

Repeated sequences in the pea genome.

University of East Anglia - A reference genome for pea provides insight into legume genome evolution

Summary:

- Current plant genomes result from repeated cycles of partial and complete **duplications**, followed by **reductions** and **modifications** of duplicated sequences.
- There are no genomes without **redundancy**.
- Plant genomes are still very **dynamic**.
- High portion of plant genomes consists of **repetitive DNA (TEs)**.

Description: -

-Repeated sequences in the pea genome.

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Notes: Thesis (Ph.D), University of East Anglia, School of Biological Sciences, 1990.

This edition was published in 1990



Filesize: 57.61 MB

Tags: #Repetitive #DNA #in #the #pea #(#Pisum#sativum #L.) #genome: #comprehensive #characterization #using #454 #sequencing #and #comparison #to #soybean #and #Medicago #truncatula

Kinetic determination of the genome size of the pea

The gene space covers a narrow, 0.

Repeated sequence (DNA)

Multiple-marker techniques based on PCR are highly informative in genetic analysis. These were used for the development of bionano maps and for resequencing at GENOSCOPE and University of Western Australia. Kolodner R, Tewari KK: Physicochemical characterization of mitochondrial DNA from pea leaves.

Repeated Sequence Markers in Pea (*Pisum sativum*) on JSTOR

Several complementary strategies conducted by the different groups of the consortium were undertaken in order to produce this reference sequence. Murray MG, Peters DL, Thompson WF: Ancient repeated sequences in the pea and mung bean genomes and implications for genome evolution. With a growing open access offering, Wiley is committed to the widest possible dissemination of and access to the content we publish and supports all sustainable models of access.

Rearrangements in the chloroplast genomes of mung bean and pea

StringTie enables improved reconstruction of a transcriptome from RNA-seq reads.

Repeated Sequence Markers in Pea (*Pisum sativum*) on JSTOR

Studies on Male Meiosis in Cultivated and Wild Vigna Species.

Kinetic determination of the genome size of the pea

The physical location of this locus corresponded to 25,106 bp on Psa1. Genomic and transcriptomic analyses revealed candidate genes responsible for the differences in pod color between JI128 and JI4. Gene 1980, 11 1-2 , 21-31.

Pea Genome project

Nature 1980, 283 5747 , 602-603. Zellweger A, Ryser U, Braun R: Ribosomal genes of Physarum: Their isolation and replication in the mitotic cycle. To check for specificity of this assay, control experiments were run using probe sequences differing in a single-base substitution within the repeat monomer TTA C G n and TTTA C G n.

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