

# Transcriptional control by G-quadruplexes: *in vivo* roles and perspectives for specific intervention

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## **Abstract**

G-quadruplexes are non-canonical DNA secondary structures involved in several genomic and molecular processes. Here we summarize the main G-quadruplex features and evidences proving the *in vivo* role on the transcriptional regulation of genes required for zebrafish embryonic development. We also discuss alternative strategies for specifically interfering G-quadruplex *in vivo*.

According to the model proposed by James D. Watson and Francis Crick in 1953, the DNA molecule consists of two polynucleotide chains wound around each other to form a clockwise double helix. This structure is known as B form of DNA (B-DNA), and is the predominant conformation adopted by DNA under relaxed conditions. However, non-canonical DNA secondary structures are widespread in all living organisms where they have profound effects on replication, transcription and genome stability. Guanine quadruplex (G-quadruplex), i-motifs, triplexes, cruciforms and hairpins secondary structures can lead to double strand breaks; induction or inhibition of transcription; and initiation or stalling of replication (Figure 1A). The formation of secondary structures may contribute to the generation of genetic diversity, polymorphism, and genome evolution. Conversely, they may result in a variety of genetic disorders, hereditary diseases and cancer through chromosomal rearrangements, mutagenesis, dysregulation of gene expression, and changes in the DNA replication process.

Among various non-canonical DNA structures, G-quadruplexes have attracted enormous research attention as prospective targets for chemical intervention of biological functions. Guanine rich single-stranded DNA has a strong propensity to fold into G-quadruplex *in vitro*. The consensus sequence  $[G_3N_{1-7}G_3N_{1-7}G_3N_{1-7}G_3]$  allows four sets of G triplets to form into three layers of G tetrads stabilized by Hoogsteen hydrogen bonding and  $K^+$  chelation<sup>1, 2</sup>. There are 376,000 putative quadruplex sequences (PQS) in the human genome that have been identified through genome-wide surveys based on quadruplex folding rules<sup>3, 4</sup>. PQS are highly frequent in proto-oncogene promoters<sup>5, 6</sup>; however, not all of them may exist *in vivo*. A prerequisite for the formation of G-quadruplex is the destabilization of the B-DNA double-strand helix, which is highly stable. The current hypothesis states that transcription bubble generates regions of positive and negative supercoiling, which can be propagated along the DNA-helix until reaching sites susceptible of structural transitions. In this condition, transiently exposed single-strand segments become able to fold as G-quadruplexes<sup>7</sup> (Figure 1B). G-quadruplexes may affect gene transcriptional activity either by

upregulation or downregulation, a function that can be evidenced by stabilizing or disrupting G-quadruplex formation through both interacting small ligands (drugs) and/or specific nucleic acid binding proteins <sup>8,9</sup>.

The validation of drug-targeted G-quadruplex DNA and the modulation of oncogenes expression intensely increased in the recent past. Despite a few of new anticancer drugs have entered preclinical or clinical trials <sup>10, 11</sup>, the selectivity of these compounds has yet to be improved. Up to now there are no drugs able to discriminate between G-quadruplexes affecting genome stability from those ones controlling gene expression. Even more, drugs cannot discern between G-quadruplexes controlling the transcription of oncogenes from those ones controlling the transcription of other essential genes. In this context, a novel strategy consisting of the use of short antisense DNA sequences or oligonucleotides (ASO) blocking the formation of a specific G-quadruplex has been recently reported <sup>12-14</sup>.

Numerous studies performed *in cellulo* have demonstrated the influence of different PQS patterns and loop lengths <sup>15, 16</sup>, the effect of ions <sup>17, 18</sup> and the action of specific G-quadruplex ligands <sup>8, 9, 19</sup> on G-quadruplex stability and the transcriptional process. Mostly, these studies consisted in assessing the effect of specific G-quadruplex ligands on the transcriptional expression of reporter genes governed by promoter elements containing PQS. Several reports suggest that G-quadruplexes act as transcriptional repressors by impeding transcription factor binding to duplex-DNA or stalling the progression of RNA polymerase, mostly when they are located downstream the transcription start site in the template strand <sup>2, 20-22</sup>. Conversely, other reports showed that G-quadruplex may enhance the transcription of particular genes by favoring the binding of specific transcription factors <sup>2, 12, 22</sup> or by holding the DNA molecule open thus facilitating the re-initiation of transcription <sup>2, 7, 14, 22</sup> (Figure 1B). Therefore, the hypothesis about a common behavior of G-quadruplexes on transcriptional control would be erroneous.

The *in cellulo* existence and potential impact of G-quadruplex on pathological processes is now accepted, but questions regarding their functions and mechanisms of action *in vivo* remain to be fully addressed. It was reported that microinjection in zebrafish embryos of small G-quadruplex ligands caused G-quadruplex stabilization along with downregulation of *Cdh5* transcription and the generation of embryonic phenotypes mimicking *Cdh5*-morphants<sup>23</sup>. However, such study was unable to conclusively demonstrate that phenotypes were due to the tested ligand on the *Cdh5* G-quadruplex. In view of the high number of PQS present in zebrafish genome<sup>14</sup>, the possibility of nonspecific or pleiotropic effects of such ligands could not be ruled out.

Although in past years the knowledge about the biochemical features and cellular roles of the G-quadruplex has made significant progress, the challenge was to demonstrate the direct role of these structures on a specific biological process carried out by complex multicellular organisms. The embryonic development resulted as an appropriate scenario to accomplish this goal. During embryonic development, gene expression is orchestrated by specific and highly evolutionarily conserved mechanisms that take place accurately, both at spatial and temporal levels<sup>24</sup>. An intricate array of *cis*-regulatory sequences controlling individual genes leads to a fine-tuning of gene expression. The last decades have provided compelling evidence that not only protein-mediated transcriptional control but also chromatin state play essential roles in orchestrating stages of embryonic development<sup>25, 26</sup>. Although the enrichment of G-quadruplex in promoter regions of developmentally regulated genes had been found in *in silico* analyses several years ago<sup>27</sup>, no experimental evidences proving the role of G-quadruplex in vertebrate embryonic development had been reported. In a recent work, evolutionarily conserved G-quadruplexes located within the proximal promoter region of genes required for proper craniofacial cartilage formation, notochord elongation and eye development were identified. The disruption of these G-quadruplexes *in vivo* by microinjection of specific ASOs in developing zebrafish resulted in lower transcription of the targeted genes, as well as in the recapitulation of the embryonic and larvae phenotypes reported for the respective morphants or mutants<sup>14</sup> (Figure 2). This pioneer work demonstrated the role *in vivo*

of G-quadruplexes as *cis*-acting elements contributing to the transcriptional regulation during the embryonic development, one of the most regulated processes of vertebrate's biology.

PQS in gene promoters may contain more than four G-stretches or more than three guanines in each stretch, thus resulting in a mixture of conformational isomers in a multiple dynamic equilibrium. Additionally, PQS genetic polymorphisms in G-stretches or even loop-regions may modify G-quadruplex formation and/or stability, thus significantly affecting gene expression among individuals<sup>28</sup>. In a particular cellular context, specific proteins could associate with a subpopulation of conformational isomers shifting the equilibrium toward a particular structure or bind differentially to polymorphic PQS. Consequently, both G-quadruplex alternative conformation and PQS polymorphisms might function as molecular switches enabling gene expression modulation by transitions in DNA structure. Of note, several proteins were identified associated with PQS; most of them are highly conserved zinc-finger DNA binding proteins. Because the versatility of zinc-finger binding pocket is remarkable, it is interesting to consider the implications of G-quadruplex–zinc-finger interactions as a pair<sup>29</sup>. In this context, variations in G-quadruplex conformational isomers, PQS genetic polymorphisms and protein domains may contribute to a fine tuning of transcriptional control.

### **Conclusions and perspectives**

Knowledge about G-quadruplex structure and biochemical features opens up a new field for exploring their biological functions, which might be relevant for understanding the regulation of several cellular and biological processes. G-quadruplexes existence had already been shown both *in cellulo* and *in vivo* and their role in transcriptional regulation is now evident. Profound insights into the mechanisms of G-quadruplex folding, polymorphism affecting G-stretches or even loop-regions, drugs and proteins binding affecting G-quadruplex stability should now be the focus of the scientific community.

G-quadruplexes have been linked with diseases such as cancer, neurodegenerative and genetic disorders, thus providing new clues for the customized design of novel therapeutic strategies. The design of specific molecules capable to discriminate among G-quadruplexes could be helpful at the moment of planning efficient strategies to fight against diseases. The ASO approach allows blocking *in vivo* the formation of a specific G-quadruplex, thus controlling the expression of defined genes. This and similar approaches would emerge as alternative tools to selectively modulate the G-quadruplex-mediated transcription of precise genes allowing to inhibit either disease development or progression reducing undesired collateral effects.

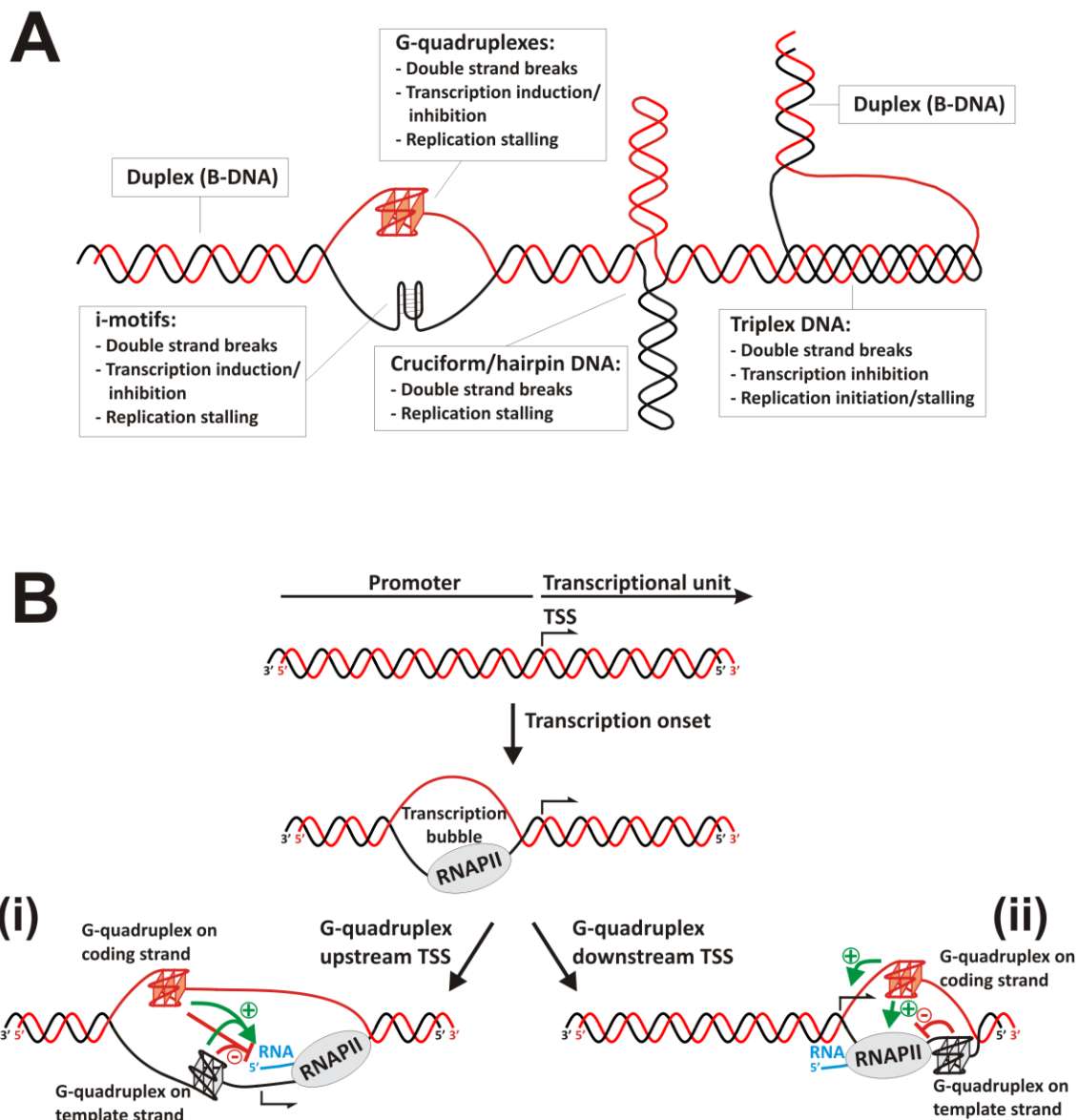
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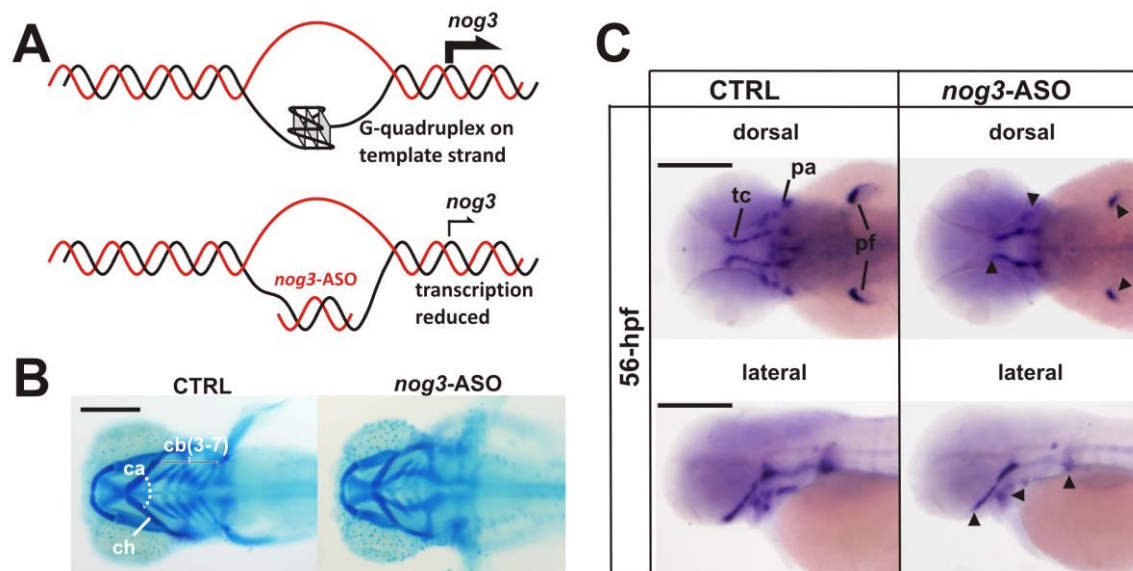


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**Figure 1. Non-canonical DNA secondary structures influencing transcription.** **A.** Scheme representing the most relevant non-canonical DNA secondary structures and their effects on genome and gene expression. **B.** Transcriptional regulation by G-quadruplexes. After transcription onset, transcription bubble generates transiently exposed single-strand segments able to fold as G-quadruplexes. Two putative scenarios are represented: (i) G-quadruplexes may form upstream the transcription start site (TSS), causing positive or negative effects on transcription depending on

their capability of interfering with RNA Polymerase II or transcription factors binding, recruiting G-quadruplex binding proteins or maintaining an open DNA conformation that facilitates transcription re-initiation. (ii) G-quadruplexes may form downstream the TSS, usually causing positive effects on transcription when located in the coding strand due to favoring transcription re-initiation, or negative effects on transcription when located in the template strand due to stalling the progression of RNA polymerase.



**Figure 2. *Noggin 3* (*nog3*), a gene required for proper craniofacial cartilages development, is regulated *in vivo* by G-quadruplex. A.** Strategy to specifically block G-quadruplex formation using an antisense oligonucleotide (*nog3*-ASO) microinjected in zebrafish embryos. **B.** Alcian blue staining showing craniofacial cartilages (ca: ceratohyal cartilages angle; cb (3-7): ceratobranchial cartilages 3 to 7; ch: ceratohyal cartilage) of 4 days post fertilization (4-dpf) larvae. Compared to controls (CTRL), *nog3*-ASO microinjected larvae display reduced head structures and abnormal craniofacial cartilage pattern. **C.** Lateral and dorsal views of whole-mount *in situ* hybridizations showing reduced expression of *nog3*-mRNA in 56 hours post-fertilization (56-hpf) larvae microinjected with *nog3*-ASO when compared with controls (CTRL). pa: pharyngeal arches; pf: pectoral fin; tc: trabeculae cranii. Scale bars = 200  $\mu$ m.