механических свойств клеток, 14,7% понимают физический смысл модуля Юнга, а 71,3% никогда не слышали об атомно-силовой микроскопии. Это указывает на необходимость совершенствования образовательных программ в области современных методов диагностики. Несмотря на низкий уровень информированности, студенты демонстрируют высокий интерес и доверие к инновационным технологиям: 87,6% опрошенных считают перспективным использование механических свойств клеток в диагностике, 89,2% готовы пройти обследование методом АСМ, а 79,1% хотели бы получить дополнительные знания по данной теме в рамках учебного процесса.

Повышение осведомленности будущих врачей о возможностях современных диагностических методов будет способствовать более раннему выявлению онкологических заболеваний и улучшению прогноза пациентов.

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IN SILICO SCREENING FOR G-QUADRUPLEX FORMING SEQUENCES IN THE *SLC7A11* GENE AS A BASIS FOR FERROPTOSIS RESEARCH

Introduction

Ferroptosis is a recently characterized form of regulated cell death driven by iron-dependent phospholipid peroxidation and subsequent membrane damage. It is genetically and biochemically distinct from apoptosis, necrosis, and autophagy [1]. In oncology, ferroptosis acts as a natural tumor suppression mechanism; however, cancer cells often develop resistance to ferroptosis to survive metabolic and oxidative stress. Therefore, identifying novel regulatory elements that control the expression of ferroptosis-related genes is a critical step toward developing new targeted cancer therapies [1].

The *SLC7A11* gene (solute carrier family 7 member 11) encodes the xCT light chain subunit of the cystine/glutamate antiporter system Xc^-. This transporter plays a pivotal role in importing cystine for glutathione synthesis, thereby protecting cells from oxidative stress and acting as a key negative regulator of ferroptosis [1]. Dysregulation of *SLC7A11* expression is implicated in various cancers and neurodegenerative diseases, making it an important target for therapeutic intervention.

G-quadruplexes (G4s) are non-canonical secondary structures formed in guanine-rich DNA or RNA sequences. They consist of planar arrays of four guanines (G-quartets) stabilized by

Hoogsteen hydrogen bonding and monovalent cations [2]. G4 motifs are enriched in regulatory regions of the genome, including promoters, untranslated regions, and introns, where they function as molecular switches to modulate transcription, replication, and translation [3]. The presence of stable G4 structures in the promoter regions of oncogenes (such as *MYC*, *KRAS*, and *BCL-2*) has been well documented, and targeting these structures with small-molecule ligands has emerged as a promising strategy to suppress oncogenic expression [4].

Given the critical role of *SLC7A11* in ferroptosis and tumor suppression, a comprehensive *in silico* analysis of its G4 landscape can reveal new regulatory hotspots. This study presents a foundational *in silico* screen for G4-forming motifs in the *SLC7A11* gene. The obtained dataset has been subsequently integrated into a broader multi-omics investigation of the gene's role in ferroptosis and oncology, which included analysis of protein–protein interactions and clinically relevant genetic variants [5]. Thus, the present work provides the essential groundwork for understanding the epigenetic regulation of *SLC7A11* via G-quadruplexes and for identifying potential targets for future drug design.

Goal

To identify and characterize putative G-quadruplex forming sequences in the human *SLC7A11* gene using strict bioinformatic criteria.

Material and methods of research

The genomic sequence of a human gene associated with ferroptosis regulation was retrieved from the NCBI Datasets Gene database. The sequence was downloaded in FASTA format. This file was submitted to the G4IPDB online prediction tool (), which analyzes both sense and anti-sense strands for canonical G4 motifs ($G_{+-3}N_xG_{+-3}N_xG_{+-3}N_xG_{+-3}$). The output table included the strand, start/end positions, putative G4 sequence, and three confidence scores: cG (total guanine score), cC (total cytosine score), and the cG/cC ratio. Sequences with a cG/cC ratio >20 or marked as "INF" (where cC=0, indicating extremely high G-richness without competing C-richness) were considered high-confidence predictions. The data were compiled and analyzed in Microsoft Excel.

The results of the research and their discussion

The G4IPDB analysis identified a total of 82 putative G-quadruplex forming sequences within the analyzed ferroptosis-associated gene. Among these, 40 were located on the sense strand and 42 on the anti-sense strand, indicating a nearly equal distribution and a dense G4 landscape within the locus.

A selection of the most significant high-confidence G4 sequences (cG/cC>20 or INF) is presented in Table 1. The cG/cC score reflects the ratio of guanine to cytosine content; values above 20, especially "INF" values, denote sequences with a very high probability of stable G4 formation in vivo due to minimal competition from complementary C-rich strands.

Table 1 – High-confidence putative G-quadruplex forming sequences in a ferroptosis-associated gene

Strand	Start Position (bp)	Putative G4 Sequence (5'–>3')	Length (bp)	cG Score	cC Score	cG/cC Score
Sense	1602	GGGTTTTGGGGGGCTGGGGG	21	1010	10	101
Sense	1412	GGGGCTGGGGTGGGGGG	18	900	10	90
Sense	2387	GGCGGGGGTAGG	13	430	10	43
Sense	6385	GGACTGGGGAGTTGGGAGG	20	390	10	39
Sense	1936	GGCAGGGGAAAAGGGAGG	19	380	10	38
Sense	2340	GGGGACGGGGGCGGTGGAGAGGG	24	740	20	37
Sense	1469	GGGAGAGGAGAAGGCAGAGGG	22	310	10	31
Sense	3989	GGGGCGGGGTGGCAGGG	18	540	20	27

End of table 1

Strand	Start Position (bp)	Putative G4 Sequence (5'–>3')	Length (bp)	cG Score	cC Score	cG/cC Score
Anti-sense	571	GGGGAAGGTGGGGAGG	16	480	0	INF
Anti-sense	588	GGGGAGGGTGGGGAGGG	17	600	0	INF
Anti-sense	3833	GGGGAAGGGATGGGAGG	17	440	0	INF
Anti-sense	4691	GGGGGTTGGAGG	12	430	0	INF
Anti-sense	6118	GGGATGGTGGTGGTTGGG	18	320	0	INF
Anti-sense	4270	GGGCGGGGGAAGG	13	490	10	49

Note. "INF" denotes a cG/cC score approaching infinity due to a cC score of 0, indicating an exceptionally G-rich sequence with no competing cytosine runs.

Several key observations emerge from this analysis. First, the most stable G4s on the sense strand, such as the sequence at position 1602 (cG/cC=101) and 1412 (cG/cC=90), possess extremely long G-runs and exceptionally high cG scores. These are highly likely to form stable structures in vitro and in vivo that could impede polymerase progression during transcription or affect alternative splicing [3].

Second, the presence of multiple "INF" sequences on the anti-sense strand (e.g., at positions 571, 588, 3833) is particularly intriguing. These sequences lack any cytosines in the motif, making them obligate G4–formers when the strand becomes single-stranded during transcription or replication. They may serve as critical transient regulatory switches [4]. The anti-sense sequence at position 4270 (cG/cC=49) also represents an exceptionally strong candidate.

Third, a notable pattern of sequence repetition was observed. Several motifs, such as the sequence at 328 bp and its identical copy at 7930 bp, appear twice in the gene, suggesting possible gene duplication events or the presence of conserved structural elements required for gene regulation [5]. This clustering of G4 motifs may create a complex "G4 landscape" that finely tunes the expression of this ferroptosis-related gene in response to cellular stress. The novel high-confidence G4s identified here, especially those with "INF" scores and those located near the promoter-proximal region, represent promising candidate targets for future drug design. Targeting these structures with specific G4–stabilizing ligands could provide a novel strategy to modulate ferroptosis sensitivity in cancer cells, either by suppressing the expression of ferroptosis inhibitors (like GPX4 or SLC7A11) or by enhancing the expression of ferroptosis inducers [1].

Conclusion

1. The analyzed ferroptosis-associated gene harbors 82 putative G-quadruplex forming sequences, with a nearly equal distribution between the sense (40) and anti-sense (42) strands, indicating a dense G4 landscape.

2. Fourteen high-confidence G4 motifs with cG/cC scores greater than 20 or "INF" values were identified as the most promising candidates for stable structure formation in vivo.

3. The presence of five "INF" sequences on the anti-sense strand (cC=0) suggests that these regions are obligate G4–formers and may serve as critical regulatory elements during transcription.

4. The identified high-confidence G4 sequences represent novel potential therapeutic targets for small molecules aimed at modulating ferroptosis pathways in human cancers.

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PUBLIC AWARENESS OF CHOLESTEROL AND OMEGA-3 FATTY ACIDS

Introduction

This report investigates public awareness and practices related to cholesterol and Omega-3 fatty acids. The objective was to evaluate knowledge levels, identify common misconceptions, and highlight gaps between public awareness and evidence-based scientific understanding. The findings aim to support healthcare professionals in designing targeted educational interventions [1–3].

Goal

The aim of this study was to assess public understanding of cholesterol metabolism and the physiological roles of Omega–3 fatty acids. Furthermore, it examines the perceived relationship between dietary fats and cardiovascular risk, as well as awareness of practical dietary strategies for lipid management.

Material and methods of research

An online survey was conducted among participants aged 18 to 60+ years. Demographic variables included gender, educational level, and family medical history. Secondary data were obtained from sources which included ScienceDirect and publications from the National Institutes of Health (NIH).

The results of the research and their discussion

Survey results indicate that while general awareness of cholesterol-related diseases exists, detailed scientific understanding remains limited. Many respondents primarily associated cholesterol with cardiovascular diseases, atherosclerosis, and diabetes (Figure 1).

Cholesterol

Cholesterol is a vital biological molecule involved in membrane structure, hormone synthesis, and cellular signaling. However, elevated low-density lipoprotein (LDL) and oxidized LDL (oxLDL) are recognized as significant contributors for cancers. Cholesterol levels have a dual effect on the immune response depending on the concentration.