

## Supplementary Materials: Cross-Species, Amplifiable EST-SSR Markers for *Amentotaxus* Species Obtained by Next-Generation Sequencing

Chiuan-Yu Li <sup>1,2,†</sup>, Tzen-Yuh Chiang <sup>3,†</sup>, Yu-Chung Chiang <sup>4,†</sup>, Hsin-Mei Hsu <sup>5</sup>, Xue-Jun Ge <sup>6</sup>, Chi-Chun Huang <sup>7</sup>, Chaur-Tzuhn Chen <sup>5</sup> and Kuo-Hsiang Hung <sup>2,\*</sup>

**Table S1.** Characteristics and functional annotations of 26 microsatellite primers were developed in *Amentotaxus formosana*.

Locus	Repeat Motif	Primer Sequence(5'-3')	Allele Size (bps)	<i>Ta</i>				Cross Amplification	Accession Number	BLAST Top Hit Acc. No.	Description	<i>e</i> -Value
				Ar	Fo	Yu	Po					
Amen03	(TGTTGC) <sub>4</sub> (GTT) <sub>4</sub>	F: CATTCTGATTAGTTGCTTC R:TAATGGTCAATCTGCTAGTC	179–187	50	50	50	50	4/4	LN907616	XP_002269363.2	PREDICTED: <i>Vitis vinifera</i> hypothetical protein	0
Amen04	(GGAATG) <sub>6</sub>	F:GAGAACATTACAGGAAGTCA R:AGGCATAATTGAACTGATT	178–196	50	50	50	48	4/4	LN907617	XP_001757450.1	<i>Physcomitrella patens</i> subsp. <i>patens</i> predicted protein	4.77 × 10 <sup>-41</sup>
Amen07	(ATTTT) <sub>3</sub> (ATTTTT) <sub>3</sub>	F:CATGGAGAGTCCTGATAGTA R:CTCATACGGTCTGTAGAAAA F:CATAGCACTTGAGATCACTT	203–208	54	54	54	54	4/4	LN907618	ACN26960.1	<i>Zea mays</i> unknown protein	2.92 × 10 <sup>-62</sup>
Amen10	(CCA) <sub>4</sub> (CCT) <sub>12</sub>	R:GCATTATAGAGTTTGACGA	349–358	50	50	50	50	4/4	LN907619	XP_002534324.1	<i>Ricinus communis</i> putative arginine/serine-rich splicing factor,	6.90 × 10 <sup>-15</sup>
Amen13	(CTATCC) <sub>4</sub>	F:ATATCACTGGCAGTCTCTT R:ATATCTATATGGTTGGCCTC	254–290	50	50	50	50	4/4	LN907620	CAN74005.1	<i>Vitis vinifera</i> hypothetical protein VITISV_006236	4.54 × 10 <sup>-17</sup>
Amen15	(CTG) <sub>3</sub> (GATTGG) <sub>4</sub>	F:CTATTGTCAGAGAAATCGAA R:GAAAGAGAAAGAGAAAGTGG	264–279	53	53	53	53	4/4	LN907621	XP_002265605.1	<i>Vitis vinifera</i> PREDICTED: partial hypothetical protein	1.22 × 10 <sup>-41</sup>
Amen18	(AAGTGG) <sub>4</sub>	F:CATCTCGCTTCTATTCAT R:AAAGCTTTATTGAACTTCG	273–279	48	48	48	48	4/4	LN907622	None	None	None
Amen19	(TGATGG) <sub>4</sub>	F:TAGGACAAAGAAGATAGCAG R:CATCAACACCATCACTGT	245–257	50	50	50	50	4/4	LN907623	XP_002285304.1	<i>Vitis vinifera</i> PREDICTED: hypothetical protein	1.45 × 10 <sup>-56</sup>

Table S1. Cont.

Locus	Repeat Motif	Primer Sequence(5'–3')	Allele Size (bps)	<i>Ta</i>				Cross Amplification	Accession Number	BLAST Top Hit Acc. No.	Description	<i>e</i> -Value
				Ar	Fo	Yu	Po					
Amen20	(CGGGAT) <sub>4</sub> N(GAGACG) <sub>3</sub> N (GGAAGG) <sub>4</sub>	F:AAATCCTAGAAACGGTATTT R:TTGTCTCAGCAGTTTCTTAT	279–300	50	50	50	50	4/4	LN907624	None	None	None
Amen24	(TCCTGC) <sub>6</sub>	F:CTCTTTATAACAGCCTCCTC R:GAAGGCTTCTATTCTCTGT	206	51	51	51	51	4/4	LN907625	XP_002525143.1	<i>Ricinus communis</i> conserved hypothetical protein	3.49 × 10 <sup>-19</sup>
Amen25	(CCT) <sub>7</sub>	F:GAATCTACTCAATGTATGCG R:GAGTAGAGACGTTCCAGTG	236	49	49	49	49	4/4	LN907626	XP_002518826.1	<i>Ricinus communis</i> conserved hypothetical protein	0
Amen26	(AGGAAG) <sub>6</sub>	F:TATCTAGAGTGCTGTGTTGG R:TTGAATTAGCATTAAATAGGG	239–251	52	52	52	52	4/4	LN907627	ABK24854.1	<i>Picea sitchensis</i> unknown protein	1.07 × 10 <sup>-96</sup>
Amen27	(AGGATT) <sub>4</sub>	F:TGTATGGATTAAATAGGGA R:AATCCTAATCCTAACCCCTAA	164–172	50	50	50	50	4/4	LN907628	XP_002973804.1	<i>Selaginella moellendorffii</i> hypothetical protein SELMODRAFT_100054	2.10 × 10 <sup>-146</sup>
Amen30	(CTGCC) <sub>4</sub>	F:GCATAGGTGTAGCTATGAAC R:ATACTTGTGCAGTTTGATTT	402–414	50	50	50	50	4/4	LN907629	XP_002300693.1	<i>Populus trichocarpa</i> predicted protein	1.62 × 10 <sup>-58</sup>
Amen35	(GAT) <sub>10</sub>	F:CATTGGGCAAATTCAGTGTC R:GCCTCCCACCCATTAGTAGA	237–252	50	50	50	50	4/4	LN907630	XP_002268183.1	<i>Vitis vinifera</i> PREDICTED: hypothetical protein	0
Amen38	(CCA) <sub>9</sub>	F:AAGAAATCTGGGGCACTGGA R:TGCACATCTTCTTCGTCACA	119–137	50	50	50	50	4/4	LN907631	ADE77044.1	<i>Picea sitchensis</i> unknown protein	0
Amen40	(CA) <sub>12</sub>	F:ACCCAGCTCAATACCAAAGC R:GCGAAATGTTGGTGACAGAC	350–380	51	51	51	51	4/4	LN907632	None	None	None
Amen41	(AGAA) <sub>6</sub>	F:CATGCAAATTGAGGCCAGTA R:ATAGGAGGAGAGGGCAAGGT	146–158	50	50	50	50	4/4	LN907633	EEC84662.1	<i>Oryza sativa</i> Indica Group hypothetical protein OsI_31560	5.08 × 10 <sup>-10</sup>
Amen42	(AGA) <sub>9</sub>	F:TGATGAGGAAGATGGGATGA R:CTTGGAGCATTCTCTGATGC	206	50	50	50	50	4/4	LN907634	XP_002523095.1	<i>Ricinus communis</i> putative U3 small nucleolar RNA- associated protein	1.25 × 10 <sup>-22</sup>

Table S1. Cont.

Locus	Repeat Motif	Primer Sequence(5'-3')	Allele Size (bps)	<i>Ta</i>				Cross Amplification	Accession Number	BLAST Top Hit Acc. No.	Description	<i>e</i> -Value
				Ar	Fo	Yu	Po					
Amen43	(TGG) <sub>10</sub>	F:AAGGTCTGTTGAAGTTTCGC R:AAGGGAGCGATTATTGGTTG	180–210	50	50	50	50	4/4	LN907635	XP_002969636.1	<i>Selaginella moellendorffii</i> hypothetical protein SELMODRAFT_231344	5.07 × 10 <sup>-136</sup>
Amen44	(GGAGA) <sub>4</sub>	F:GAGCACGTGGGGTTCTATG R:GAGCGAGGGCAATAAAGAG	95–100	50	50	50	50	4/4	LN907636	ABK23596.1	<i>Picea sitchensis</i> unknown protein	1.07 × 10 <sup>-68</sup>
Amen46	(AGTTG) <sub>6</sub>	F:GTGTATAGGCCGACCTTTT R:TGCACCTGCAACAACAAC	169–174	50	50	50	50	4/4	LN907637	CAN59753.1	<i>Vitis vinifera</i> hypothetical protein VITISV_036639	6.37 × 10 <sup>-178</sup>
Amen47	(CTCC) <sub>8</sub>	F:GGAAACTGGAATAGTCGGGA R:ATTTGCTGCAACAGAGCAAG	148–203	50	50	50	50	4/4	LN907638	ABK23165.1	<i>Picea sitchensis</i> unknown protein	8.39 × 10 <sup>-54</sup>
Amen48	(CT) <sub>15</sub>	F:ATTTTATGGGCAGTCAAGGC R:TAGAGGGAGAAGGAGACGGA	237–267	52	52	52	52	4/4	LN907639	None	None	None
Amen50	(ATAGA) <sub>10</sub>	F:CATAGACTACGCTCACCCCA R:CTCCCCTACCTACCCTACCC	220–260	53	53	53	53	4/4	LN907640	None	None	None
Amen52	(AATAG) <sub>8</sub>	F:TAGGGCATACTATCTGCCA R:GCCTCCAGGCCATAGATA	288–318	50	50	50	50	4/4	LN907641	None	None	None

The forward (F) and reverse (R) sequences, repeat motif, allele size (bps), annealing temperature when run individually (*Ta*), cross amplification, the GenBank accession number and Blast analysis are indicated. Abbreviations Ar, Fo, Yu, and Po indicate *A. argotaenia*, *A. formosana*, *A. yunnanensis*, and *A. poilanei*, respectively.