Detection of active LTR retrotransposons via eccDNA analysis in *Helianthus annuus* L., *Arabidopsis thaliana* and triticale

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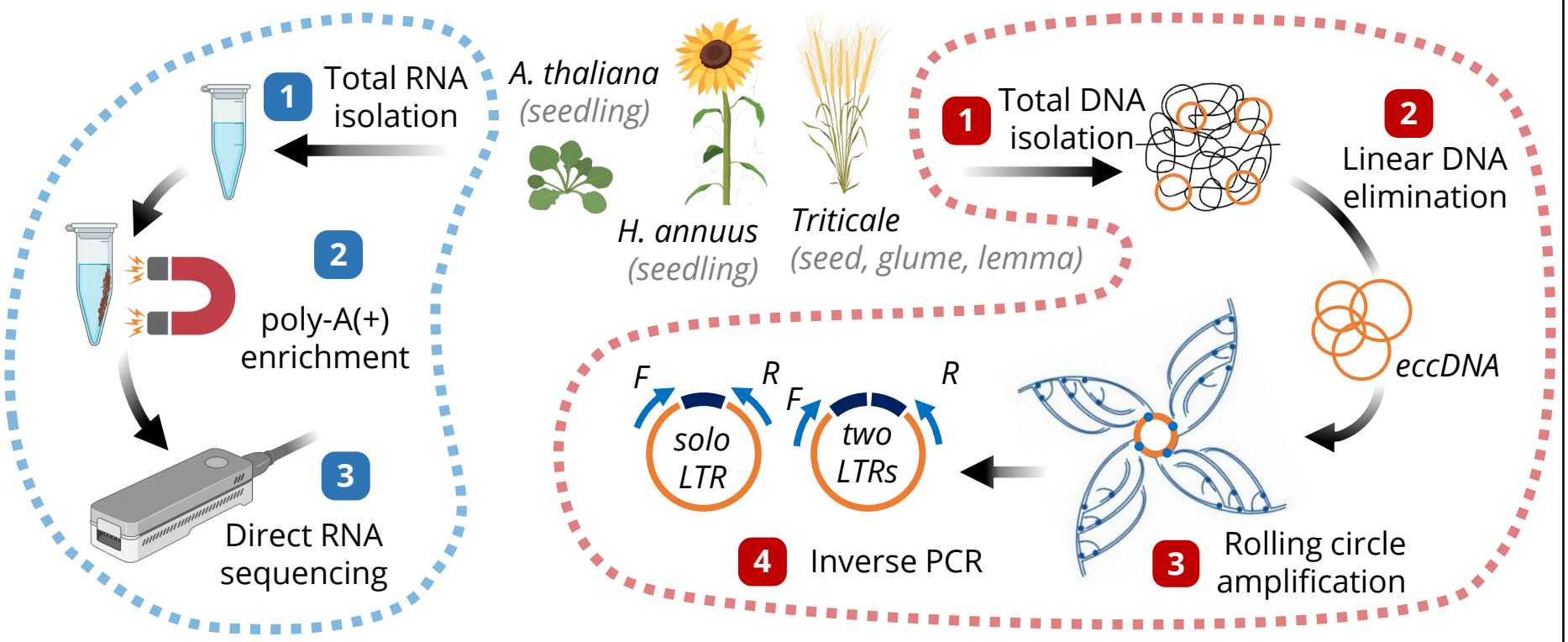
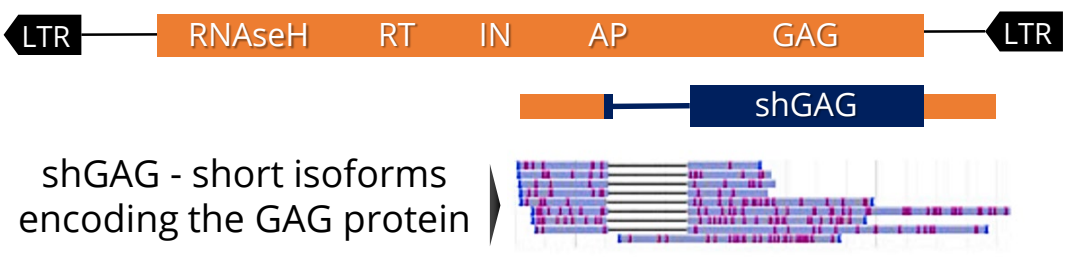
Summary. LTR retrotransposons present a subclass of mobile genetic elements and can produce extrachromosomal circular DNA (eccDNA) as a byproduct of their life cycle. Recent studies showed that the amount of LTR retrotransposon eccDNA molecules is individual for each element and often correlates with the transposition ability. In this way, eccDNA can be used for experimental detection of active retrotransposons in plants as an alternative to whole-genome sequencing. In our study, we aimed to reveal active retrotransposons in *Arabidopsis thaliana*, *H. annuus,* and triticale (x *Triticosecale* Wittmack). We performed an eccDNA enrichment followed by inverse PCR with specific primers. In *H. annuus* & triticale we detected two LTR retrotransposons (named *Gagarin* & *MIG*, respectively) producing eccDNA molecules. Using RT-PCR analysis and direct RNA Nanopore sequencing we also detected different isoforms for these retrotransposons.

Materials & methods



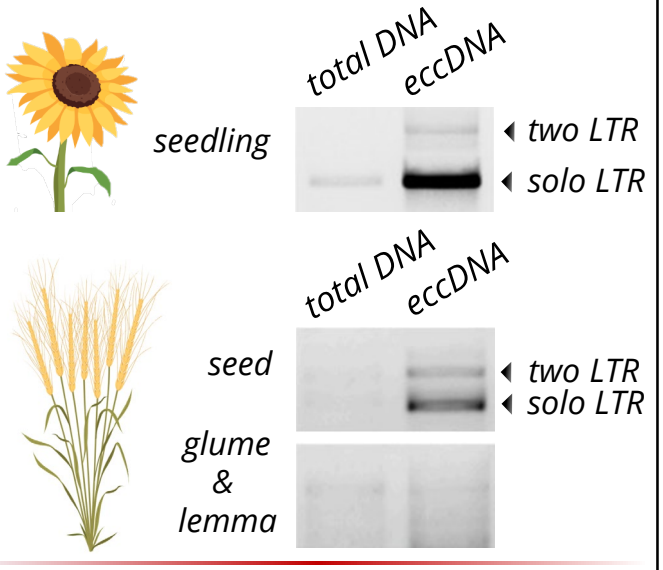
Results

TaeST2.45518.1 (*MIG*)



shGAG - short isoforms encoding the GAG protein

Nanopore direct RNA sequencing revealed shGAG isoforms for retrotransposon TaeST2.45518.1 (MIG)



Detection of extrachromosomal circular DNA (eccDNA) for Gagarin and MIG retrotransposons by inverse PCR

In conclusion, eccDNA detection is an accurate method for the identification of active LTR retrotransposons in large and repetitive plant genomes.