

Category	: 8th Rice Genetics Symposium
Select Theme	: Genome biology: Structure, Function and Comparison
Endorsement email	:
Genome biology Structure Function and Comparison Keyword 1	: Comparative genomics
Genome biology Structure Function and Comparison Keyword 2	: Genome evolution
Genome biology Structure Function and Comparison Keyword 3	: Phylogeny
Title of Entry	: Identification and characterisation of G-quadruplex forming regions in rice and their evolutionary perspective
Presenting author	: Rohini Garg
Presenting author email	: rohini.garg@snu.edu.in
Co author 1	: NA
Co author 2	: NA
Co author 3	:
Co author 4	:
Co author 5	:
Co author 6	:
Co author 7	:
Co author 8	:
Co author 9	:
Co author 10	:
Co author 11	:
Co author 12	:
Co author 13	:
Co author 14	:

Affiliation presenting author : Department of Life Sciences, School of Natural Sciences, Shiv Nadar University, Gautam Budh Nagar, India

Affiliation 1 :

Affiliation 2 :

Affiliation 3 :

Affiliation 4 :

Affiliation 5 :

Affiliation 6 :

Affiliation 7 :

Affiliation 8 :

Affiliation 9 :

Affiliation 10 :

Affiliation 11 :

Affiliation 12 :

Affiliation 13 :

Affiliation 14 :

Select only one type of presentation : 3-5 minute flash talk

Abstract : There is increased interest in recent years to unravel the structure based functionality of non-coding parts of the genome for controlling gene expression. DNA, in addition to the canonical B-form, can acquire a variety of alternate structures, such as G-quadruplexes. These structures have been implicated in several cellular processes. In this study, we have identified different types of G-quadruplex forming sequences (GQSeS) in rice and other sequenced plants and analyzed their distribution in various genomic features, including gene body, and coding, intergenic and promoter regions. G2-type GQSeS were most abundant in all the plant species analyzed. A strong association of G3-type GQSeS with intergenic, promoter and intronic regions was found. However, G2-type GQSeS were enriched in genic, CDS, exonic and untranslated regions. Further, we identified GQSeS present in the conserved genes among monocots. The genes involved in development, cell growth and size, transmembrane transporter, and regulation of gene expression were found to be significantly enriched. A strong association of GQSeS were found in genes differentially expressed under abiotic stress response in rice. Further, we validated the structure formation of several putative rice GQSeS, demonstrated their effect on stalling in-vitro replication and revealed their interaction with plant nuclear proteins. We also identified rice proteins that interact with G-quadruplex forming regions suggesting that G-quadruplexes might interact with various proteins to regulate various processes in plants. Our data provide insights into the prevalence of GQSeS in plants, establish their association with different genomic features and functional relevance.

Uploaded Files »

No files found.