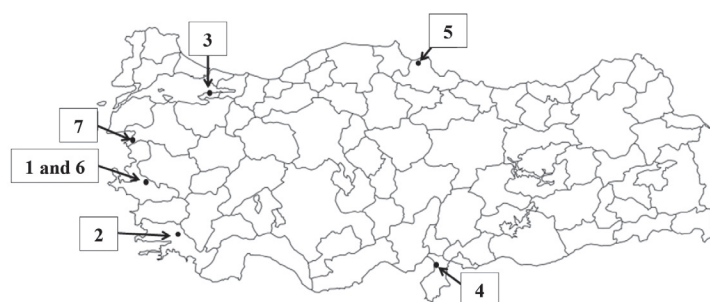
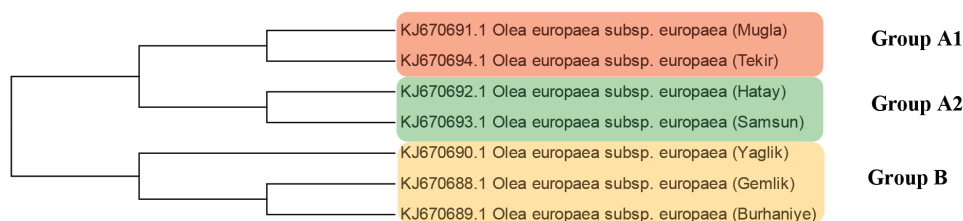


GENETIC RELATIONSHIP OF TURKISH OLIVES BASED ON *trnL-F*

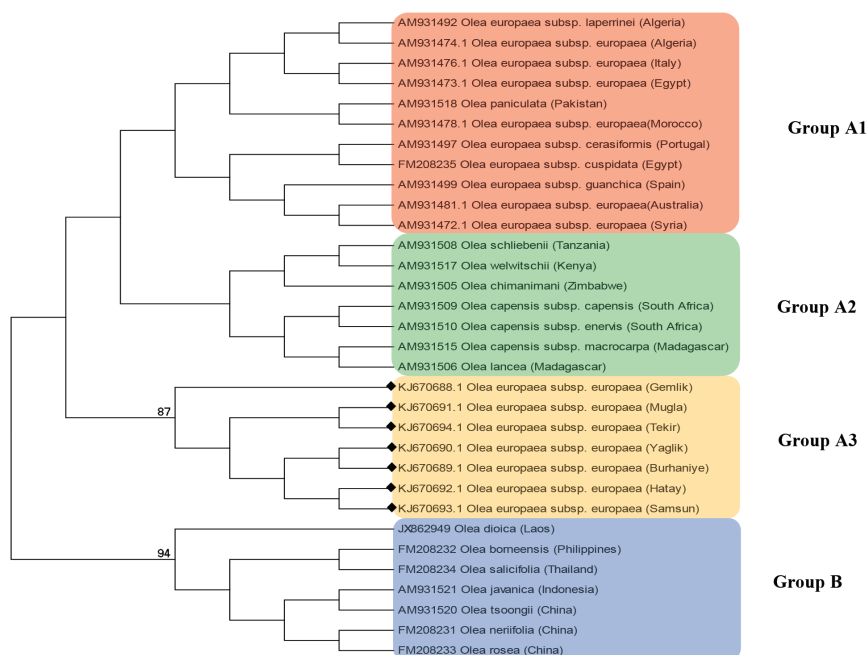
On-line Suppl. Fig. 1. Biogeographic distribution of seven Turkish olive cultivars. Numbers indicate the location of genotype sources; 1: Yaglik, 2: Mugla, 3: Gemlik, 4: Hatay, 5: Samsun, 6: Tekir, and 7: Burhaniye

On-line Suppl. Tab. 1. The pairwise similarity matrix of seven Turkish olive cultivars. Bold-underlined values show the lowest and highest distances between cultivars.

	Gemlik	Burhaniye	Yaglik	Mugla	Hatay	Samsun	Tekir
Gemlik	–	0.982	0.956	0.944	0.962	0.973	0.959
Burhaniye	0.982	–	0.965	0.950	0.973	0.979	0.962
Yaglik	0.956	0.965	–	<u>0.927</u>	0.985	0.973	0.962
Mugla	0.944	0.950	<u>0.927</u>	–	0.941	0.947	0.938
Hatay	0.962	0.973	0.985	0.941	–	<u>0.988</u>	0.968
Samsun	0.973	0.979	0.973	0.947	<u>0.988</u>	–	0.956
Tekir	0.959	0.962	0.962	0.938	0.968	0.956	–



On-line Suppl. Fig. 2. Phylogenetic tree of seven Turkish olive cultivars (*Olea europaea* subsp. *europaea*). Tree was constructed using *trnL-F* sequences with maximum likelihood method.



On-line Suppl. Fig. 3. Phylogenetic tree of various *Olea* members, including Turkish cultivars. Tree was constructed using *trnL-F* sequences with maximum likelihood method for 1000 bootstraps. Turkish olive cultivars were indicated with diamond symbol.