

	1	10	20	30	40	50	60
rps3_fertile	MARKGNPISVRLKNRSSDSSRFSDYYGKSVYQDVNMRSYFGSIRPPTRLTLGFRPGRCLILHFPKR						
rps3_sterile	MARKGNPISVRLKNRSSDSSRFSDYYGKSVYQDVNMRSYFGSIRPPTRLTLGFRLGRCCLILHFPKR						
	70	80	90	100	110	120	130
rps3_fertile	TFIHLFLPRRPRRLKRREKSRPGKKKKGRWWAFGKVGPGCLHSSDDTEKERNEVRGGETGKRVGSI						
rps3_sterile	TFIHLFLPRRPRRLKRREKSRPGKKKKGRWWAFGKVGPGCLHSSDDTEKERNEVRGREITGKRVGSI						
	140	150	160	170	180	190	200
rps3_fertile	GLDDREKQNEIRIWPKKKQRYGYHDRSPSIKILLSKSLRVSGAFKHPKYAGVVNDIAFLIKNDDSF						
rps3_sterile	GLDDREKQNEIRIWPKKKQRYGYHDRSPSIKILLSKSLRVSGAFKHPKYAGVVNDIAFLIKNDDSF						
	210	220	230	240	250	260	270
rps3_fertile	TKFLKLEFFQKKFRSDSPTSHLLKRTLPAVRPSLNL SVMQYYLLNTKNKMHFDPVVVLNHFLASGVAE						
rps3_sterile	TKFLKLEFFQKKFRSDSPTSHLLKRTLPAVRPSLNL SVMQYYLLNTKNKMHFDPVVVLNHFLASGVAE						
	280	290	300	310	320	330	340
rps3_fertile	PSTMGGANAQGRSLDKRIRSRIAFFVES SAGEKKSLAEAKKRLTRLIRLANDLRFAGTTKTTISPFPF						
rps3_sterile	PSTMGGANAQGRSLDKRIRSRIAFFVES SAGEKKSLAEAKKRLTRLIRLANDLRFAGTTKTTISPFPF						
	350	360	370	380	390	400	
rps3_fertile	FGATFFFPRDGVGVYKNLFFEDAREPLLGLRKKCWNL MGKDKVMELIEKFIGLGGIGELIKGIEMLL						
rps3_sterile	FGATFFFPRDGVGVYKNLFFEDAREPLLGLRKKCWNL MGKDKVMELIEKFIGLGGIGELIKGIEMLL						
	410	420	430	440	450	460	470
rps3_fertile	EILLRNRIIPYGYNSYLNVEVKKMRSLLFNRTNTNTLIESVKIKSVYQSASPIAQDISFQPRNKTRSFR						
rps3_sterile	EILLRNRIIPYGYNSYLNVEVKKMRSLLFNRTNTNTLIESVKIKSVYQSASPIAQDISFQPRNKTRSFR						
	480	490	500	510	520	530	540
rps3_fertile	SIFSKI VKDIP LVMKKGVEGIRICCSGRLKGAEIARTECGKYGKTSRNVFNQKIDYAPAEVSTRYGIS						
rps3_sterile	SIFSKI VKDIP LVMKKGVEGIRICCSGRLKGAEIARTECGKYGKTSRNVFNQKIDYAPAGVSTRYGIS						
	550	553					
rps3_fertile	GVK V W I S Y						
rps3_sterile	GVK V W I S Y S						

Figure S1 Amino acid alignment of ribosomal protein small subunits 3 (rps3) retrieved from the mtDNA of male fertile (MF, rps3 fertile) and cytoplasmic male sterile (CMS, rps3 sterile) accessions of *Foeniculum vulgare*

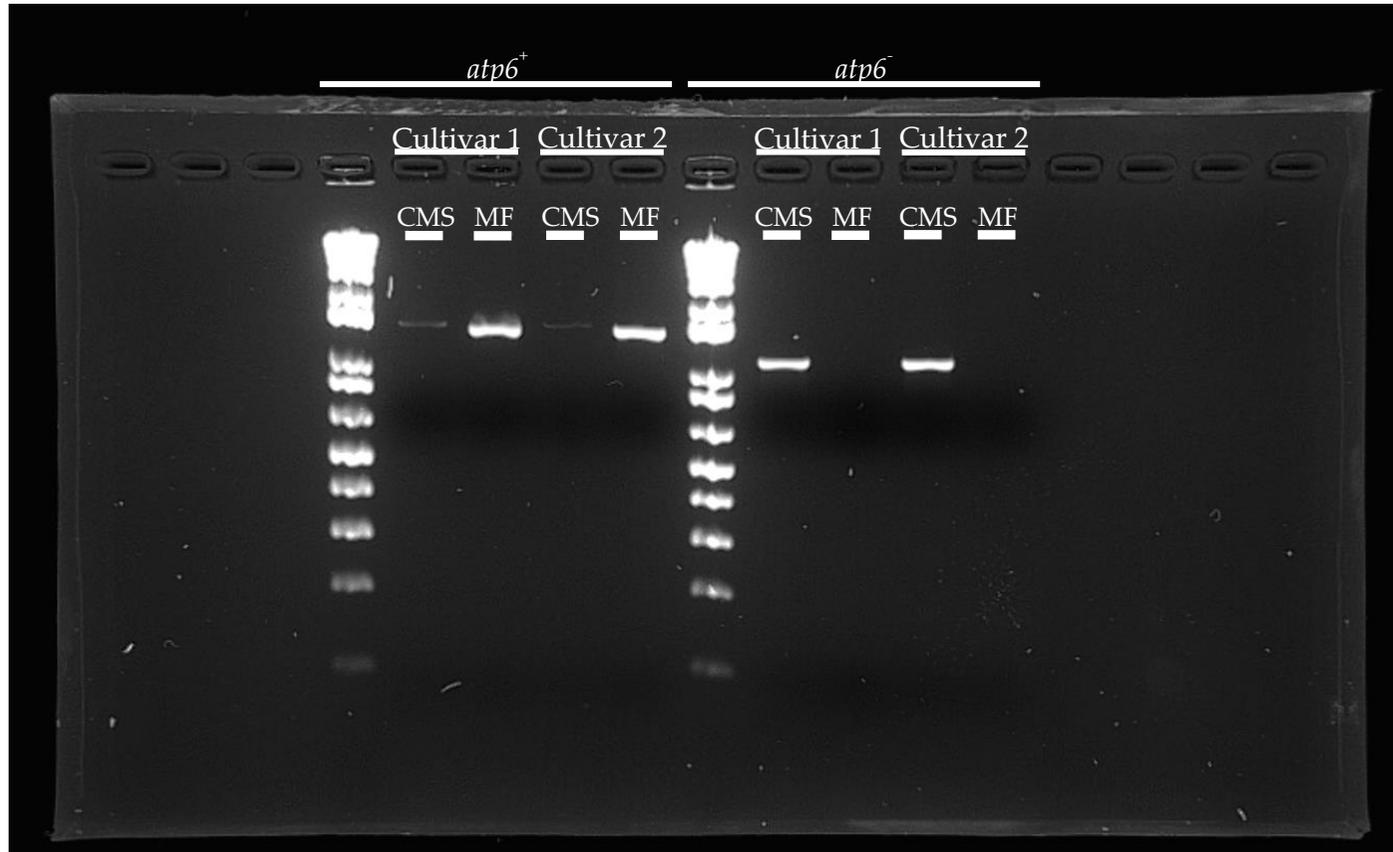


Figure S3. PCR amplification of two cytoplasmic male sterile individuals (CMS) from as many commercial lines and their two isogenic fertile maintainers (MF). In details, for the analysis of the wt copy of the *atp6* gene (*atp6*⁺), the following primers were used: F1: ATCGACCTGAACAACATATACGGA R1: GCTGGCGATTTCCGACAAGT. For the amplification of the mutated form (*atp6*⁻), F2: TCACTGAGCACTGTCTG and R2: CCTAGAGTCTTTCGATACTATA were employed.

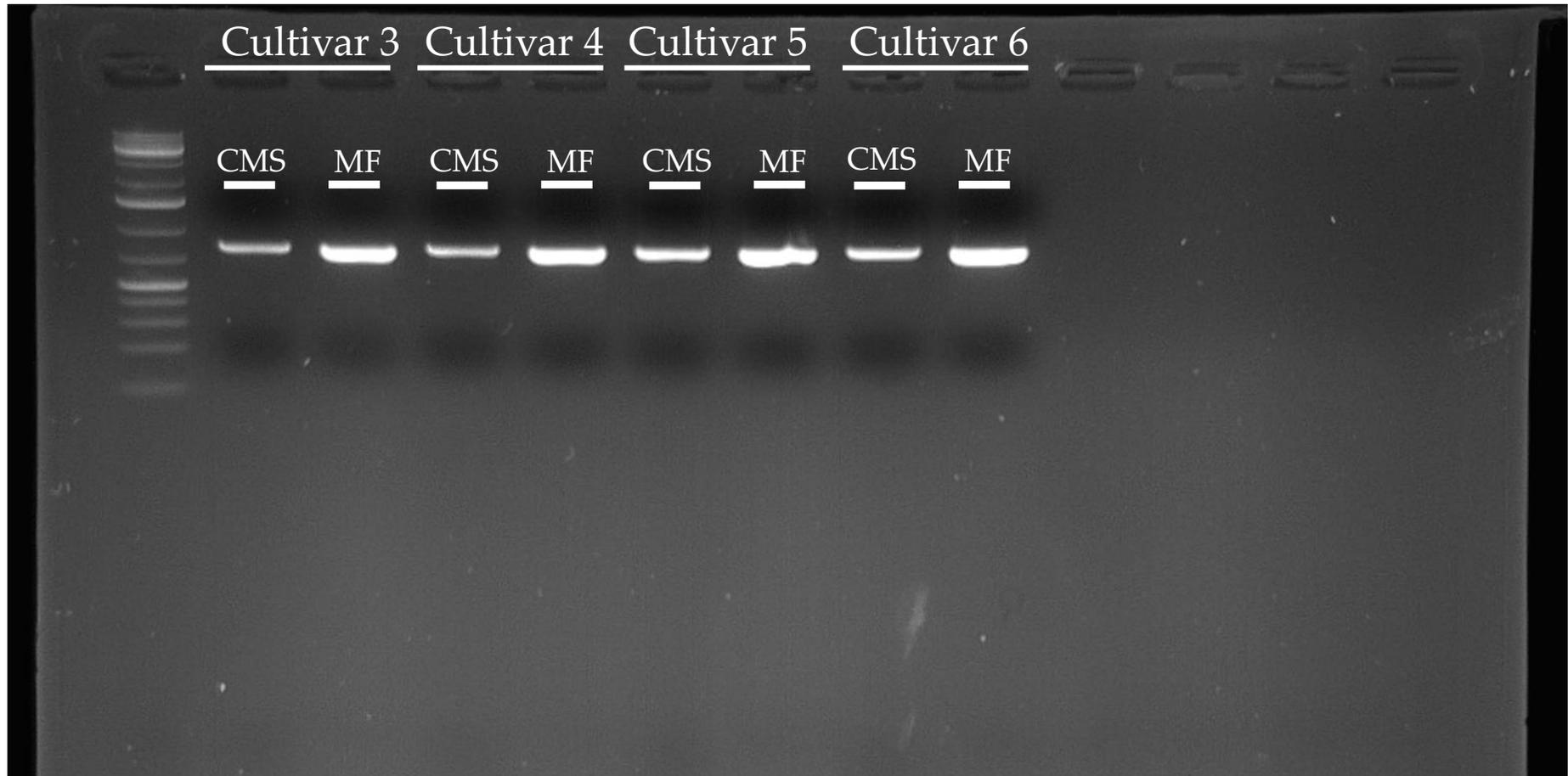


Figure S4. Additional PCR amplifications of the *atp6+* gene performed on four cytoplasmic male sterile individuals (CMS) from as many commercial lines (different from those ones used in the preliminary amplifications shown in Figure S3) and their isogenic fertile maintainers (MF).