

1. Record Nr.	TD12029459
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Titolo	Analisi della struttura genomica di <i>Arabidopsis thaliana</i> L. [Tesi di dottorato]
Editore	Universita' degli studi di Sassari, 2011-02-24
Lingua di pubblicazione	Italiano
Formato	Tesi di dottorato
Livello bibliografico	Monografia
Note	In relazione con http://eprints.uniss.it/4939/
Sommario	<p>The present thesis provides an insight on the genomic structure of plant species, by taking in exam the model organism <i>Arabidopsis thaliana</i>. The research activity pointed towards three directions. Initially the correlation between the expression profile and some structural properties such as the sequence length and the GC (guanine + cytosine) content was studied. The results revealed that in plants highly expressed genes undergo a selection for miniaturization which is probably due to the need to minimize the cost of the transcription/translation process. In a successive phase the usage of the synonymous codons (i.e. nucleotide triplettes which code for the same amino acid) was investigated within 15 <i>Arabidopsis</i> tissues. The results showed that genes specifically expressed in certain tissues use a definite set of codons, whereas more widely expressed genes feature a codon composition which is, at a certain extent, a compromise between the codons used in the single tissues. Finally the nucleotide composition as a function of the position in the gene was studied in two monocots and two dicots. For all the analyzed bases compositional gradients were revealed. The observed trends, mostly describable with a linear model, underlined marked difference between monocots and dicots.</p>
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