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DESCRIPTION

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A Group of Genes Expressed in Human Dendritic Cells

Technical Field

The invention of this application relates to a group of genes expressed in dendritic cells derived from human monocyte. More particularly, it relates to an aggregate of genes comprising 100 genes which are highly expressed in human dendritic cells; to an aggregate comprising 100 genes each being highly and lowly expressed in human dendritic cells as compared with in human monocyte; to a cDNA group for each of those gene groups; to novel gene contained in such gene groups; and to an aggregate of oligonucleotides for specifying those genes and cDNAs.

Background Art

Dendritic cells (DCs) play a very important role in an immune system by, for example, providing $CD4^+$-naïve T cells with antigen. It has been also reported that DCs directly participate in a T cell tolerance and an immunoglobulin production by B cells. In lymphocytes and nonlymphoid DCs, surface markers and function of each of them are different whereby they have different names. (For example, Langerhans cells in skin; interdigitating DC in lymph node; interstitial DC in heart, lung, kidney and testicle; thymus DC in thymus; etc.)

Although DCs have been believed to belong to a type different from monocyte and macrophage, macrophage and DCs have been reported to be derived from common stem cells. It has been also reported that human DCs are generated from $CD34^+$ precursor cells isolated from cord blood and bone

marrow in the presence of granulate-macrophage colony stimulating factor (GM-CSF) and tumor necrosis factor α (TNF-α). It is further reported that blood monocyte incubated with GM-CSF and interleukin-4 (IL-4) is differentiated to non-adhesive $CD1a^{+}CD14^{low/-}$ having morphological and functional characteristics of DCs. It is furthermore reported that DCs change to mature DCs expressing CD38 by a stimulation TNF-α, CD40 ligand, LPS or monocyte conditioned medium.

However, it is the present state that, although DCs are known to be the cells differentiated from monocyte, a process for the differentiation has not been clarified at all.

Clarification of a differentiation process of monocyte to DCs is quite important not only for understanding the function of an immune system but also for developing the novel means for diagnosis and therapy of various human diseases in which the dendritic cell is participated. In order to clarify the process of differentiation of monocyte to DCs, it is one of the effective means to specify a gene group which is expressed with a high frequency or a low frequency in each of the cells.

The invention of this application has been achieved under the circumstances as mentioned above and its object is to provide a gene group comprising the preceding 100 genes which are most abundantly expressed among the genes expressed in human dendritic cell.

Another object of this application is to provide a cDNA group comprising each cDNA of the gene group; novel gene contained in the gene group; and an oligonucleotide group for specifying the gene group and the

cDNA group.

Still another object of this application is to provide a gene group comprising each of the preceding 100 genes from the highly expressing part and the preceding 100 genes from the lowly expressing part in human dendritic cells derived from human monocyte as compared with in human monocyte. Further object is to provide a cDNA group, a novel gene group and an oligonucleotide group for each of those gene groups.

Disclosure of Invention

As an invention for solving the above-mentioned problems, this application provides a human dendritic cell-expressed gene group comprising 100 genes at the highest expression frequency among genes expressed in human dendritic cells derived from human monocytes, wherein the cDNAs of the individual genes individually contain nucleotide sequences of SEQ ID N0: 1 to 100 consecutive to the nucleotide sequence 5'-CATG-3' closest to the poly A region; a cDNA group comprising each cDNA of this gene group; a novel gene contained in this gene group; a novel protein encoded by the novel gene; an antibody and antagonist; and an oligonucleotide group comprising each nucleotide sequence of SEQ ID NO:1 to NO:100 consecutive to the nucleotide sequence 5'-CATG-3'. Incidentally, in the gene group which most abundantly expresses the human dendritic cell, it is a preferred embodiment that the expression frequency of the gene encoding the cDNA containing the nucleotide sequence of SEQ ID N0: 1 is the highest and the expression frequencies of the remaining 99 genes are in the order of SEQ ID N0: 2 to 100

This application also provides a human dendritid cell-expressed gene

group comprising 100 genes expressed more in human dendritic cells derived from human monocytes than in human monocytes, wherein the cDNAs of the individual genes individually contain nucleotide sequence of SEQ ID NO:101 to 200 consecutive to the nucleotide sequence 5'-CATG-3' closest to the poly A region; a cDNA group comprising each cDNA in this gene group; a novel gene group contained in this gene group; a protein encoded by the novel gene; an antibody and an antagonist; and an oligonucleotide group comprising each of the nucleotide sequences of SEQ ID NO:101 to NO:200 consecutive to the nucleotide sequence 5'-CATG-3'. In the gene group where an expression increases in this human dendritic cell, it is a preferred embodiment that the difference between the expression frequency of the gene encoding the cDNA containing the nucleotide sequence of SEQ ID N0: 101 and the expression frequency of this gene in human monocytes is largest, and the expression frequencies of the remaining 99 genes are in the order of SEQ ID N0: 102 to 200.

This application further provides a human dendritid cell-expressed gene group comprising 100 genes expressed less in human dendritic cells derived from human monocytes than in human monocytes, wherein the cDNAs of the individual genes individually contain nucleotide sequence of SEQ ID NO:201 to 300 consecutive to the nucleotide sequence 5'-CATG-3' closest to the poly A region; a cDNA group comprising each cDNA of this gene group; a novel gene group contained in this gene group; a protein encoded by the nobel gene; an antibody and an antagonist; and an oligonucleotide group comprising each of the nucleotide sequences of SEQ ID NO:201 to NO:300 consecutive to the nucleotide sequence 5'-CATG-3'. In the gene group where expression lowers in this human dendritic cell, it is a preferred embodiment that the difference between the expression frequency of the

gene encoding the cDNA containing the nucleotide sequence of SEQ ID N0: 201 and the expression frequency of this gene in human monocytes is largest, and the expression frequencies of the remaining 99 genes are in the order of SEQ ID N0: 202 to 300.

Each of the gene groups provided by the above-mentioned inventions is each aggregate of the genes specified by a tag sequence of SEQ ID NO:1 to NO:300 consecutive to the nucleotide sequence 5'-CATG-3' and the gene information comprising 14 bp is sufficient for identifying the full length of each gene and is useful, for example, for diagnosis, monitoring and judgement of prognosis of human infectious diseases and inflammatory diseases via cloning, protein expression and functional analysis thereof. In addition, the cDNA group and the oligonucleotide group are useful as the material for microarray, DNA chip, etc. for such a diagnosis, etc. Further, since the novel gene group has a high possibility of participating in the cause of human infectious diseases and inflammatory diseases, protein for which each of those gene codes and antibody and antagonist thereof are useful as the materials for development of pharmaceuticals.

Brief Description of Drawing

Fig. 1 is a result of a flow cytometry where the surface type of DCs derived from monocyte of human blood was analyzed; Fig. 2 is a result of comparison of gene expression in monocyte and DCs; and Fig. 3 is a result of the RT-PCR analysis of nine genes in monocyte, GM-macrophage and DCs of four blood donors (A, B, C and D).

Best Mode for Carryig Out the Invention

Each of the gene groups expressed in the human dendritic cell

according to this invention is an aggregate of 100 genes having different types expressed in the dendritic cell derived from human monocyte and has been identified by the known SAGE: serial analysis of gene expression method (Science 276:1268, 1997; Cell 88:243, 1997; Science 270:484, 1995; Nature 389:300, 1997; U. S. Patent 5,695,937). This SAGE method determines ten base pairs of DNA sequence (tag) which characterize each of cDNA prepared from genes expressing in any of the cells. It is also possible that, when the ratio of each tag is calculated from all of the resulting tag, expression frequency (copy numbers) of each gene is determined. Until now, the following gene expressions have been analyzed using this SAGE method. Thus, G2 arrest in colorectal cancer irradiation (Molecular Cell 1:3-11, 1997); oleate medium and pig 2q regulation (18th International Conference on Yeast Genetics and Molecular Biology s107:58, 1997); rat embryo fibroblast cells (Oncogene 15:1079-1085, 1997); p53 expression (Nature 389:300, 1997); yeast genome (Cell 88:243, 1997); and gastrointestinal tumors (Science 276:1268, 1997). The inventors of this application also specified the gene group which most abundantly expresses in human monocyte and human macrophage and the gene group which has a difference in terms of expression frequency between in human monocyte and in human macrophages by a SAGE method and have filed a patent application already (Patent Application No. 304550/1998).

Each of the gene groups expressed in human dendritic cell according to this invention is an aggregate of the genes specified by a method mentioned in the above-mentioned literatures and U. S. Patent, and is a gene aggregate where each cDNA contains the nucleotide sequences of SEQ ID NO:1-100, No:101-200 and NO:201-300, respectively, consecutive to 5'-CATG-3' closest to the poly A region. Those genes can be isolated, for

example, by means of a screening of a human genomic library using each oligonucleotide comprising 14 bp of this invention as a probe.

Further, the cDNA group of this invention is a cDNA of the gene constituting each of the above-mentioned gene groups and is an aggregate of cDNA (or a partial sequence thereof) having SEQ ID NO:1-100, NO:101-200 and NO:201-300 each by connecting to 5'-CATG-3' closest to the poly A region. Such a cDNA can be isolated, for example, by means of a screening of a human cDNA library using each oligonucleotide comprising 14 bp of this invention as a probe.

The information of 14 bp constituting each of the oligonucleotides of this invention is sufficient for identifying the full length of each gene and cDNA.

Incidentally, the cDNA group of this invention includes a DNA fragment (10 bp or longer) containing any of the partial nucleotide sequences of each cDNA. In addition, DNA fragment comprising sense and antisense strands are included in this cDNA group as well.

Usually, polymorphism due to the difference among individuals is frequently noted in human gene. Accordingly, gene and cDNA where one or more nucleotide(s) is/are added, deleted and/or substituted with other nucleotide or modified nucleotide in the gene group and cDNA group of this invention are included within the coverage of this invention.

The novel gene group of this invention is an aggregate of genes which have no corresponding genes as a result of retrieval of database and that

which are specified only by means of EST (expression sequence tag). Such novel gene group can be concretely specified, for example, by a positional cloning using each oligonucleotide of this invention as a marker, by a screening of a cDNA library using the oligonucleotide as a probe, by a retrieval of a gene bank, etc. It is also possible to prepare a novel protein for which a novel gene codes and an antibody to this novel protein from the novel gene. The protein can, for example, be prepared by a method where the novel gene cDNA or a partial sequence thereof is subjected to an *in vitro* transcription or a method where it is expressed in a large quantity by a suitable host-vector. The antibody can be also prepared as a polyclonal antibody or a monoclonal antibody according to a known method.

The antagonist of this invention is one to an expression of each gene belonging to each gene group of this invention and, for example, it is an antagonist to a transcription factor of each gene. Further, the antagonist of this invention is one to an activity of the protein expressed by each gene belonging to each gene group and is, for example, an antagonist to a receptor of each protein or an antagonist to a receptor of a target protein to which each protein in bonded. Thus, the gene belonging to each gene group of the invention is a gene which is abundantly expressed in human DCs or an aggregate of genes which is expressed abundantly or in a small amount as compared with in human monocyte and, since there is a high possibility that it is participated in onset or progress of human infectious diseases, inflammation, etc., the antagonist to those gene and protein is useful as an ingredient of the pharmaceuticals for prevention or therapy of infectious diseases and inflammation.

Incidentally, the antagonist can be specified, for example, by an *in*

vitro expression system of each of the above-mentioned genes or by a known screening method where each protein is a subject. Alternatively, it can be prepared by means of chemical synthesis, etc. as a result of structural analysis, etc. of the protein or a receptor thereof.

As hereunder, concrete specifying methods for each gene group of this invention and the specified gene groups will be illustrated.

(A) Preparation of cells

Peripheral blood mononuclear cells (PBMC) were extracted by a conventional method from venous blood of eight healthy persons and passed through a magnetic cell separation system to separate the monocyte and a suspension of the cells was incubated to give a highly purified monocyte.

Further, the monocyte was incubated together with GM-CSF according to a conventional method to prepare macrophage (GM-macrophage).

In addition, the monocyte which was positive to peripheral blood CD14 was incubated for five days together with GM-CSF, IL-4 and TNF-α whereupon DCs were prepared. Thus, under such an incubating condition, monocyte was differentiated to non-adhesive $CD14^-$, $CD1a^+$, $CD80^{low/+}$, $CD86^{low/-}$, $HLA\text{-}DR^+$, $CD33^+$ and $CD83^-$ (cf. Fig. 1). Those cells had a dendritic form of immature DCs.

(B) SAGE analysis

mRNA was prepared from each of the cells prepared in the above (A) and cDNA was synthesized using a biotinated oligo(dT). The cDNA (DC library) was digested by a restriction enzyme NIaIII and the 3'-terminal of each cDNA was purified using avidin-magnet beads. Since the cleaved site

by NIaIII is 5'-CATG-3', the sequence at the 5'-terminal of the purified cDNA 3'-terminal piece is always CATG. After that, cDNA was divided into two, different linker was added to 5'-terinal of each of them and the cDNA was cleaved at the site which was 14 base pairs downstream from the 3'-terminal of the linker using a restriction enzyme BsmF1. All of those DNA fragments of 14 base pairs were common in that their 5'-terminal was a CATG sequence but, since the residual ten base pairs were different for each cDNA, the ten-base pair sequence becomes a tag for characterizing the cDNA. In order to clone the aggregate of those tags, the cleaved site of BsmF1 was made into a blunt terminal, cDNA fragments divided into two were ligated and DNA was amplified by means of a PCR using an oligonucleotide for each linker as a primer. As a result, there were manufactured DNA fragments (Ditag) wherein linker sequence (5'-GGATG-3'), 5'-CATG-3' and complementary sequences thereof were available at both terminals and different tag sequences were linked at each of the 3'-terminals. The amplified DNA fragments were cleaved by NIaIII, then each Ditag was ligated to prepare a concatemer and it was cloned to a vector pZero1.

(C) Gene group expressed in human DCs

According to the above operation, 58,540 tags were obtained from cDNA expressed in human DCs, 17,000 or more genes were specified by those tags and, among them, there were 5,000 or more genes in which same tags were present twice or more. From all of those tags, 100 tag were selected in the order of abundance of duplications (i.e., high expression frequency of cDNA designated by the tag) and shown in SEQ ID NO:1 to NO:100.

As will be apparent from the above description, the tags of SEQ ID NO:1 to NO:100 are ten base pairs which continuously exist in the nucleotide

sequence CATG existing in the position nearest the poly A region of the gene cDNA expressing in human DCs. Accordingly, when the known DNA database is searched and cDNA having a know sequence is retrieved, the nucleotide sequence CATG which is nearest the poly A region of the DNA sequence is found and subjected to a matching with ten nucleotide sequences connecting thereto whereupon it is possible to specify the cDNA designated by the tag (and gene coding for the cDNA). Table 1 and Table 2 are tags (column B), numbers of the tag (column A) of SEQ ID NO:1 to NO:100, gene (column C) specified as a result of searching the database depending upon each tag and registration numbers (columns D, E and F) of the database.

Table 1

	A	B	C	D	E	F
1	952	GTTCACATTA	p33 (HLA DR invariant chain)	X00497		
2	826	CCCTGGGTTC	ferritin L-chain	M10119		
3	667	GGGCATCTCT	HLA DR alpha chain	J00196		
4	486	TTGGTGAAGG	thymosin beta-4	M17733		
5	453	CCTGTAATCC	mlutiple match			
6	435	TGCCTGCACC	cystain C	X05607		
7	430	CAAGCATCCC	EST	AA653836	AA226653	AA230314
8	427	TTGGTCCTCT	ribosomal protein L41	AF026844		
9	393	TTGGGGTTTC	ferritin H-cahin	L20941		
10	325	GTGAAACCCC	mlutiple match			
11	318	CTAAGACTTC	mitochondrial DNA	AA467764		
12	310	GTGACCACGG	EST	H50114	H84279	
13	297	CCACTGCACT	mlutiple match			
14	273	GGGGAAATCG	thymosin beta 10	M92381		
15	256	GTTGTGGTTA	beta-2-microglobulin	AB021288		
16	254	TGTGTTGAGA	elongation factor alpha 1 subunit	X16869		
17	242	CCCATCGTCC	EST	AI357743	AI281418	AI281569
18	237	TTCATACACC	EST	AI300940	AA902681	AA070967
19	201	GTGAAACCCT	mlutiple match			
20	187	TCCAAATCGA	vimentin	X56134		
21	185	TGGGTGAGCC	cathepsin B	M14221		
22	182	TTGGCCAGGC	mlutiple match			
23	180	CACAAACGGT	ribosomal protein S27	U57847		
24	171	AGCCCTACAA	EST	AI280609	AI287963	AI374100
25	167	GGCTGGGGGC	profilin	J03191		
26	163	CACCTAATTG	mitochondrial DNA	AA226180		
27	150	CTGACCTGTG	MHC class I	M28205		
28	148	ACTTTTTCAA	No match			
29	146	TGGTGTTGAG	ribosomal protein S18	X69150		
30	141	GGAGGTGGGG	granulin	M75161		
31	140	TGTACCTGTA	alpha tubulin	K00558		
32	136	TGATTTCACT	myosin-binding protein C	AI114736		
33	125	TGCACGTTTT	ribosomal protein L32	X03342		
34	125	TCACCGGTCA	gelsolin	X04412		
35	124	CCTCAGGATA	EST	AA935174	AA224784	AA906133
36	123	ATGGCTGGTA	40S ribosomal protein S2	X17206		
37	122	GGCACAAAGG	TRAC	D43767		
38	121	GCCTGCTGGG	GPx-4 mRNA for phospholipid hydroperoxidase glutathion peroxidase	X71973		
39	121	TTCCCTTCTT	MHC class II lymophocyte Ag B-chain	M28202		
40	121	AGAAGTGTCC	LAL mRNA for lysosomal acid lipase	M74775		
41	120	CCAGAACAGA	thymidylate kinase or robosomal protein L30	L05095	L16991	
42	119	CCTAGCTGGA	peptidyl-prolyl cis-trancisomerase A	Y00052		
43	113	TAGGTTGTCT	translationally controlled tumor protein	X16064		
44	111	AGGCTACGGA	ribosomal protein L13a	AA052955		
45	111	GTGCTGAATG	myosin alkali light chain	M22918		
46	111	ACGCAGGGAC	heat shock 90kD protein 1, alpha	AB897500		
47	108	GCTTTATTTG	beta actin	V00478		
48	108	AAAACATTCT	EST	AI098657	AA069402	AA099906
49	105	CCCCCTGGAT	cell division cycle 2-like 1	AA081048		
50	105	TGAAAACTAC	SB classII histocompatibility antigen alapha-chain	X00457		

Table 2

	A	B	C	D	E	F
51	104	ATGAGCTGAC	cystain B	L03558		
52	102	TTGTAATCGT	ornithin decarboxylase	D78361		
53	101	CCCGTCCGGA	EST	AA213823	AA216620	AA251755
54	101	CTGGGTTAAT	ribosomal protein S19	M81757		
55	101	GCAGTTCTGA	MHC class II	X00699		
56	100	GGGGCAACAG	CDW52	X67699		
57	96	CCGTCCAAGG	ribosomal protein S16	M60854		
58	95	AAGACAGTGG	ribosomal protein L37a	L06499	X66699	
59	95	TGTGATCAGA	ATPase	AF092124		
60	94	AGCCACCGCA	glucose-6- ohosphatase	U01120		
61	93	TGGCCCCAGG	apolipoprotein C-I	X00570		
62	91	AGGTGGCAAG	EST	AA131091	AA151439	AA194429
63	87	GACGACACGA	ribosomal protein S28	U58682		
64	87	ACCCTTGGCC	EST	AW237867	AA482078	AA496571
65	86	CCTGTAGTCC	multiple match			
66	85	GCGACCGTCA	aldolase A	M11560		
67	84	GAAGCAGGAC	non-muscle type cofilin	X95404		
68	84	ACACAGCAAG	multiple match			
69	82	AGGGCTTCCA	cytochrome C reductase	M64241		
70	82	CGCTGGTTCC	ribosomal protein L11	X79234		
71	81	AGCACATTTG	EST	AA130191		
72	80	GGGCTGGGGT	ribosomal protein L29	U10248		
73	80	ACCGCCGTGC	cytochrome b-245	M21186		
74	77	GCCGAGGAAG	ribosomal protein S12	X53505		
75	77	CTCATAAGGA	EST	AA833550	AI086871	AI366586
76	76	GTGCGCTGAG	HLA-CW3	X58536		
77	76	GCCCCCAATA	14kD beta glycotoside-binding lectin	J04456		
78	75	CGCCGCCGGC	ribosomal protein L35	U12465		
79	75	AAGTTGCTAT	prosaposin	D00422		
80	74	TGGCTCCTCC	lymphocyte cytosolic protein 1	AA044266		
81	74	TCGAAGCCCC	No match			
82	73	AGCACCTCCA	eukaryotic translation elongation factor 2	Z11692		
83	73	CGCCGGAACA	ribosomal protein L4	X73974		
84	71	AGGTCAGGAG	multiple match			
85	71	GTGTGTTTGT	TGF-B Induced gene ptoduction	M77349		
86	71	GTAATCCTGC	No match			
87	71	CACCACGGTG	EST	AA019224	AA019897	AA021231
88	70	CCATTGCACT	atacia relangiectasia phosphatidylinoditol 3-kinase homolog	U26455		
89	70	TAATAAAGGT	multiple match			
90	69	CACTACTCAC	No match			
91	69	CCTGGGGTAA	major histocompatibility complex, class II, DQ alpha 1	M17847		
92	68	ATTCTCCAGT	ribosomal protein L23	X52839		
93	68	ATAATTCTTT	ribosomal protein S29	L31610		
94	67	GGATTTGGCC	acidic ribosomal phosphoprotein	AB002533	M17887	
95	67	TTCACTGTGA	macrophage galactose-specific lectin	AB006780		
96	66	GAGGGAGTTT	ribosomal protein L27a	U14968		
97	66	AGCTCTCCCT	ribosomal protein L23	X53777		
98	65	ACTAACACCC	PACAP type-3Nip type2 receptor	U18810		
99	65	GCCTTCCAAT	nuclear p68 protein	X15729		
100	64	GTGAAGGCAG	ribosomal protein S3A	L13802		

As shown in Table 1 and Table 2, the gene which was most abundantly expressed in human DCs was an HLA DR invariant chain (expression frequency: 1.17%). It was confirmed that the genes which were expressed on the whole in a DC library were related to MHC Class I, Class II, protein synthesis and cell skeleton.

(D) Gene group abundantly expressed in human DCs as compared with in human monocyte

By the same manner as mentioned in the above (B), the tag for each genes expressing in human monocyte and human GM-macrophage were specified and the expressed genes in human monocyte and human DCs were compared. In those cells, most of the genes showed a similar expression pattern (cf. Fig. 2). However, with regard to 313 genes expressed in monocyte, the expression pattern in DCs was significantly ($p < 0.01$) different. Thus, among the 131 genes, the expression level of 181 genes lowered in DCs. On the contrary, 132 genes were expressed in a higher frequency in DCs than in monocyte. Table 3 and Table 4 show the preceding 100 genes which were more abundantly expressed in human DCs than in human monocyte. In Tables 3 and 4, genes expressed in GM-macrophage and in DCs were shown and compared as well. Thus, in Tables 3 and 4, column A is an expression frequency of tags in monocyte and DCs in terms of "fold"; column B is copy numbers of tags in monocyte; column C is copy numbers of tags in GM-macrophage; column D is copy numbers of tags in DCs; column E is a tag sequence (SEQ ID NO:101 to NO:200); column F is a protein accorded in GenBank data; and columns G, H and I are registration numbers at the GenBank.

Incidentally, in Table 4, the full name of the protein in line 23,

column F is "tyrosine 3-monooxygenase/tryptophan 5-monooygenase activation protein, beta polypeptide" while that in line 95, column F is "*Homo sapiens* clone 24860 Ena-VASP like protein mRNA sequence, partial cds".

Table 3

	A	B	C	D	E	F	G	H	I
1	125	0	72	125	TCACCGGTCA	gelsolin	X04412		
2	122	0	1	122	GGCACAAAGG	TRAC	D43767		
3	61	2	79	121	AGAAGTGTCC	LAL mRNA for lysosomal acid lipase	M74775		
4	47	2	2	94	AGCCACCGCA	glucose-6- ohosphatase	U01120		
5	41	0	10	41	CGTGAGCCAC	estrogen-responsive B box protein	AF096870		
6	40	0	4	40	GCCTGCAGTC	serine protease inhibitor, Kunitz type, 2	AB006534		
7	36	0	3	36	GCCCTGAAAG	No match			
8	35	1	0	35	TTGGAACAAT	EST	AA586687	AI130926	
9	34	0	0	34	CCTCTGGGCA	P450 oxidoreductase	R42191		
10	33	0	3	33	CCAAGACTTC	No match			
11	33	0	117	33	AACGGGGCCC	MDC	U83171		
12	32	0	15	32	CAGCTATTTC	fatty acid binding protein homologue	M94856		
13	31	0	0	31	CTTTCAGATG	platelet-rype phosphotroctokinase	D25328		
14	31	0	5	31	TTACTTCCCC	delta-6 fatty acid desaturase	AF126799		
15	30	1	0	30	TTGAGACCTC	factor XIII subunit	M14539		
16	28	2	20	55	CTGTTAGTGT	malate dehydrogenase	U20352		
17	25	0	31	25	TCTTGATTTA	alpha-2 macroglobulin	M11313		
18	25	0	64	25	TGTCCCAGCC	acid phosphatase type 5	X14618		
19	23	0	3	23	CCCCCGTAAT	Meisl homolog	AI203963		
20	22	0	6	22	ATGGAAGTCT	inoditol polyphosphate 5-phosphatase	X98429		
21	21	0	9	21	CTAAAAAAAA	CD81 antigen	M33680		
22	20	21	166	430	CAAGCATCCC	EST	AW275649	AA226653	
23	20	0	1	20	TGTGAACAAC	EST	AA470682		
24	20	0	0	20	ACTCACCTTA	EST	AA742376		
25	20	0	0	20	GATACAGCCA	Fc-epson receptor CD23 antigen	M14766		
26	19	0	5	19	CTGATCTCCA	EST	AI088488		
27	19	0	19	19	ACCCAGGGTA	EST	AA115735		
28	19	2	3	37	TTTGCTCTCC	vinculin	M33308		
29	18	0	1	18	CTATATTTTT	cathepsin C	X87212		
30	18	0	0	18	AAGGGATGCT	MCP-4	U46767		
31	18	0	2	18	AACGAGGAAT	No match			
32	18	0	3	18	CCCTCGGTCC	No match			
33	18	0	15	18	GCCTACCCGA	pancreatic carcinoma marker GA733-1	X13425		
34	18	0	34	18	GATGACCCCC	EST	AA075089	AA074875	AA075567
35	17	0	1	17	GGTGTGCTTG	clone24736	AF055021		
36	17	0	0	17	AGTGCAGGGC	No match			
37	17	0	0	17	CCTCACTACC	EST	AA454170		
38	17	0	0	17	TGCAGAAGAA	mannose receptor	J05550		
39	17	0	5	17	CCGGGCGTGG	EST	R49492		
40	17	1	9	17	CCCAAGCTAG	heat shock 27kD protein 1	S74571		
41	17	0	32	17	AAGATTGGTG	CD9	M38690		
42	16	3	7	48	TGGCGTACGG	EST	AI242886	AI279985	AI301916
43	16	1	4	16	GCCAGCCCAG	KRAB-associated protein 1	U78773		
44	16	0	4	16	GGTCCCCTAC	KIAA0100 gene product	AA551245		
45	16	9	61	140	TGTACCTGTA	alpha tubulin	K00558		
46	16	6	1515	93	TGGCCCCAGG	apolipoprotein C-1	X00570		
47	15	0	0	15	CTCTGTAAGT	metalloproteinase(HME)	L23808		
48	15	0	0	15	GGAGGCAGGA	No match			
49	15	0	6	15	TTTTCTGAAA	thioredoxin(TXIV)	J04026		
50	15	7	105	104	ATGAGCTGAC	cystain B	L03558		

Table 4

	A	B	C	D	E	F	G	H	I
51	14	1	1	14	CACAAAAAAA	multiple match			
52	14	1	0	14	GTGGCGTGTG	clone23933	U79273		
53	14	1	0	14	TCCGCCTCGG	DEK gene	AI929197		
54	14	0	2	14	CTCTACAGTG	vacuolar proton-ATPase	Y15286		
55	14	0	3	14	AATGCTTTTA	dioxin-inducible cytochrome p450	U03688		
56	14	1	4	14	TTGGACTGAG	ganglioside expression factor 2	AA099173		
57	14	0	8	14	CTTTGATGTT	NORI-1	AB010427		
58	14	1	21	14	ACCACTTATC	EST	AA865837	AI080299	AI123033
59	14	0	40	14	CACCTCCTAT	No match			
60	13	1	0	13	AGCCACCACG	KIAA0149	D63483	D86864	
61	13	0	2	13	TCATTGTAAT	glutathione peroxidase 3 (plasma)	AA027858		
62	13	0	3	13	ATGGCAGGAG	EST	AA514878	AA828070	AA578984
63	13	1	3	13	CTTTTTGTGC	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase act	AA400249		
64	13	0	4	13	TGGAAACAAA	DORA protein	AJ223183		
65	13	1	8	13	TACTAGTCCT	HSP90	D87666		
66	13	1	13	13	TCCTTCTCCA	alpha-actinin	X15804		
67	13	5	4	63	CCCAGCTAAT	arachidonate15-lipoxygenase	M23892		
68	13	2	4	25	GAGGGTGCCA	complement component 1, q subcomponent, beta polypeptide	AA910242		
69	12	0	0	12	CTGAGAGCTG	growth arrest-specific protein	L13720		
70	12	0	0	12	GTGGCTTCCC	tumor necrosis factor receptor superfamily, member 5	AA147592		
71	12	0	0	12	TTCTCAATAA	CD1 mRNA for arment for HTA1 thymocyte antigen	X04450		
72	12	1	0	12	TTTGTGCACT	EST	AW085447		
73	12	0	2	12	CTGTGCGCCC	serine protease inhibitor, Kunitz type 1	AW189576		
74	12	0	2	12	TGTGTGAGCT	EST	AA056972	AA158746	
75	12	1	3	12	AGATAATGTT	fur-mRNA for furin	X17094		
76	12	0	3	12	TCCTGCTGGC	KIAA0496	AA948411		
77	12	0	7	12	TATATTTTCT	transglutaminase	M98479		
78	12	1	10	12	GACTGTGCCA	cytoplasmic dynein light chain 1	U32944		
79	12	1	31	12	TTACAGAACT	phospholipase A2, group VII	NM005084	U24577	
80	11	0	1	11	AAGTACTTCA	general transcription factor IIB	AA136737		
81	11	0	1	11	TCACTCCTGG	No match			
82	11	0	0	11	AATTGGATTG	thymocyte antigen CD1c	M28827		
83	11	0	0	11	ATTAAGAAAA	AHNAK nucleoprotein	AA027210		
84	11	0	0	11	CAAAATGCAA	EST	AA489062	AA011305	AA242818
85	11	1	0	11	GCTTTGCAGC	src-like adaptor protein	U44403		
86	11	0	0	11	TCACAAAAGA	beta1,4-galactosyltransferase	AF038663		
87	11	2	3	22	CAGGATGACG	EST	AA461521	AA565978	AA6097147
88	11	0	2	11	TTCCTGGTAG	KIAA0788	AB018331		
89	11	0	3	11	GGAAGGGGGA	cofilon 1	T34499		
90	11	0	5	11	CTGGGTTGTG	EST	AA256831	AA600012	AA699963
91	11	0	5	11	GGGGACTGGT	protein kinase C, delta	AA505643		
92	11	0	9	11	TCAGGGCTGA	EST	AA488396	AA582282	AA834210
93	11	1	16	11	TGTTTATCCT	diazepam binding inhibitor or endozepine	M14200		
94	11	0	39	11	ACATTCTTTT	NMB	X76534		
95	10	7	15	71	CACCACGGTG	Homo sapiens clone 24860 Ena-VASP like protein mRNA seq	AF131766		
96	10	2	2	20	GAAGTCGGAA	EST	AI382431	AA575974	AI073720
97	10	0	1	10	CACAAAAAGA	integrin, alpha X	AA989341		
98	10	0	0	10	AAGTTGACTT	No match			
99	10	1	0	10	AGCAAACTGA	Homo sapiens leucine aminopeptidase mRNA	AF061738		
100	10	0	0	10	ATTAAGAGGG	No match			

As shown in Table 3 and Table 4, GM-macrophage and DCs showed the similar gene expression patterns. On the other hand, the gene showing higher expression frequency in DCs as compared with in monocyte was a gene coding for the proteins participated in cell structures such as gelsolin and vinculin, the proteins participated in lipid metabolism such as lysosome acid lipase and apolipoprotein C-1 and the chemokines such as TARC and MDCMCR-4. In addition, gelsolin, lysosome acid lipase, MDC, fatty acid-bonded protein homologs, acidic phosphatase type 5, GA 733-1, CD 9, HPS 27, etc. increased both in macrophage and DCs. On the other hand, expression in a high frequency is specifically noted in TARC, hepatocyte growth accelerating inhibiting factor type 2 (HAI-2), phosphofructokinase of a platelet type, factor XIII, CD 23, cathepsin C, MCP-4 and metalloprotease (cf. Fig. 3).

(E) Gene group which is less expressed in human DCs as compared with in human monocyte

Genes expressed in human monocyte and human DCs were compared by the same manner as mentioned in the above (D) and 100 genes where the expression frequency decreased in DCs as compared with in monocyte are shown in Tables 5 and 6. Form of indication is the same as that in Table 3 and 4. Incidentally, in Table 6, line 58 of column F is "nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha" and line 59 of column F is "monocyte activation antigen or urokinase-type plasminogen activator receptor".

Genes where the expression was most reduced in DCs were complement proteins (ficolin and properdin), DNA-bonded proteins (GOS3, GOS2 and c-fos) and a surface protein (CD14). The genes where expression

was reduced in DCs showed the same tendency in GM-macrophage as well. Further, the genes where a reduction of expression in 10-fold or more as compared with GM-macrophage was noted were MRP-14, MRP-1α, CD14, alpha 1 antitypsin, HLA-B and tranleolase. Incidentally, a reduction in CD14 in DCs was also confirmed by the result of a flow cytometry analysis as shown in Fig. 1.

Table 5

	A	B	C	D	E	F	G	H	I
1	532	1064	47	2	GTGGCCACGG	MRP-14	X06233		
2	287	287	0	0	TACCTGCAGA	MRP-8	X06234		
3	244	244	3	0	CCCACAACCT	ficolin-1	D83920		
4	105	105	19	0	GCACCAAAGC	MIP-1a	D00044		
5	97	97	0	0	TGGAAGCACT	IL-8	M17017		
6	84	84	10	0	TGGTCCAGCG	CD14	M86511		
7	77	77	0	1	CTTGACATAC	protein tyrosine phosphatase	X68277		
8	66	66	10	1	GGAAAAGTGG	alpha 1-antitrypsin	M26123		
9	65	65	22	1	GCTGTTGCGC	ribosomal protein S20	AA076625		
10	65	65	2	0	GGCCACGTAG	D component of complement	AA302667		
11	63	63	0	0	TCTACACGTG	complement compoment properdin	M83652		
12	63	63	0	0	CTGATGGCGA	S100 calcium-binding protein A9	AA587283		
13	55	55	0	0	CTGTACTTGT	GOS 3	L49469		
14	51	51	0	0	TGGAAAGTGA	v-fos FBJ murine osteosarcoma viral oncogene homolog	NM005252		
15	48	48	10	1	CTGACTTGTG	MHC class I HLA-B	M15470		
16	46	46	0	0	ACATTTCCAA	Human G0S2 protein gene	AA594415		
17	44	88	5	2	TCACAGCTGT	B-cell translocation gene 1, anti-proliferative	AA024842		
18	44	44	0	1	ATGGTGGGGG	zinc finger protein	M63625		
19	44	44	19	1	TTGGCAGCCC	ribosomal protein L27a	H73560		
20	34	34	2	0	TGGGCAGCTG	multiple match			
21	33	33	20	0	TTGCGTGTGT	protein phosphatase PAC-1	L11329		
22	31	31	1	0	CTCCATCCAG	G-CSF receptor	M59819		
23	31	31	0	0	AGTGCACGTG	ribosomal protein L29	AA157635		
24	31	31	0	0	GGCCAGGACT	formyl peptide receptor1	M60627		
25	27	27	2	1	GTCCCCCCAA	EST	AI217285		
26	27	27	0	0	CCCTGAGGCC	cDNA DKFZp566F184	AI148871		
27	25	25	0	0	GTGGGCCACG	Homo sapiens SNC73 protein (SNC73) mRNA	AI735130		
28	23	70	20	3	GCCGCCATCT	transketolase	L12711	U55017	
29	22	112	16	5	CTGTTGGCAT	ribosomal protein L21	T41133		
30	21	21	1	0	ACCATTCTGC	IFN-inducible mRNA	X57351		
31	21	21	3	0	ACTTTAATGA	C5a anaphylatoxin receptor	M62505		
32	21	21	11	0	AATTAAATTA	eukaryotic translation initiation factor 4 gamma, 1	AA622573	AA082100	
33	20	20	7	1	GGTAGCCCAC	trinucleotide repeat containing 5	AA468594		
34	20	20	0	0	GCCGCCGTGC	No match			
35	19	19	0	1	CTTTTTTCCC	CD48	M59904		
36	19	19	4	0	CTTGGGATGT	endoplasmic reticulum lumenal protein	AA074076		
37	19	37	11	2	ATGGAGCGCA	tumor necrosis factor receptor superfamily, member 1B	M32315		
38	18	18	2	1	ACGCTCTCGA	CD37	X14046		
39	18	18	0	0	TAGCCCCCTG	TNF	M10988		
40	18	18	0	0	TTGGAGCACT	EST	AA724726		
41	18	18	0	0	TTTCTGTATG	H3 histone, family 3B (H3.3B)	AA400294		
42	18	18	6	0	ATGGCTTGGT	ribosomal protein S2	AA064604		
43	17	17	0	0	TAATGCTAAA	helix-loop-helix basic phosphoprotein	L13463		
44	16	48	0	3	TGAAGTAACA	putative translation initiation factor	AJ012375		
45	16	48	2	3	GGGAAACAGG	EST	AA970435		
46	16	16	0	1	TGAGTCTGGC	core promoter element binding protein	AL117595		
47	16	16	8	1	GCGACAGCTC	ribosomal protein L24	AI375511		
48	16	79	18	5	GCTGAACGCG	CCAAT, enhancer binding protein (C/EBP), beta	AA135498		
49	15	15	1	0	TGTTTTCATA	small inducible cytokine A4	AA777287		
50	15	15	0	0	CTCACTTTTT	NF-IL6 beyta	M83667		

Table 6

	A	B	C	D	E	F	G	H	I
51	15	15	0	0	GCGGCGGCTC	ribosomal protein L28	AI340623		
52	15	15	2	0	ACTACAAATA	ribosomal protein L9	AW169101		
53	14	14	0	1	TCAACTTCTG	solute carrier family 2 (facilitated glucose transporter), member 3	AA101267		
54	14	14	0	0	ATCCGGACCC	growth arrest and DNA-damage-inducible 34	U83981		
55	14	14	0	0	CAATTTGTGT	IL1b	AF043335		
56	14	14	0	0	TTGAAGGGCC	delta sleep inducing peptide, immunoreactor	AL110191		
57	14	14	0	0	TTGCTGCCAG	EST	AI275804		
58	14	14	2	0	GACTTGTATA	nuclear factor of kappa light polypeptide gene enhancer in B-cells i	AI285391		
59	14	14	6	0	AACCACATTG	monocyte activation antigen or urokinase-type plasminogen activat	M83246	U08839	
60	13	13	4	1	GCGTGCTCTC	ribosomal protein L18a	AI815745		
61	13	13	1	0	ATGGCGATCT	ribosomal protein S24	AI333064		
62	13	51	7	4	GGCCTTTTTT	histone HIX	D64142		
63	12	12	3	1	TAGAAAGGCA	butyrate response factor 2	AA039882		
64	12	12	7	1	TTGACCTGTG	major histocompatibility complex, class I, B	AW072760		
65	12	12	1	0	GCGAGACCCC	No match			
66	12	12	1	0	TAAACTGTTT	ribosomal protein S14	N22003		
67	12	12	1	0	TTGGGTCCTC	ribosomal protein L41	AA484882		
68	12	12	1	0	TTTCAATAGA	EST	AI243522	AI698759	
69	12	12	1	0	GACTGGACCG	No match			
70	12	12	1	0	TACGTTGTCT	tumor protein, translationally-controlled 1	AI719912		
71	12	12	0	0	CTGGGCCAGC	vesicle-associated membrane protein 5 (myobrevin)	AI066491		
72	12	12	0	0	TACCTGCAAA	P47-phox(NcF1) pseudogene	M25665	M55067	
73	12	12	0	0	AACTCCCAGT	negative growth-regulatory protein	AF090950		
74	12	12	0	0	TGTTGTAACT	EST	AA947175		
75	12	12	2	0	GGGCCAAAAC	EST	AA047668		
76	12	12	4	0	GGCCTGGCAC	EST	AI223741		
77	12	12	9	0	GCGCGGGCGA	ribosomal protein, large, P1	AA190821	90827	AA304860
78	12	35	3	3	GCGGCTTTCC	gDNA homologous to yeast ScoI	AL021683		
79	11	22	3	2	CCCCCACCTA	differentiation dependent AU protein	L09604		
80	11	11	0	1	CTTAATCTTG	BTG2	U72649		
81	11	11	0	0	ACTCGAATAT	K12 protein precursor	U77643		
82	11	11	0	0	ACTGCCTACA	small inducible cytokine A3-like 1	AW059858		
83	11	11	0	0	TCTATCCCCC	multiple match			
84	11	11	2	0	TTGAAGGCAG	No match			
85	11	11	8	0	TACCCCACCT	H2A histone family, member Y	C75515		
86	11	11	39	0	CTGGGGTTTC	No match			
87	11	42	0	4	TACATTCTGT	myeloid cell leukemia sequence 1	L08246		
88	11	21	5	2	GAGATCCGCA	IFN-r or preproprolactin-releasing peptide	AB0154		
89	10	30	2	3	GCAGAGAAAA	actin binding protein P57	D44497		
90	10	10	0	1	CTGAGGTGTG	DEBP2ac1 acute myeloid leukoemia	Z35278		
91	10	10	0	1	GGAGGTGGAG	multiple match			
92	10	10	0	1	TCCGTCCGGA	No match			
93	10	10	12	1	ATCGTGCGCT	No match			
94	10	10	18	1	CATCCCGTGA	leukotriene A-4 hydrolase	J02959		
95	10	10	26	1	CTCTGGGTTC	No match			
96	10	10	0	0	TTTGGGACCC	pleckstrin homology, Sec7	AI51287		
97	10	10	0	0	AGGAGATGCT	leukocyte immunoglobulin-like receptor, subfamily B, member 2	AF011566	AF025528	
98	10	10	0	0	ATACCTGGAT	TYRO protein tyrosine kinase binding protein	AI299346		
99	10	10	0	0	GGGTTCCAGT	bone marrow stromal cell antigen 1	D21878		
100	10	10	0	0	TATATTGATT	B-cell translocation gene 1, anti-proliferative	X61123		

Incidentally, an SAGE analysis of each gene expression as mentioned above was carried out using the cells prepared from the blood of the eight persons. Now, in order to check whether the difference in each gene expression is dependent upon the difference in gene of blood donors, an RT-PCR was carried out for the blood samples for four persons with a target of 9 genes. The result is as shown in Fig. 3 and it was confirmed that the result of the SAGE analysis was not due to the difference in the gene of the blood donor but was dependent upon the difference in the gene expression frequencies in monocyte, GM-macrophage and DCs.

Further, the cDNA group of this application is an aggregate of cDNAs of gene constituting the above-mentioned each gene group connecting to 5'-CATG-3' which is nearest nucleotide sequence to the poly A region having the nucleotide sequence of SEQ ID NO:1 to NO:100, NO:101 to NO:200 and NO:201-NO:300 or a partial sequence thereof. The cDNA group of this invention covers DNA fragments (10 bp or more) containing any partial nucleotide sequence of each cDNA. Further, DNA fragment comprising sense chain and antisense chain is covered by this cDNA group as well.

In human genes, polymorphism due to the difference among individuals is frequently noted in general. Accordingly, in the gene group and cDNA group of this invention, gene and cDNA where one or more nucleotide(s) is/are added, deleted and/or substituted with other nucleotide are also included within a coverage of this invention.

As mentioned hereinabove, all of the gene groups provided by this invention including novel genes are genes which are expressed in human DCs and, particularly, the preceding 100 genes having the most abundant

expressing amount. Further, the gene group provided by this invention is a gene group having a relatively high expressing amount and that having a relatively low expressing amount in human DCs (and GM-macrophage) as compared with in human monocyte. Accordingly, those gene group and cDNa group as well as the aggregation of tags designating them are useful, for example, in the following fields.

(1) Specification of novel genes

With regard to the novel gene (group) provided by this invention, it is possible to specify such novel gene by means of, for example, a positional screening using an oligonucleotide where 5'-CATG-3' is added to the 5'-side of its tag sequence as a marker, a screening of a cDNA library using the said oligonucleotide as a marker or a search of the gene bank. It is also possible from the novel gene to prepare a novel protein for which the gene codes and also an antibody and an antagonist to the said protein. The protein can be prepared, for example, by a method where the novel gene cDNA or a partial sequence thereof is subjected to an *in vitro* transcription or by a method where expression in a large quantity is carried out using an appropriate host-vector. With regard to an antibody, it can be prepared as a polyclonal antibody or as a monoclonal antibody according to a known method. With regard to an antagonist, it can be prepared by means of chemical synthesis, etc. as a result of elucidation of structure of the protein or the receptor thereof.

(2) Specification of morbid gene

There is a high possibility that the causative gene for the diseases in which human DCs are participated (such as atopic dermatitis and asthma) is a gene which is expressed in a high frequency in DCs. That is, for example,

an excessive expression of the specific gene contained in the gene group expressed in DCs provided by this invention, decrease or deletion of expressed amount, gene mutation, etc. In addition, as mentioned already, there are genes showing clearly different amounts between in monocyte and in DCs. Accordingly, such genes showing different expressing amount are also the candidates for useful gene for the diseases in which each cell function is participated. As such, each gene group provided by this invention is useful for clarification of those morbid gene and an onset mechanism thereof.

(3) Development of pharmaceuticals

Clarification of the causative gene and of the onset mechanism as mentioned in the above (2) is useful in the development of therapeutic agents for the above-mentioned diseases. Examples are pharmaceuticals which lower the expressing amount of excessively expressing gene.

(4) Development of diagnostic means

There is a usefulness in the development of a diagnostic means for the diseases in which human DCs are participated. Examples are a kit for EIA and RIA utilizing an antibody to protein expressed by the causative gene and a DNA chip in which a partial or a full-length DNA of the gene is incorporated. Particularly, a DNA chip is useful for diagnosis of the diseases in which plural genes are participated but, since the DNA fragment numbers which can be incorporated on the substrate are limited, it is necessary to select the gene which is essential for the diagnosis. This invention provides gene and cDNA having an abundant expressing amount and, since it goes without saying that they are an aggregate of gene playing an important role in cell functions and cDNA thereof, they are quite useful as

the candidates for DNA constituting a DNA chip. In addition, since the oligonucleotide group of this invention containing a tag sequence is a sequence which correctly specifies each gene, it can be also utilized as a minimum DNA sequence being incorporated in a DNA chip.

Further, the gene information comprising 14 bp of a novel gene provided by this invention is an information which is sufficient for identifying the full length of each gene and it relates to the development of pharmaceuticals and antagonists via cloning, protein expression and function analysis thereof.

Industrial Applicability

In accordance with the invention of this application, there are provided a gene group comprising 100 genes which are highly expressed in human DCs and a gene group which is expressed in a high frequency and in a low frequency in human DCs as compared with in human monocyte. Those gene groups are quite useful not only for understanding of the differentiation process from monocyte to DCs but also for developing the novel means for diagnosis and therapy of various human diseases in which monocyte and DCs play an important role.

CLAIMS

1. A human dendritic cell-expressed gene group comprising 100 genes at the highest expression frequency among genes expressed in human dendritic cells derived from human monocytes, wherein the cDNAs of the individual genes individually contain nucleotide sequences of SEQ ID N0: 1 to 100 consecutive to the nucleotide sequence 5'-CATG-3' closest to the poly A region.

2. A human dendritic cell-expressed gene group of claim 1, wherein the expression frequency of the gene encoding the cDNA containing the nucleotide sequence of SEQ ID N0: 1 is the highest and the expression frequencies of the remaining 99 genes are in the order of SEQ ID N0: 2 to 100.

3. A human dendritic cell-expressed gene cDNA group comprising the cDNAs or partial sequences thereof of the individual genes composing a human dendritic cell-expressed gene group of claim 1, wherein the cDNAs individually contains nucleotide sequences of SEQ ID N0: 1 to 100 consecutive to the nucleotide sequence 5'-CATG-3' closest to the poly A region.

4. A human dendritic cell-expressed novel gene group included in a human dendritic cell-expressed gene group of claim 1, wherein the cDNAs of the individual novel genes individually contain nucleotide sequences of SEQ ID NO:7, 12, 17, 18, 24, 28, 35, 48, 53, 62, 64, 71, 75, 81, 86, 87 or 90 consecutive to the nucleotide sequence 5'-CATG-3' closest to the poly A region.

A novel protein encoded by the gene of the dendritic cell-expressed novel gene group of claim 4.

6. An antibody to the novel protein of claim 5.

7. An antagonist to the expression of each gene belonging to the gene group of claim 1.

8. An antagonist to the activity of protein expressed by each gene belonging to the gene group of claim 1.

9. A group of oligonucleotides individually having the nucleotide sequence of SEQ ID NO:1 to NO:100 consecutive to the nucleotide sequence 5'-CATG-3'.

10. A human dendritid cell-expressed gene group comprising 100 genes expressed more in human dendritic cells derived from human monocytes than in human monocytes, wherein the cDNAs of the individual genes individually contain nucleotide sequence of SEQ ID NO:101 to 200 consecutive to the nucleotide sequence 5'-CATG-3' closest to the poly A region.

11. A human dendritic cell-expressed gene group of claim 10, wherein the difference between the expression frequency of the gene encoding the cDNA containing the nucleotide sequence of SEQ ID N0: 101 and the expression frequency of this gene in human monocytes is largest, and the expression frequencies of the remaining 99 genes are in the order of SEQ ID

NO: 102 to 200.

12. A human dendritic cell-expressed gene cDNA group comprising the cDNAs or partial sequences thereof of the individual genes composing a human dendritic cell-expressed gene group of claim 10, wherein the cDNAs individually contains nucleotide sequences of SEQ ID NO: 101 to 200 consecutive to the nucleotide sequence 5'-CATG-3' closest to the poly A region.

13. A human dendritic cell-expressed novel gene group included in a human dendritic cell-expressed gene group of claim 10, wherein the cDNAs of the individual novel genes individually contain nucleotide sequences of SEQ ID NO: 107, 108, 110, 122-124, 126, 127, 131, 132, 134, 136, 137, 139, 142, 148, 158, 159, 162, 172, 174, 181, 184, 187, 190, 192, 196, 198 or 200 consecutive to the nucleotide sequence 5'-CATG-3' closest to the poly A region.

14 A novel protein encoded by the gene of the dendritic cell-expressed novel gene group of claim 13.

15. An antibody to the novel protein of claim 14.

16. An antagonist to the expression of each gene belonging to the gene group of claim 10.

17. An antagonist to the activity of protein expressed by each gene belonging to the gene group of claim 10.

18. A group of oligonucleotides individually having the nucleotide sequence of SEQ ID NO:101 to NO:200 consecutive to the nucleotide sequence 5'-CATG-3'.

19. A human dendritid cell-expressed gene group comprising 100 genes expressed less in human dendritic cells derived from human monocytes than in human monocytes, wherein the cDNAs of the individual genes individually contain nucleotide sequence of SEQ ID NO:201 to 300 consecutive to the nucleotide sequence 5'-CATG-3' closest to the poly A region.

20. A human dendritic cell-expressed gene group of claim 19, wherein the difference between the expression frequency of the gene encoding the cDNA containing the nucleotide sequence of SEQ ID N0: 201 and the expression frequency of this gene in human monocytes is largest, and the expression frequencies of the remaining 99 genes are in the order of SEQ ID N0: 202 to 300.

21. A human dendritic cell-expressed gene cDNA group comprising the cDNAs or partial sequences thereof of the individual genes composing a human dendritic cell-expressed gene group of claim 10, wherein the cDNAs individually contains nucleotide sequences of SEQ ID N0: 201 to 300 consecutive to the nucleotide sequence 5'-CATG-3' closest to the poly A region.

22. A human dendritic cell-expressed novel gene group included in a human dendritic cell-expressed gene group of claim 10, wherein the cDNAs of the individual novel genes individually contain nucleotide sequences of SEQ ID NO:225, 234, 240, 245, 257, 265, 268, 269, 274-276, 284, 286, 292,

293 or 295 consecutive to the nucleotide sequence 5'-CATG-3' closest to the poly A region.

23 A novel protein encoded by the gene of the dendritic cell-expressed novel gene group of claim 22.

24. An antibody to the novel protein of claim 23.

25. An antagonist to the expression of each gene belonging to the gene group of claim 19.

26. An antagonist to the activity of protein expressed by each gene belonging to the gene group of claim 19.

27. A group of oligonucleotides individually having the nucleotide sequence of SEQ ID NO:201 to NO:300 consecutive to the nucleotide sequence 5'-CATG-3'.