

Accessory Publication

Deletions in an endopolygalacturonase gene cluster correlate with non-melting flesh texture in peach

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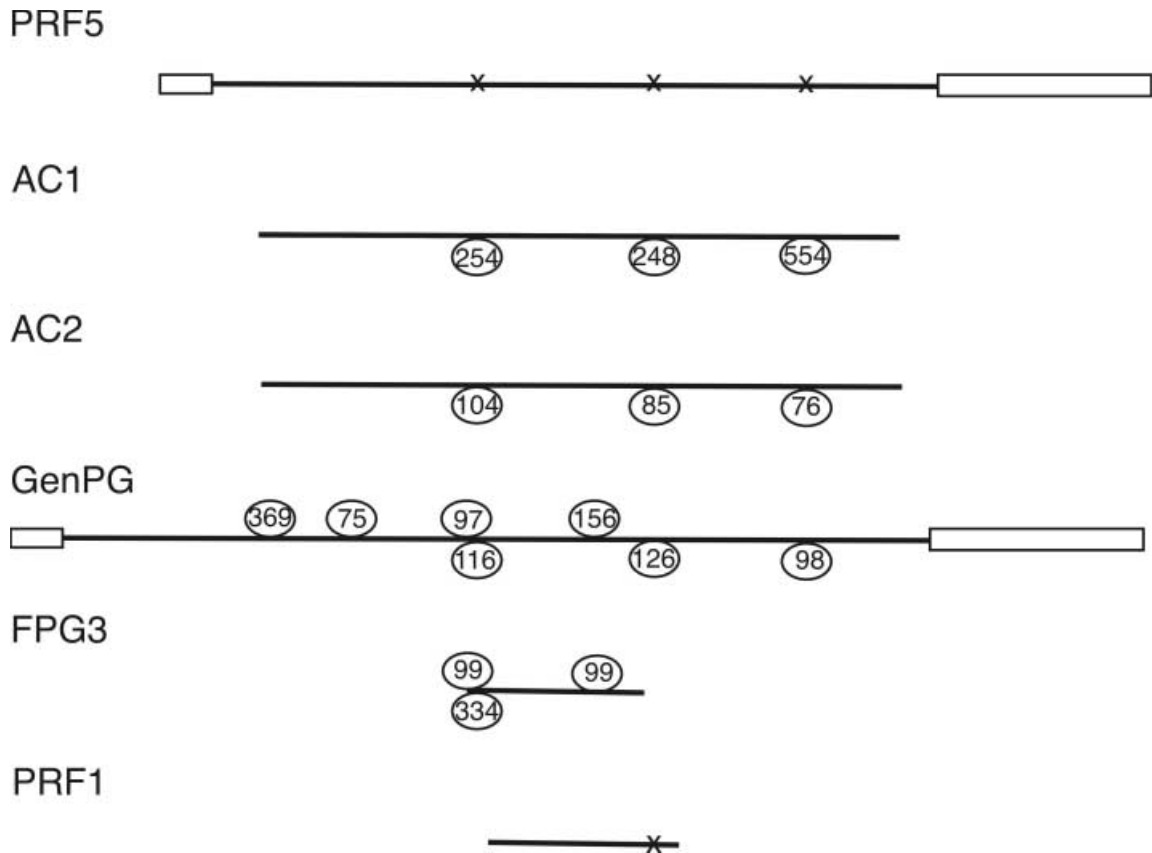


Fig. A1. Schematic that represents the six known peach polygalacturonase sequences. Boxes represent the 5' and 3' non-coding sequences of PRF5 and GenPG. Lines represent the coding sequence and ovals represent introns with the size inside. The small × symbols represent potential splice junctions in cDNA sequences.

		60
PRF5	MANRRSLFSLSLIFVFMINSIAIASPLTYNVASLGAKADGKTDSTKAFLSAWAKACASMNP	
AC1	*****	
AC2	*****G****E*****I*****AE*	
GenPG	*NF***GN*A-D*T*A*EK**KA**S*NGA	
		120
PRF5	GVIYVPAGTFFLRDVFVSGPCKNNAITFRIAGTLVAPSDYRVIGNAANWIFFHHVNGVTI	
AC1	*****	
AC2	A****R*R*L*HN***A*****D**S*ED*E****	
GenPG	I*LV**QK*YLV*PIE*****SH-L*MQ*Y**IE*SD*RS*YKDVTH*LI*DN*QSLLV	
		180
PRF5	SG-GILDGQGTALWACKACHGES--CPSGATTLG-FSDSNNIVVSGLASLNSQMFHIVIN	
AC1	*****S*****	
AC2	*****K**D*****-A*K*****S**N**DI****VI*****	
GenPG	V*P*TIN*N*NRW*ENSCKRKPP*NEQ*P*AVT*NKC**L**KN*KIQDA*QM*VRFQ	
FPG3	G*TIN*N*EQW*QNSCKINK*KP*K-D*P*ALI*QKCK*LR*NN*NIQDA*QI*VSFQ	
		240
PRF5	DFQNVQMVGVRVSRSGNSPNTDGIHVQMSSGVTILNSKIATGDDCVSIGPGTSNLWIEGV	
AC1	*C*****A*****	
AC2	GCH**K**S*K**A**Q*****S*****D***NI	
PRF1	****M*IGR**NIN*TGAE*K*****L*D*SQQIN**K*	
GenPG	NCK**EASHLT*TAPED*****ITNTKNIT*SS*V*G****I**VS*SQRVQATDI	
FPG 3	KCM**ASNLIIAPEK*****TDTQNIL*TN*V*****L**VN*CEKVQATNI	
		300
PRF5	ACGPGHGIGISIGSLGKEQEEAGVQNVTVKTVTFSGTQNGLRKISWGRPSTGFARNILFQHA	
AC1	*****T*****	
AC2	K*****D*****SI**FN*****KD*****	
PRF1	K*****RYHD*QP*TG***RNC*I*N*S**V***T*	
GenPG	T*****EDNANDH*SG*F*NGAKI**S**V***T*Q-GGS*S*S**V**NV	
FPG3	T*****	
		360
PRF5	TMVNVENPIVIDQHYPDNKG--CPGQVSGVQISDVITYEDIHGTSATEVAVKFD CSPKHP	
AC1	*****	
AC2	V*L**Q*****N*****K*****Q*****S*Y*	
GenPG	E*ND*T**I**N**-*H*NKD*TR*R*A**VKN*L*QN*R***STD*IT*N**QSV*	
		399
PRF5	CREIKLEDVKLTYKNQAAESSCSHADGTTTEGVVQPTSCLE	
AC1	*S*****E*	
AC2	*SN**MK*****A*****	
gene	*QG*V*QNIQLQ--NAR*--KCNMVKPAYK*A*S*R-*	

Fig. A2. A predicted amino acid comparison of the six known peach PG genes. * Represents a consensus sequence to PRF5, – represents a gap. GenPG, PRF5, PRF1 were previously sequenced (GenBank accession nos. X77231, X76735, and Lester *et al.* 1994, respectively) and AC1, AC2, FPG3 are from this paper.

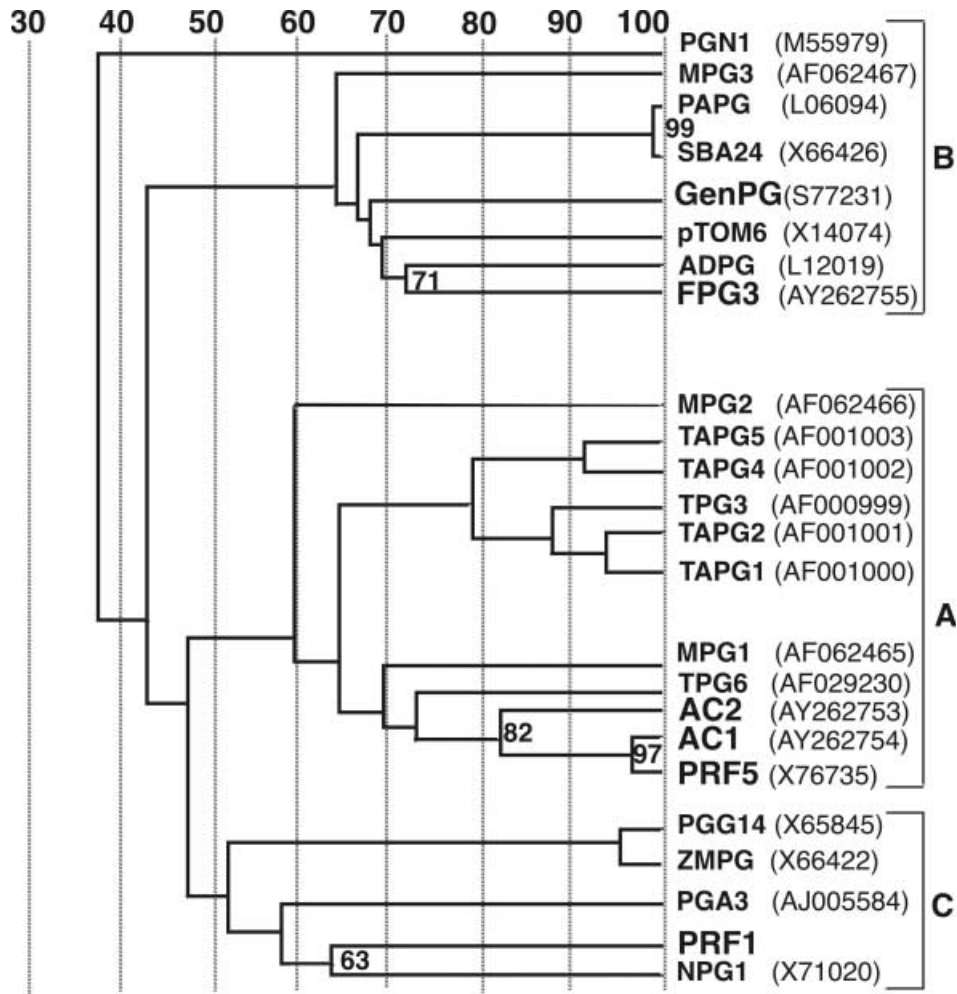


Fig. A3. Similarity of derived polypeptide sequences representing polygalacturonase. A similarity tree of the region of greatest conservation (Scott-Craig *et al.* 1990) was generated using the MAP123 alignment program (Gracy and Sallantin 1994). Dotted vertical lines indicate percent similarity based on the similarity matrix generated by the alignment. Numbers on the tree refer to percent similarity between the genes indicated. A fungal gene, PGN1, encoding an endopolygalacturonase was used as an outlier to assist in generating the tree. PGN1 (*Cochliobolus carbonum*); MPG1, MPG2, MPG3 [*Cucumis melo* (muskmelon)]; PAPG, SBA24 [*Persea americana* (avocado)]; GenPG, PRF5 [*Prunus persica* (peach)]; PRF1 (*P. persica*, Lester *et al.* 1994); AC1, AC2, FPG3 (*P. persica*, this paper); pTOM6, TAPG1, TAPG2, TPG3, TAPG4, TAPG5, TPG6 (*Lycopersicon esculentum*); ADPG (*Actinidia deliciosa*); PGG14, ZMPG (*Zea mays*); PGA3 (*Arabidopsis thaliana*) NPG1 (*Nicotiana tabacum*).