

Table 1. AM fungal rRNA types from root nucleic acid fractions

Root	DNA/RNA	Glo3	Glo27	Glo23	Glo8	Glo26	Glo2	Glo28	Glo29	Glo46	Glo57	Glo58	Glo59	Glo60	Acau13	Acau14	Acau15	Scut5	Total
<i>T. repens</i> sample A1	DNA*	1	4	5	20														30
	Unlabeled RNA [†]	7		2	18														27
	¹³ C-labeled RNA [‡]			11	17														28
<i>T. repens</i> sample A2	DNA*	24			1	1	3												29
	Unlabeled RNA [†]	13			8	4													25
	¹³ C-labeled RNA [‡]	19				6													25
<i>A. capillaris</i> sample A1	DNA*	2			2			1	4	10					5		1	4	29
	Unlabeled RNA [†]	14			8			1	2						2	1		2	30
	¹³ C-labeled RNA [‡]	7			10			3								3	5		28
<i>A. stolonifera</i> sample B1	Unlabeled RNA [§]				14							5	8	3					30
	¹³ C-labeled RNA [¶]				18						9	2	5						34

Total nucleic acids from roots of *T. repens*, *A. capillaris* (experiment A), or *A. stolonifera* (experiment B) were fractionated on a density gradient. AM fungal rRNA sequences were amplified from each fraction, products were cloned, and 25–30 representative clones were sequenced. Number of clones of each phylotype (Fig. 3) is shown.

*Cloned from PCR of total DNA.

[†]Cloned from RT-PCR of gradient fractions 9 and 10 (Fig. 2).

[‡]Cloned from RT-PCR of fractions 17 and (for A1 only) 18.

[§]Cloned from RT-PCR fraction 9.

[¶]Cloned from RT-PCR fraction 17.