

# Genome-Wide Identification, Phylogenetic and Expression Analysis of Expansin Gene Family in *Medicago sativa* L.

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MsEXPA113	.....MNMVTKELRVESAVWQQAHAATFYGGSDASGTMGGACGYGNLYTDGYGIKSAALSTALFNDGKSCGGCYQIVCDARQVP	78
MsEXPA114	.....MVEVMPQEQ.....WIVCDARQVP	19
MsEXPA118	MEKFIICVLLLLMNMVTKELRVESAVWQQAHAATFYGGSDASGTMGGACGYGNLYTDGYGIKSAALSTALFNDGKSCGGCYQIVCDARQVP	90
MsEXPA119	MEKIIICVLILLINLLTKELRVESVWQQAHAATFYGGSDASGTMGGACGYGNLYTDGYGIKSAALSTALFNDGKSCGGCYQIVCDARQVP	90
MsEXPA120	MEKFIICVLLLLMNMVTKELRVESAVWQQAHAATFYGGSDASGTMGGACGYGNLYTDGYGIKSAALSTALFNDGKSCGGCYQIVCDARQVP	90
MsEXPA121	MEKIIICVLILLINLLTKELRVESVWQQAHAATFYGGSDASGTMGGACGYGNLYTDGYGIKSAALSTALFNDGKSCGGCYQIVCDARQVP	90
MsEXPA122	.....MNMVTKELRVESAVWQQAHAATFYGGSDASGTMGGACGYGNLYTDGYGIKSAALSTALFNDGKSCGGCYQIVCDARQVP	78
MsEXPA123	MEKIIICVLILLINLLTKELRVESVWQQAHAATFYGGSDASGTMGGACGYGNLYTDGYGIKSAALSTALFNDGKSCGGCYQIVCDARQVP	90
Consensus	ivcdarqvp	
MsEXPA113	QWCLRGTSITITATNFCPPNFALPNDNGGWCNPPRPHFDMSPAFQTIKYRAGIVPILYRRVGCKRSGNIRFTINGRDYFELVLISNVG	168
MsEXPA114	QWCLRGTSITITATNFCPPNFALPNDNGGWCNPPRPHFDMSPAFQTIKYRAGIVPILYRRVGCKRSGNIRFTINGRDYFELVLISNVG	109
MsEXPA118	QWCLRGTSITITATNFCPPNFALPNDNGGWCNPPRPHFDMSPAFQTIKYRAGIVPILYRRVGCKRSGNIRFTINGRDYFELVLISNVG	180
MsEXPA119	QWCLRGTSITITATNFCPPNFALPNDNGGWCNPPRPHFDMSPAFQTIKYRAGIVPILYRRVGCKRSGNIRFTINGRDYFELVLISNVG	180
MsEXPA120	QWCLRGTSITITATNFCPPNFALPNDNGGWCNPPRPHFDMSPAFQTIKYRAGIVPILYRRVGCKRSGNIRFTINGRDYFELVLISNVG	180
MsEXPA121	QWCLRGTSITITATNFCPPNFALPNDNGGWCNPPRPHFDMSPAFQTIKYRAGIVPILYRRVGCKRSGNIRFTINGRDYFELVLISNVG	180
MsEXPA122	QWCLRGTSITITATNFCPPNFALPNDNGGWCNPPRPHFDMSPAFQTIKYRAGIVPILYRRVGCKRSGNIRFTINGRDYFELVLISNVG	168
MsEXPA123	QWCLRGTSITITATNFCPPNFALPNDNGGWCNPPRPHFDMSPAFQTIKYRAGIVPILYRRVGCKRSGNIRFTINGRDYFELVLISNVG	180
Consensus	qwclrgtsititatanfcppnfalpndnggwcnprrphfdmsqfafqtiakyragivpilyrrvgckrsgnirftingrdyfelvlisnvg	
MsEXPA113	GGGEISKVWIKGSKKNKWEPMMSMNWGANWQSLSYLNGQSLSFRIQLKNGKTRTAINVAPSNWRFQGSYKSNVQ	241
MsEXPA114	GGGEISKVWIKGSKKNKWEPMMSMNWGANWQSLSYLNGQSLSFRIQLKNGKTRTAINVAPSNWRFQGSYKSNVQ	182
MsEXPA118	GGGEISKVWIKGSKKNKWEPMMSMNWGANWQSLSYLNGQSLSFRIQLKNGKTRTAINVAPSNWRFQGSYKSNVQ	253
MsEXPA119	GGGEISKVWIKGSKKNKWEPMMSMNWGANWQSLSYLNGQSLSFRIQLKNGKTRTAINVAPSNWRFQGSYKSNVQ	253
MsEXPA120	GGGEISKVWIKGSKKNKWEPMMSMNWGANWQSLSYLNGQSLSFRIQLKNGKTRTAINVAPSNWRFQGSYKSNVQ	253
MsEXPA121	GGGEISKVWIKGSKKNKWEPMMSMNWGANWQSLSYLNGQSLSFRIQLKNGKTRTAINVAPSNWRFQGSYKSNVQ	253
MsEXPA122	GGGEISKVWIKGSKKNKWEPMMSMNWGANWQSLSYLNGQSLSFRIQLKNGKTRTAINVAPSNWRFQGSYKSNVQ	241
MsEXPA123	GGGEISKVWIKGSKKNKWEPMMSMNWGANWQSLSYLNGQSLSFRIQLKNGKTRTAINVAPSNWRFQGSYKSNVQ	253
Consensus	gggeiskvwikgskknkwepmmsmnwganwqslsylingqslsfriqlkngkt tainvapsnwrfqgsyksnvq	

Figure S1. Homology comparison among eight tandem duplication genes on the scaffold.