
view of evolution as p-adic evolution implied by the basic quantum theory,
should be a crucial element of the picture. Together with p-adic length

scale hypothesis, with Combinatorial Hierarchy model for genetic code
allowing to interpret genes as Boolean statements, and general vision
about quantum control and coordination based on a hierarchy of weakly
coupled super conductors, the notion of many-sheeted DNA leads to precise
quantitative predictions and a general model for genetic program. In
particular, one can understand the mystery of introns. What interesting
from the point of view of our consciousness is that it might be possible to
interpret the Boolean statements represented by the exon and intron parts
of genes as a physical representation for our belief system. Thus genes
would code both matter-- and mind like hardware of the living system.

The notion of magnetic body is central in the TGD inspired theory of living
matter. Every system possesses magnetic body and there are strong reasons
to believe that the magnetic body associated with human body is of order
Earth size and that there could be hierarchy of these bodies with even much
larger sizes. Therefore the question arises what distinguishes between the
magnetic bodies of Earth and human body.

The vision about dark matter hierarchy labelled partially by a hierarchy
of values of effective Planck constant coming as integer multiples of the
ordinary Planck constant leads to a rather concrete view about the
hierarchy of magnetic bodies and implies a natural generalization leading
to the notion of super- and hyper genes. The original model assumption
$\hbar_{eff} = \lambda^{k_d}\hbar_0$, $\lambda\simeq 2^{11}$, is however
un-necessarily strong.

Super genes consist of genes in different cell nuclei arranged to threads
along magnetic flux sheets like text lines on the page of book whereas
hyper genes traverse through genomes of different organisms. Super and
hyper genes provide an enormous representative capacity and together

with
the dark matter hierarchy allows to resolve the paradox created by the
observation that human genome does not differ appreciably in size from that
of wheat.