



# MOLECULAR CHARACTERIZATION OF GENES CONTROLLING DEHISCENCE IN PISTACHIO (*PISTACIA VERA*)

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## BACKGROUND

The existing commercial varieties of pistachio widely differ in the percentage of dehiscent fruits. This factor determines the destination of the product, the investment required for fruit processing operations and its final price in the market (**Figure 1**). Dehiscence is a complex biological process that involves not only environmental but also genetic factors. Two types of genes are concerned: a first group controls the valve margin identity and signals *replum* cells that eventually will constitute the dehiscence zone and the separation layer, while a second group conducts lignification of these cells and the opening of the fruit.

Cultivar	% Dehiscent fruits
Ashoury	99%
Ohadi	94%
Sirora	93%
Siirt	92%
Amiry	91.20%
Aegina	90%
Syrizi	86.70%
Mateur	70-90%
Uzun	70%
Kirmizi	67%
Kerman	40-80%
Napoletana	>25%



**Figure 1.-** Some representative *P. vera* cultivars and their average % of dehiscence (1). Types of dehiscence in pistachio from left to right: indehiscent fruit, dehiscence at the apex, partial dehiscence along the dorsal ridge, dehiscence along both longitudinal ridges and at the apex.

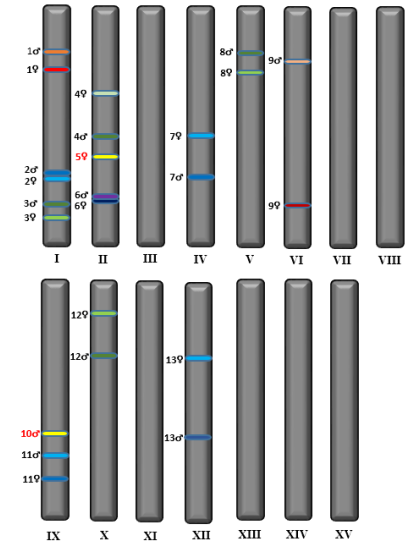
## RESULTS

Using WGS of three varieties of pistachio (female cultivars Batoury and Siirt, and male cultivar Bagyolu), 15 genes proved previously to be responsible for dehiscence in *Arabidopsis thaliana* (2) and *Vicia faba* (3) were characterized *in silico* and assigned to different chromosomes (**Figure 2**). Positive matches were found for all genes investigated except for YAB3 (4) that was only found in female genomes and RPL found only in male genomes.

To test these results and for future gene expression profiling, primers were designed for 9 genes. All of them were amplified and sequenced in *P. vera* cultivars Peter (♂) and Kerman (♀) suggesting that *in silico* results obtained for YAB3 and RPL genes might be due to incompleteness of the assembly in that particular chromosome regions.

Additionally, the presence of these genes was investigated in non-dehiscent species *P. terebinthus* (terebinth) and *P. lentiscus* (lentisk). All of them yielded positive PCR amplifications in both species except for FUL that was not found in lentisk. Since terebinth and pistachio are more closely related, this could be a reflection of the phylogeny of this group of species.

ID	Name	Chr	Length
1	SHP1	1	5.570
2	YAB1	1	2.870
3	SPT	1	3.527
4	FUL	2	4.120
5	YAB3	2	2.597
6	NST1/3	2	1.823
7	ADPG1/2	4	2.694
8	AP2	5	3.529
9	JAG	6	7.975
10	RPL	9	3.755
11	IND	9	786
12	ALC	10	3.874
13	SHP2	12	7.898



**Figure 2.-** List of genes investigated and their location in *P. vera* genome. In red: genes exclusively found in one sex, in bold: paralogous genes reduced to a single locus in *P. vera*.

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