

(54) Title of the invention : A GENOME-INFORMED SYSTEM FOR IDENTIFYING AND FUNCTIONALLY UTILIZING SIMPLE SEQUENCE REPEAT MARKERS IN FAGOPYRUM TATARICUM

(51) International classification	:C12Q 1/68, C12N 15/11, G16B 30/10, G16B 20/20, C12Q 1/6895	(71) <b>Name of Applicant :</b> <b>1)Swami Rama Himalayan University</b> Address of Applicant :Swami Rama Himalayan University, Swami Ram Nagar, Jolly Grant, Dehradun-248016 Dehradun Uttarakhand India (72) <b>Name of Inventor :</b> <b>1)Garima Kishore</b> <b>2)Anjali Uniyal</b> <b>3)Geeta Bhandari</b> <b>4)Sanjay Gupta</b>
(31) Priority Document No	:NA	
(32) Priority Date	:NA	
(33) Name of priority country	:NA	
(86) International Application No	:	
Filing Date	:01/01/1900	
(87) International Publication No	: NA	
(61) Patent of Addition to Application Number	:NA	
Filing Date	:NA	
(62) Divisional to Application Number	:NA	
Filing Date	:NA	

## (57) Abstract :

The present invention relates to a genome-informed system and method for identification, classification, and functional utilization of simple sequence repeats (SSRs) derived from nucleotide sequences of Fagopyrum tataricum. The invention employs curated, non-redundant genomic and gene-associated sequences and applies an in-silico repeat mining approach to detect di-, tri-, tetra-, penta-, and hexanucleotide repeat motifs. The identified SSRs are systematically classified based on repeat length, motif composition, and frequency distribution to generate a refined, species-specific marker resource. The resulting SSR markers are suitable for genetic diversity analysis, polymorphism characterization, linkage map construction, and marker-assisted selection in breeding programs. The disclosed approach reduces cost and time associated with traditional marker development methods and provides a scalable framework adaptable to other plant species with limited genomic information.

No. of Pages : 23 No. of Claims : 10