



Transcriptomics of Actinorhizal Symbioses Reveals Homologs of the Whole Common Symbiotic Signaling Cascade

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Table S1 : *Alnus glutinosa* and *Casuarina glauca* expressed sequence tag (EST) and cluster collection s

<i>Alnus glutinosa</i>		SUBTRACTIVE LIBRARIES		
	Root	Nodule	2 days post inoculation	7 days post inoculation
Number of ESTs sequenced	16215	16487	1812	2939
<i>EST summary</i>				
Number of high quality EST	13872 (86%)	14156 (86%)	1707 (94%)	2856 (97%)
Mean EST length (bp)	532	539	450	468
Range of EST size (bp)	101-843	101-825	101-859	101-856
Non valid sequences	2343 (14%)	2331 (14%)	105 (6%)	83 (3%)
- Small size sequence (< 100 bp)	2089	2084	32	42
- Low quality sequences	254	247	73	41
<i>Cluster summary</i>				
Number of ESTs assembled	13872	14156	1707	2856
Number of clusters	1675	2252	326	517
Number of singletons	4211	4171	299	1136
Number of contig sequences	1880	2431	330	529
Mean contig length (bp)	692	675	500	567
Range of contig size (bp)	121-1865	118-1889	126-1297	129-1770
Redundancy	70%	71%	82%	60%

<i>Casuarina glauca</i>		SUBTRACTIVE LIBRARIES		
	Root	Nodule	2 days post inoculation	7 days post inoculation
Number of cDNA sequenced	13869	14682	1862	2021
<i>EST summary</i>				
Number of high quality EST	13017 (94%)	13700 (93%)	1826 (98%)	1982 (98%)
Mean EST length (bp)	551	510	535	597
Range of EST size (bp)	101-845	101-830	101-845	101-865
Non valid sequences	852 (6%)	982 (7%)	36 (2%)	39 (2%)
- Small size sequence (< 100 bp)	682	786	18	17
- Low quality sequences	170	196	18	22
<i>Cluster summary</i>				
Number of ESTs assembled	13017	14682	1826	1982
Number of clusters	1337	1442	351	316
Number of singletons	5416	4361	669	251
Number of contig sequences	2261	1606	366	327
Mean contig length (bp)	757	745	646	698
Range of contig size (bp)	114-2261	131-1923	145-1580	137-1722
Redundancy	58%	68%	63%	87%