# Structure and Intracellular Localization of Mouse ADP-Ribosylation Factors Type 1 to Type 6 (ARF1-ARF6)<sup>1</sup>

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ADP-ribosylation factors (ARFs) are a family of small GTP-binding proteins that are proposed to be involved in the formation of coated transport vesicles. Although six ARF sequences have been reported in mammals to date, it has been unclear how many ARF members are present in a single organism. In this study, we provide the first direct evidence by cDNA cloning for the presence of all six ARF members in mouse. These proteins are highly conserved across mammalian species and Northern blot analysis revealed that mRNAs for all the members were expressed ubiquitously. Transfection of cells with epitope-tagged ARFs revealed that ARFs 1-3 displayed a perinuclear Golgi localization, while ARFs 4-6 appeared to be widely dispersed throughout the cytoplasm. These results suggest that although all the ARF proteins play fundamental and critical roles in cellular function, they are involved in different vesicular transport processes.

Key words: ADP-ribosylation factor, epitope tagging, Golgi complex, small GTP-binding protein, vesicular trafficking.

Multiple small GTP-binding proteins belonging to the Rab, ADP-ribosylation factor (ARF), and Sar1 subfamilies, and heterotrimeric G proteins are key regulators of vesicular trafficking through the exocytic and endocytic pathways in eukaryotic cells (for reviews, see Refs. 1–7). Genetic and biochemical studies have revealed that Rab proteins play an essential role in various vesicular transport steps. Distinct Rab proteins are associated with almost every intracellular membrane compartment, suggesting that these small GTP-binding proteins function in vesicular targeting and/ or fusion (1, 3, 4, 6). Sar1 is required for vesicle budding from the endoplasmic reticulum (ER) (8–10).

The ARF family includes six members of ARFs and several structurally related ARF-like proteins (11-14; for reviews, see Refs. 7 and 15). ARF was first discovered as the cofactor required for the cholera toxin-catalyzed ADP-ribosylation of the  $\alpha$  subunit of the heterotrimeric G

protein, G, (16, 17). More recently, ARF proteins have been shown to play a critical role in vesicular trafficking along the exocytic and endocytic pathways (18-23). Vesicle formation is triggered by the attachment of cytosolic ARF to the membrane of donor compartments. The exchange of GDP for GTP on ARF, which is inhibited by a fungal metabolite, brefeldin A (24-26), promotes membrane binding of ARF, the binding of which is apparently a prerequisite for the membrane binding of coatomer, a complex of seven COP proteins (27), and that of HA-I/ AP-1 clathrin adaptor, a complex of four adaptor proteins (28), from the cytosol (5, 29-31). Subsequently, budding of COP-coated vesicles from the Golgi and that of clathrincoated vesicles from the trans-Golgi network occur (32). Furthermore, recent evidence suggests that ARFs are capable of activating phospholipase D (33, 34). The stimulation of phospholipase D activity by ARFs could promote vesicle budding at distinct membrane domains, possibly by acting to direct coat protein binding in transport vesicle assembly (35).

Although six ARF sequences have been reported in mammals (for reviews, see Refs. 7, 15, and 36), there is uncertainty with respect to the number of ARF family members in a given organism. Bovine ARF1 and ARF2 (37, 38) and human ARFs 1 and 3-6 (11, 12) have been cloned to date, but there has been no report of human ARF2. In this study, however, we cloned cDNAs for all the ARF members from mouse, demonstrating that ARFs 1-6 are present in a single organism.

The six ARF proteins are highly homologous to one another and are assigned to three classes on the basis of the sequence similarity: class I, ARF1, ARF2, and ARF3; class II, ARF4 and ARF5; class III, ARF6 (12, 36). Owing to the

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Abbreviations: ARF, ADP-ribosylation factor; ER, endoplasmic reticulum; TGN, *trans*-Golgi network; HA, hemagglutinin.

high sequence similarity of ARFs, antibodies that specifically recognize each ARF member are not available, though recently D'Souza-Schorey *et al.* (23) have raised antiserum that reacts specifically with ARF6, and have shown that ARF6 is localized at the cell periphery and is involved in receptor-mediated endocytosis. One way to approach this problem is the epitope-tag method. Using this method, ARF1 has been shown to be localized in the

## A. ARF1

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A1	000 G	GG	AA H	TA' I	TC1	F	TQC A	XA N	AC	CT L	сп F	ĸ	00 6	Ľ	F	по 6	GCA K	K	AAG E		TG	coc R	AT I	τςτ L	CAT	OGT V	GGC	i L	D	A TO	TO A	CAOC 6	igaag K	168 30
AC T	T	CA	AT I	TC L	TAT	T AI Y	CAA K	L	т	iaa K	CC1	600 6	CG E	m i	TTG V	TGA T	CCA T	сс А 1	P	<u>س</u>	æ	ATT I	rog G	ПП F	CAA H	TGI	E	NGA T	rigi V	TG E	NTA Y	K	IGAAT N	258 60
A1 1	S	x	TT F	CAI T	ά	31) V	GTG W	0G 0	AT	GT V	660 6	CCCC G	ĉ	NOG D	K	AGA' I	TCC R	SGC P	- CCC	TGT	<b>GO</b>	coc R	жа Н	CTA Y	СП F	τυ 0	GN N	T	ę	vac G	хт L	IGA1	CTTC F	348 90
G1 ¥	AG V	TG I	GA D	CA S	ж Г	44 H	tga D	CA R	G	GA E	900 R	nG ¥	'GA N	KCG E	AGG A	CCCO R	ettg E	MG	AGC	TCA	TG	agg R	AT H	OCT L	A00	TG/ E	NG/ D	E	L L	R	GAG D	ATGC A	лоп V	438 120
CT L	сг L	ſĢ	GT V	GT F	П¢	30	CAA N	CA K	AG	СА 0	D D	cت د	CCI P	XA N	ATG A	CCA'	TGA. N	ATG A	CGG	CCG E		ATC I	ж Т	AGA D	CM K	GCT L	660 6	ioci L	СС/ Н	CTO S	דר L	raci R	ICCAC H	528 150
ac R	iga N	10	TG F	GT/ Y	ŝ	AT I	TCA Q	.0G	<b>C</b> C	AC T	cto C	TGC A	CAI T	XA S	9009 G	2000 D	<b>ACG</b> 6	SCC L	TCT Y	ATG		6C.4 6	CT.	AGA D	П	10C1 L	1010 S	TA N	лси Q	CCT L	rcca R	3GAV N	CCAG Q	618 180
AA K	бTI	34	AO	CAC	jA(	æ	ст	œ	ст	00		τ¢	сп	œ	гст	ста	209	x	TCA	OCT	π	ССТ	ст	CAT	GTG	æ	~	GTO	iCG/	ст	16	GGT	CCTG	706 161
AC	лa	x	AG	~	c	ſG	тст	œ	AT	60	जा	661	ĊA	AG	TGTI	CA.	TOG	200	CGT	сст	GT.	AC.A	TG	TGC	AGA	00	x	xπ	CAG	w	GG	m	TAT	798

TAATGTAAATASTITICTGTTTCCACTGAGGCAGTTTCTGGTACICCTATGCAATATTACTTAGCTTTTTTAATGTAAAAGAATCAAC 899 TCAACTGTCAGTACTGAGAAGGGATTTGGGTGTAGGGGCACTGGCCTCGGGGAGCCATTGGGCTGTAGACTGGTGGGGTATCCATTTG GTGGTTGGTTTTTAACCCAAACTCAGTGCATTTTTTAAAAATAGTTAAAAATAC 1032

### B. ARF2

	TCOOCCOAGTAGCATTTTCGTGAGTGOCTTTGTGAAGGTGTTCGCTGCGGAGACAGGTTGCAGAATTCAGCTACA 75																													
AT	000	GAA	TGI	сп	TGA		601	GTT	TAA	AAG	сст	ATT	тос	GM	w	<b>6</b> 6/	**	000	GAT	nci	CAI	GGT	600	хΠ	AG/	TGC	AGC	TOG		165
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ĸ	GAC	GAT	сп	GTA	cm	ATT	GAA	GCT	AGG	AGA	GAT	TGT	GAC	wC	CAT	œ	TAC	CAT	AGG	π	CN	TGI	6G/	GAC	AGT	KA	6TA	¢.M		255
T	т	I	L	Y	K	L	K	L	G	E	I	۷	T	T	I	Ρ	T	I	G	F	N	۷	E	T	۷	E	Y	K	N	80
AT	CAG	сπ	CAC	ACT	стө	GGA	TÜT	TGG	TGG	CCA	OGA	2	**1	TAG	ACC	Π	GTG	000	ACA	TT/	сп	100/	GN	CAC	TCA	AGG	TCT	GAT	TTTĈ	345
١	S	F	T	۷	Ħ	D	۷	G	0	٥	D	ĸ	I	R	Ρ	L	W	R	н	Y	F	0	N	т	٥	6	L	I	F	90
бT	OGT	TGA	CAG	TAA	TGA	<b>cc</b> a	AGA	GCG	GGT	CAA	TGA	860	cas	CGA	AGA	ATT	GAC	CA (	AAT	CCT	ACC	10	101	TGA	сст	CAG	AGA	TOC	AGTC	435
۷	ITBGTTGACAGTAATGACCGAGAGGGGGGCAATGABGCCCCCCGGAAGAATTGACCAGAATGCTACAGAAGAGGACGCGAGAATGCAGG / V D S N D R E R V N E A R E E L T R M L A E D E L R D A V															120														
Π	GΠ	OGT	GTT	TGT	***	cm	ACA	OGA	TCT	τœ	TAA	TOC	TAT	CAA	TGC	жc	AGA	GAT	CAC	AGA	cv	CCT	TOC	сп	KA	стc	œτ	ТСС	CCAG	525
L	L	۷	F	Ŷ	N	K	Ó	D	L	P	N	٨	H	N	٨	٨	E	I	T	D	K	L	G	L	H	5	L	R	0	150
AG	***	стg	GTA	CAT	TCA	60C	TAC	CTG	TGC	GAO	CAG	TOG	AGA	TOC	GCT	TTA	CGA	AGG	CCT	0GA	сто	ICCT	CTC	×.	œ	GCT	CAA	~	CCAG	615
R	N	W	Y	1	0	٨	T	С	٨	т	5	G	D	G	L	Y	E	Ģ	L	D	T	L	S	N	Q	L	K	N	٥	180
ĸ	GTG	ATC	AGA	AGC	MC	αCA	TIC	œc	ATG	CAT	TGT	00C	***	ecc	AGC	T00	CCT	π	009	TUT	90/	וסו	GAC	CGT	GTG	AGG	AGC	CCA	66666	705 181

## C. ARF3

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a	GTI		STC	cπ	XA	TA	œA	ACC	AO	CAC	x	:TA	w	ω	IGA'	ПА	x	TGCI	cc	τœ	CTG	660	x	TAT	ΠG	ACT	TN	ACC		CAC	.T61	ATC	19
A1 M	roci G	SCA N	ATA I	tci F	Π : (	601 G	GAA N	αı	ПC L	TG/	<b>u</b> 0	GAG S	CCT L	- -	rcci G	ж К	GA K	AOG E	AGA H	tgc) R	OCA 1		TG	ATC N	90T V	000 G	L L	06/ D	ATOC	ТӨС А	2000 G	GAAG K	26. 3
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A1	IC.A	ст	FCA	CAC	TC	TG	GGA	co	rag	610	o	хA	GGJ	c,	GA	пα	60	æ	TCT	GGA	GAC	ACT	ĸ	π	œ	GAJ	ca	æ	war	сп	GAT	ATT	45
1	S	F	Ŧ	1	1		D	۷	G	G	,	0	D	ĸ	1	R	P	L		R	Н	1	r	F	0	н	T	0	G	L	I	F	96
G	IGG	ΠG	AC.A	œ	uT	GA'	TCG	GG/	GC	GAG	π	344	œ	GGC	xo	00G	WG	ACC	TGA	TGA	GGA	TCC	TG	60	064	GGJ	TG	GCI	m		Tec	TETE	55
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N K	GT	ж	100	CAG	IGC./	AGI	000	TCI	CT	GAC	T,	100	ω		:																		77: 18

Fig. 1. Nucleotide and deduced amino acid sequences of mouse ARF1 (A), ARF2 (B), ARF3 (C), ARF4 (D), ARF5 (E), and ARF6 (F).

Golgi region, and ARF6 in the cell periphery and endosomes (39, 40). However, little is known about the subcellular localization of other ARF members. In the present study, we also applied this method and determined the subcellular localization of all the ARF proteins.

## D. ARF4

	CCAGACCCCCTCCTTTTGACCGTCAAGTGCCACCACCGCT 4														- 40															
¥.	ATGGGGCTCACCATCTCTCTCTCTCGCGCCGCTTCGGCAAGAGCACATGCGCATTTGATGGTTGGATGGA															130														
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T	TILYKLKLGEIVTTIPTIGFNVETVEYKN															60														
¥.	пπα	π	CAC	AG	TATG	0G/	TGT	TGG	TGG	TCA	AGJ	TM	MT	TAG	600	тст	ста	GAG	GCJ	πı	сπ	œ	GV	TAC	CCA	660	itci	CAT	ππ	310
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G	IGGI	AG	TAC	x	TGA	TCO	TG/	MG	AAT	CCA	GG/	400	AOC	AOC	TGT	GCT	GCA	GAA	M	001	Incl	GG/	NGI	TGA	ост	°C/	<b>0</b> 6/	TGC	AGTO	400
۷	۷	D	S	N	D	R	Ε	R	I	0	E	e	A	٨	۷	L	0	ĸ	M	L	L	Ε	D	E	L	٥	D	٨	۷	120
сı	IGCT	œ	τп	ΠGC		cu	ĸ	GGA	TCT	600		<i>c</i> oc	TAT	66C	CAT	CAG	TGA	GAT	GAC	JCJ	cM	GCT	AGG	пст	TCC.A	атс	TCI	ccs		490
L	٤	L	F	A	N	ĸ	Q	0	ι	P	N	٨	Ĭ	٨	T	5	Ε	Ľ	Ţ	D	K	L	6	L	Q	S	L	A	N	150
A		ATC	GT/	TGI	ICCA	AGC	C.K	πс	TGC	TAC	ĸ	AGG	MC	TGG	тст	GTA	TGA	0GG	ACT	GGJ	TTG	GCT	GTC		TGA	ACT	π		acgt	580
R	T	W	Y	۷	0	A	т	с	٨	T	۵	G	т	G	Ł	Y	Ε	G	L	D	W	L	5	N	Ε	L	S	ĸ	R	180
T/	w	GAA	607	GC/	TAT	CTA	ACC.	MG	GAC	ATG	т	GAT	AGA	ATT	GGT	CTA	GGC	TTG	TTA	w	cm	<b>AA</b> T	TAG	π	œA	тст	та	ITTA	ΠM	670
A	GAT	ATC	TG	GAC	AGG	ш	600	CAG	m	TTA	CAG	CGT	TTA	***	ĊТТ	GTT	TIG	TTG	œ	٨П	ATT	GΠ	TAC	cM	GM	c.	TGI	тас	TAT	760
T/	00	ATA	TOC	т	OGT	TTA	AGI	GAA	ATT	стс	сп	666	***	ĢAA	MG	TAT	CCA	TTA	TT	TGC	ПС	αn	TGA	ACC	TAA	ATG	cci	GGA	TACA	850
G	GCT	ATC	cπ	ж	ССТ	TTA	GAC	AGA	тст	GAO	TGG	m	TTG	AGC	CCA	~~	Ç,M	TAA	TGT	π	***	GП	ATT	œ	ΠG	ATA	сП	TAC	TGAG	940
A	хп	TAT	CAI	πα	TCA	GAC	AGT	CTG	CTG	ATT	TAA	m	TÜT	AGC	AΠ	œ	π	GTA	m	ATT	тст	ACC	сΠ	TGC	CM	~	GAI	Π	TCTA	1030
AI	M	GCT	TGI	×.	600	CAA	000	CGT	GGT	CCA	~~	CAC	TAT	TCA	GTT	πс	TIG	TAC	TGA	QC/	τα	œ	CAC	ccc	ACC					1107

#### E. ARF5

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A1																139 30														
AC T	CTACCATCCTGTACMACTGAMGTTGGOOGMGATTGTCACCACCACCACCCACTATAGGCTTCAATGTGGAMCAGTGGAATATAAGAC TTILYKLKLGEIVTTIPTIOFN VETVEYKN															229 60														
AT I	NTCTGTTTCACAGTGTGGGATGTTGGAGGCCAGGATAAGATTCGGCCTCTGTGGGGGGCACTACTTCCAGAACACTCAGGGCCTCATCTTT C F T V W D V G G O D K I R P L W R H Y F Q N T O G L I F															319 90														
GT V	TOSTAGACAGCAACGAGCGGGAGCGGGGTCCAGGAGTCTGCTGATGAACTCCAGAAGATGCTGCAGGAGGATGAGGTGCGGGTGCGGGT 'V D S N D R E R V 0 E S A D E L 0 K II L 0 E D E L R D A V															409 120														
CT L	6C1 L	GG V	IGTI F	TQ A	CA N	K	6C/ 0	000 D	CAT	QCC P	CAA N	100 A		OCC P	CGT V	GAG S	E	OCT L	GAC T	TG/ D	CAA K	001 L	GCC G	ĩ	ТСА 0	оси Н	<del>در</del> ۲	GCCG R	TAGC S	499 150
CG R	C <b>AC</b> T	GTO W	GTA Y	CG V		1004 A	<b>XA</b> T	с С	TCC A	CAC T	сса 0	A00 6	CAC T	AGG 6	CCT L	GTA Y	TGA D	T00 G	OCT L	ogj D	CTG W	001 L	GTC S	CCA H	CCA E	ECT L	етс S	ĸ	OCOC R	589 180
TA	600	ACC	XA	3000	τ.	3000	xci	GCT	000	<b>COC</b>	MG	стс	<b>CCG</b>	ωī	GCA	TCC	COG	GAT	GAC	CAC	АСТ	æ	OGA	стс	стс	AGG	CAG	TGC	ccπ	679
α	τα	æ	сто	:110	xπ	200	Ś	GAC	A00	αt	CTG	сто	CIG	<b>CGC</b>	СТG	αст	90/	TOC	тст	сто	TIG	πα	ITTQ	GA0	œτ	0G/	600	TTG	стст	769
ст	GGG	CAC	AGA	600	СТС	TG	:101	α	900	TOC	T00	GAC	CTG	TGG	ATG	GGC	πο	сто	000	***	000	000	ICI	TCC	AGG	0GA	OGA	OCA	GOGA	859
TC	TOG	ATI	TA	l Π	GGI	Ш	961	m	GGT	ш	TTG	ATT	ш	ш	TCT	ш	ш	тст	пс	Π	Π	ш	GTT	TTG						933

#### F. ARF6

		. 34
CREGARGATCEATGACCTGACCREGECGARCCREGETCGTCGTC9000GTG	GTGACCGGGGTCOGTGCCGAGTCCGGTGCTCGCAGGCC	12
98CAG8069CCGCAGTTGGAGCC00CBC9T9CCGAGGCGCCGGA8GAGCTGT	COGCOGCOCTTOCTCOCTCOCTCOCTCOCCCCCCCCCCC	21(
GCGGGGGGGAAGGGCAGTTCCGGGCGGGCGGCGCGCCTCGCCTCGCTTG	ACAGGCGGCGGCTCTCCCGGCGCAGACGCAGGGCCC	30
CORCERCERCEATECCOLAGTEAGEOCARECCEGOCCCCTGCTUCCCTARC	CBBCABCTTCBCSCABBCCGCABGBCGTCCTCGCAGCG	39
SCGCSGCSACGTTTC:SCGCTCGCGGCGCGTTGTAGGCTTGAGGGGACCCGG	GACACCTGAATGCCCCCGGCCCCGGCTCTTCCGACGCG	48
ATGGGGAAGGTGCTATOCAAGATCTTCG9GAACAAGGAAATGCOGATCCTCA	TECTEGECCTEGACECAGCCOGCAAGACAACGATCCTE	571
IGKVLSKIFGNKEBRILM	ILGLDAAGKTTIL	3
TACANGTIGANGCIENNOCAN TENGTENCENCENCENCENCIGTENDECTICA	ACETEGAGACHETGACTTACAAAAACETCAACTTCAAC	
YKLKLGQ <b>SV</b> TTIPTVGFN	VETVTYKNVKFN	6
GTGTOOGATGTOGGCGGCCAGGACAAGATCCGGCCGCTCTGGCGGCATTACT	ACADOGGEACCCAGOGTCTGATCTTCGTQGTAGACTGC	75
<b>V W D V G G Q D K I R P L W R H Y Y</b>	Τ G T O G L I F V D C	90
GODEACCECEACCECATOGACEADECCOGCCAGGAGCTGCACCECATTATCA	ATGACOGOGAGATGAGOGACOCCATCATCCTCATCTTC	84
A D R D A I D E A R O E L H R I I N	ID RENROAIILIF	12
BOCAACAAGCAGGACCTBCCCGATGCCATGAAACCCCCATGAGATCCAGGAGA	AACTIGGGCCTGACCECIGATTCGGGACAOGAACTGGTAT	936
<b>ANKOOLPOAWKPHEIQEK</b>	LGLTRIRDRNWY	150
STSCASCOCTECTISTICCCACCTECGGOGAEGGAETETATGAGGOBETEACAT	GETTAACCTCTAACTACAAATCCTAATGAGCGTCCTCC 1	021
V Q P S C A T S G D G L Y E G L T W	ILTS NYKS	17
NOCCASCOCCOSSANGSAGASAAATOCAAAACOCATTOCTASSATTATOSOC	ACCTOCATCACCTCTTTGAATTGCCACTCTCTTTTTG 1	116
MTCTGAACTCTGGAGTTACT6TTCTACAGTTTAGTGGGGGTTGGGGGGTTTTC	ппоппесии плитиппессоности и	206
ICCGTTAGGATECTCTGATCTGACATTTGACACGAATACAGTGCTAGATGCC	TTGTGACTTOCAGCAAACGGGGTGGGGGTAATAQCAACT 1	296
CITEGTAAAGIOCTITATAATAATOGFITGATTTTTTATFICGAGAGAATC	TTCCCCCCCATGTATGCTTTTTTTCCTTTTTGCCCAGG 1	386
FICTTATEACTIGETIGTAGATOGETTATTTTGEATTEATGEAGACTATGTTC	CANGTETGTTTCATCTAGTAAACTGAAAATTATTGETT 1	47
ATCAMETECCETTEETCTTTTATATTTANGECC	1	511

## EXPERIMENTAL PROCEDURES

Cloning of Mouse ARF cDNAs—Approximately  $5 \times 10^5$ phages of a mouse brain library in the  $\lambda$ gt10 vector (41) were screened using a bovine ARF1 cDNA fragment covering the entire coding sequence (a kind gift from Dr. Richard A. Kahn, Emory University School of Medicine, Atlanta, GA; 37) under low stringency conditions. The number of obtained cDNA clones for each ARF is shown in Table I. By this screening, cDNAs covering the entire coding sequence were obtained for ARFs 1, 3, 4, and 6, while all the cDNAs for ARF2 and ARF5 were partial. Therefore,  $\sim 2 \times 10^5$  phages of mouse liver library (41) were then screened using the partial ARF2 and ARF5 cDNAs, and full-length ones for both ARFs were obtained. The cDNAs were separately subcloned into the NotI site of pBluescript-II (Stratagene, La Jolla, CA) and sequenced using a *BcaBest* sequencing kit (Takara Shuzo, Kyoto).

Northern Blot Analysis—Total RNAs  $(10 \mu g)$  isolated from mouse tissues and cell lines were denatured with glyoxal, electrophoresed on a 1.5% agarose gel, and blotted

TABLE I. ARF cDNA clones isolated from mouse brain library. Approximately  $5 \times 10^5$  clones were screened as described in "EXPERIMENTAL PROCEDURES."

DIG DIGHTDI I I I	ос <i>до</i> отщо.
ARF	Number of clones isolated
ARF1	7
ARF2	3
ARF3	6
ARF4	8
ARF5	1
ARF6	5
Total	30

mARF1	MGNIFANLFKGLF	) KREMRILMV <mark>gld</mark>	)AAGK <mark>TTILYKLKLGEIVTTIPTIGFNVETVEYKNI</mark>	61
harf1	• • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	61
mARF2	•••V•EK•••S•••	• • • • • • • • • • • • • • •	· • • • • • • • • • • • • • • • • • • •	61
barf2	•••V•EK••S•••	• • • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	61
mARF3	•••••G••L•S•I	• • • • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	61
har <b>f</b> 3	••••G••L•S•I	• • • • • • • • • • • • • •	• • • • <mark>• • • • • • • • • • • • • • • </mark>	61
marf4	••LTISS••SR••	• • • Q • • • • • • • • • •	• • • •	61
harf4	••LTISS••SR••	• • • Q • • • • • • • • • • •	• • • • <mark>• • • • • • • • • • • • • • • </mark>	61
mAR#5	··LTVSA··SRI·	• • • Q • • • • • • • • • • •	• • • • • • • • • • • • • • • • • • • •	61
hARF5	••LTVSA••SRI•	• • •Q • • • • • • • • • •	• • • • <mark>•</mark> • • • • • • • • • • • • • • •	61
mAR₽6	• • KVLSKI•	N · · · · · · L · · ·	•••••	57
harf6	••KVLSKI•	N••••L	•••••	57
	** *		************	
marf1	SFTVWDVGGQDKI	PLWRHYFQNTQG	LIFVVDSNDRERVNEAREELMRMLAEDELRDAVLL	122
hARF1	••••• <mark>••••</mark> ••••	• • • • • • • • • • • • • •	••••••••••	122
mARF2	•••••	• • • • • • • • • • • • •	•••••	122
barf2	•••••	• • • • • • • • • • • • • •	••••••	122
mARF3	••••	• • • • • • • • • • • • • •	•••••••••••••	122
harf3	•••••	• • • • • • • • • • • • • •	••••••••••••••	122
marf4	C • • • • • • • • • • • • •	• • • • • • • • • • • • •	••••••••••••••••••••••••••••••••••••••	122
harf4	C • • • • • • • • • • • • • • • • • • •	•••к•••••	••••••••••••••••••••••••••••••••••••••	122
marf5	C • • • • • • • • • • • • •	•••••	••••••••••••••••••••••••••••••••	122
harf5	C • • • • • • • • • • • • •	•••••	••••••••••••••••••••••••••••••	122
mARF 6	к•ы•• <mark>••••</mark> ••••	•••••¥TG•••	••••••CA••D•ID•••Q••H•IINDR•M•••II•	118
har <b>f</b> 6	к•ы•• <mark>••••</mark> •••••	•••••¥TG•••	•••••CA••D•ID•••Q••H•IINDR•M•••II•	118
	* ******* **	*** ** ***	***** ** * * * * * * *	
marf1	VFA <mark>NKQD</mark> LPNAMNI	AEITDKLGLESL	RHRNWYIQAT <mark>CAT</mark> SGDGLYEGLDWLSNQLRNQK :	181
harf1	••• <mark>••••</mark> •••••	•••••	· • • • • • • • • • • • • • • • • • • •	181
mARF2	••v••••••••••	••••	•Q••••• <del>•</del> •••	181
bar <b>f</b> 2	••••••••••••••••••••••••••••••••••••••	•••••	•Q••••• <b>K</b> •••	181
mARF3	•••• <mark>••••</mark> ••••••	••••	•••••••••••••••••••••••••••••••	181
hARF3	••••	• • • • • • • • • • • • •	••••••••••••••••••••••••••••••••••••••	181
marf4	L • • • • • • • • • • • • • • • • • • •	S•M•••••Q••	•N•T••V••• <mark>•••</mark> Q•T•••••••• <b>•</b> E•-SKR	180
harf4	L • • • • • • • • • • • • • • • • • • •	S•M•••••Q••	•N•T••V•••	180
mAR <b>F</b> 5	••••	'S•L•••••QH•	•S•T••V•••	180
hAR <b>F</b> 5	••••	5•L•••••QH•	•S•T••V•••	180
mar <b>y</b> 6	I••••••		•D••••V•PS <mark>•••</mark> ••••••••T••TSNYKS	175
hARF6	I••••••		•D••••V•PS <mark>•••</mark> ••••••••T••TSNYKS	175
	* **** * **	* ****	* * ** * ***	

Fig. 2. Comparison of mouse ARF amino acid sequences with those of other species. Amino acids identical with those of mouse ARF1 are indicated by dots, and gaps introduced for optimal alignment are indicated by hyphens. Asterisks indicate the positions of amino acids identical in all the ARFs. Consensus sequences for GTP-binding and hydrolysis are shown in dark boxes.

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onto a GeneScreen*Plus* membrane (Du Pont-NEN, Boston, MA) as described previously (42). The blot was hybridized with the following cDNA fragments of 5'- or 3'-untranslated region specific for each mouse ARF: ARF1, nucleotides 727-954; ARF2, nucleotides 962-1155; ARF3, nucleotides 1-170; ARF4, nucleotides 871-1086; ARF5, 640-860; ARF6, nucleotides 43-510.

DNA Construction—A vector for expressing COOH-terminally influenza hemagglutinin (HA) epitope-tagged proteins in mammalian cells (pCMV-HA) was constructed by subcloning of a double-stranded oligonucleotide coding for the HA-epitope sequence (YPYDVPDYA) between the XhoI and XbaI sites of pRcCMV (Invitrogen, San Diego, CA). Each ARF cDNA having an XhoI recognition sequence immediately behind the codon for the last amino acid, which was generated by a PCR-based method, was subcloned into pCMV-HA.

DNA Transfection and Indirect Immunofluorescence Microscopy—The expression vector for the COOH-terminally HA-tagged ARF thus constructed was transfected into monkey kidney Vero cells by using a CellPhect transfection kit (Pharmacia LKB Biotechnology, Uppsala, Sweden). The cells were cultured for 24 h, and then trypsinized, plated onto wells of eight-well Lab-Tek chamber slides (Nunc, Roskilde, Denmark), and cultured for a further 24 h. The cells were fixed, permeabilized, and blocked as described previously (43). The cells were then incubated with monoclonal mouse anti-HA antibody (12CA5, Boehringer Mannheim GmbH, Mannheim, Germany) and polyclonal rabbit anti- $\beta$ -COP antibody (a kind gift from Dr. Yukio Ikehara, Fukuoka University School of Medicine, Fukuoka; 44), followed by FITC-labeled donkey antimouse IgG (Chemicon, Temecula, CA) and Texas Redlabeled donkey anti-rabbit IgG (Jackson Immuno Research Laboratories, West Grove, PA). The stained cells were observed with a laser-scanning confocal microscope (TCS4D, Leica Lasertechnik, GmbH, Heidelberg, Germany).

## RESULTS AND DISCUSSION

By screening at low stringency of  $\sim 5 \times 10^{5}$  clones from a mouse brain library (41) with a bovine ARF1 cDNA fragment covering the entire coding sequence, 30 positive clones were obtained. Restriction endonuclease mapping and partial nucleotide sequence analysis revealed that these included cDNA clones for all known ARFs (Table I). Since the cDNAs for ARF2 and ARF5 were partial, a mouse liver library (41) was then screened with the partial cDNAs, and full-length ones for both ARF2 and ARF5 were obtained. It is particularly noteworthy that cDNAs for all six ARFs were obtained from the same library. There has been uncertainty regarding the number of ARF family members in a given organism although six ARF sequences have been reported in mammals (for reviews, see Refs. 7, 15 and 36); bovine ARF1 and ARF2 (37, 38) and human



Fig. 3. Northern blot analysis. Total RNAs  $(10 \mu g)$  of the mouse tissues and cell lines indicated were analyzed as described under "EXPERIMENTAL PROCEDURES." Positions of ARF transcripts are indicated by arrowheads. Neuro 2A, a neuroblastoma cell line; AtT-20, a corticotrophic tumor cell line; NIH 3T3, an embryo cell line; L929, a connective tissue cell line; MIN6, an insulinoma cell line.





ARFs 1 and 3-6 (11, 12) have been cloned to date, but there has been no report on human ARF2. In this study, however, we cloned cDNAs for all the ARF members from mouse, demonstrating that ARFs 1-6 are present in a single organism.

Figure 1 shows the nucleotide and deduced amino acid sequences of the six mouse ARFs. Alignment of the mouse ARF sequences with those of other mammals (Fig. 2) revealed that the ARFs are highly conserved proteins. The deduced amino acid sequences of mouse ARFs 1-3, 5, and 6, were in complete agreement with those of the human and bovine counterparts so far reported. By contrast, seven out of 180 amino acids of mouse ARF4 were different from those of human ARF4. The very high sequence conservation suggests that the whole region of each ARF protein plays a critical role in its function.

It is curious that only the mouse ARF4 sequence is not identical with that of other species. This could imply that we cloned one isoform of ARF4 and there may exist another ARF4 isoform that we failed to isolate. Nonetheless, we think that the cDNAs we cloned encode the sole mouse counterpart of ARF4, since the partial nucleotide sequences containing both the translated and untranslated regions of eight cDNA clones for ARF4 isolated from the brain library and five clones from the liver library were identical with one another (data not shown).

We then performed Northern blot analysis to examine the tissue and cellular distribution of the ARF members. In this analysis, we used a fragment covering an untranslated region of each ARF cDNA to detect specifically mRNA transcripts of each member, since the nucleotide sequences in the coding region of ARFs 1-6 are highly homologous to one another. The analysis revealed that all ARF transcripts were expressed in all examined mouse tissues (liver, kidney, intestine brain, lung, heart, testis) and cell lines (NIH 3T3, L929, AtT-20, MIN6, Neuro2A) (Fig. 3), suggesting all the ARF proteins play a fundamental role in cellular function.

Although there have been many reports on the subcellular localization and function of ARFs, most studies have been restricted to ARF1; the functions of other ARFs have not been defined. One of the reasons for this is the lack of antibodies that specifically recognize individual ARF members, since the ARF proteins are highly homologous to one another (see Fig. 2). For example, a widely used monoclonal antibody to ARF, 1D9 (45), recognizes all the ARF members (data not shown). To circumvent this problem, we first constructed expression vectors for ARFs with a COOH-terminal extension of the influenza HA epitope, since the HA epitope tag has been shown not to alter the intracellular localization of ARF1 and ARF6 (39, 40), although we could not completely exclude the possibility that such a tag affects the localization of other ARFs.

Monkey kidney Vero cells were transiently transfected with these ARF-HA constructs and were examined to determine the intracellular localization of each ARF using monoclonal anti-HA antibody (12CA5) by indirect immunofluorescence microscopy (Fig. 4). In cells expressing class I ARFs, ARF1 (panel A), ARF2 (panel D), and ARF3 (panel G), the staining was mainly restricted to a perinuclear region. For ARF1, a similar staining pattern was observed when it was tagged COOH-terminally with the human myc epitope in place of HA (data not shown). The staining of class I ARFs was superimposed on that of  $\beta$ -COP, a component of the coatomer protein complex, suggesting that these class I ARFs are localized in the Golgi region (panels A-I). Teal *et al.* (39) showed, by expressing HA-tagged ARF1 in COS-1 cells, that ARF1 colocalizes with  $\beta$ -COP in the perinuclear region. Our results thus showed that this is also the case with other class I ARFs, ARF2 and ARF3. Our results are also compatible with the previous report showing that ARF1 binding is a prerequisite for binding of coatomer to the Golgi membranes (29), and suggest that ARF2 and ARF3 play similar roles.

The staining patterns of ARFs 4-6 were different from those of ARFs 1-3. The class II and class III ARFs were localized in punctate structures throughout the cytoplasm and at the cell periphery (panels J, M, and P). Although the punctate staining was relatively intense in the perinuclear region, it was not completely superimposed on the  $\beta$ -COP staining (panels J-R). While this study was in progress, D'Souza-Schorey *et al.* (23) and Peters *et al.* (40) showed using an antibody specific for ARF6 and using the epitope tag method, respectively, that ARF6 is localized in endosome-like structures and in the plasma membrane, in accordance with our finding for ARF6. For ARFs 3-6, relatively intense nuclear staining was also observed, but its significance is currently unknown. We are now addressing this question.

In this study, we showed that ARFs constitute a protein family that is highly conserved across mammalian species and expressed ubiquitously. These findings indicate that ARF proteins play fundamental and critical roles in cellular function. However, ARF proteins belonging to classes I, II, and III appear to show different subcellular localizations, suggesting that they are involved in different vesicular transport processes. Experiments are under way in our laboratory to address this issue.

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