(12) PATENT
(19) AUSTRALIAN PATENT OFFICE

(11) Application No. AU 199655573 B2
(10) Patent No. 709733

(54) Title
Difference gel electrophoresis using matched multiple dyes

(51)[6] International Patent Classification(s)
G01N 027/447

(21) Application No: 199655573

(22) Application Date: 1996 .04 .19

(87) WIPO No: WO96/33406

(30) Priority Data

(31) Number	(32) Date	(33) Country
08/425480	1995 .04 .20	US

(43) Publication Date : 1996 .11 .07
(43) Publication Journal Date : 1997 .01 .02
(44) Accepted Journal Date : 1999 .09 .02

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(56) Related Art
US 5242796

OPI DATE 07/11/96 APPLN. ID 55573/96
AOJP DATE 02/01/97 PCT NUMBER PCT/US96/05435

AU9655573

(51) International Patent Classification 6 : G01N 27/447

A1

(11) International Publication Number: WO 96/33406

(43) International Publication Date: 24 October 1996 (24.10.96)

(21) International Application Number: PCT/US96/05435

(22) International Filing Date: 19 April 1996 (19.04.96)

(30) Priority Data:
08/425,480 20 April 1995 (20.04.95) US

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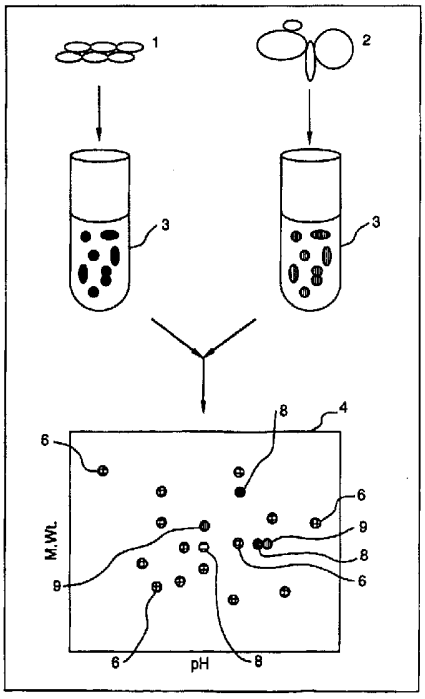
(81) Designated States: AU, CA, JP, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).

Published
With international search report.
Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.

(54) Title: DIFFERENCE GEL ELECTROPHORESIS USING MATCHED MULTIPLE DYES

(57) Abstract

A process and a kit are provided for detecting differences in two or more samples of protein. Protein extracts are prepared, for example, from each of a different group of cell samples (1, 2) to be compared. Each protein extract is labeled with a different one of a luminescent dye from a matched set of dyes. The matched dyes have generally the same ionic and pH characteristics but emit light at different wavelengths to exhibit a different color uponluminescence detection. The labeled protein extracts are mixed together and electrophoresed together. The gel (4) is observed to detect proteins unique to one sample or present in a greater ratio in one sample than in the other. Those unique or excess proteins will fluoresce the color of one of the dyes used. Proteins common to each sample migrate together and fluoresce the same.



TITLE

DIFFERENCE GEL ELECTROPHORESIS USING MATCHED MULTIPLE DYES

BACKGROUND OF THE INVENTION

Field of the Invention

The present invention relates to a process for detecting differences in the protein composition of cells and cell extracts, and more particularly, to a process utilizing a matched pair of labeling reagents for detecting such differences.

Background of the Invention

Researchers studying various aspects of cell biology use a variety of tools to detect and monitor differences in cell structure, function and development. An essential part of studying cells is studying the differences and similarities in the protein composition between the different cell types, stages of development and condition. Determining differences in the protein content between normal and cancerous cells or wild type and mutant cells, for example, can be a valuable source of information and a valuable diagnostic tool.

Mixtures of proteins can be separated into individual components according to differences in mass by electrophoresing in a polyacrylamide gel under denaturing conditions. One dimensional and two dimensional gel electrophoresis have become standard tools for studying proteins. One dimensional SDS (sodium dodecyl sulfate) electrophoresis through a cylindrical or slab gel reveals only the major proteins present in a sample tested. Two dimensional

polyacrylamide gel electrophoresis (2D PAGE), which separates proteins by isoelectric focusing, i.e., by charge, in one dimension and by size in the second dimension, is the more sensitive method of separation and will provide resolution of most of the proteins in a sample.

The proteins migrate in one- or two-dimensional gels as bands or spots, respectively. The separated proteins are visualized by a variety of methods; by staining with a protein specific dye, by protein mediated silver precipitation, autoradiographic detection of radioactively labeled protein, and by covalent attachment of fluorescent compounds. The latter method has been heretofore only able to be performed after the isoelectric focusing step of 2D PAGE. Immediately following the electrophoresis, the resulting gel patterns may be visualized by eye, photographically or by electronic image capture, for example, by using a cooled charge-coupled device (CCD).

To compare samples of proteins from different cells or different stages of cell development by conventional methods, each different sample is presently run on separate lanes of a one dimensional gel or separate two dimensional gels. Comparison is by visual examination or electronic imaging, for example, by computer-aided image analysis of digitized one or two dimensional gels.

Two dimensional electrophoresis is frequently used by researchers. O'Farrell, P.H., "High resolution two-dimensional electrophoresis of proteins", Journal of Biological Chemistry, 250:4007-4021 (1975), separated proteins according to their respective isoelectric points in the first dimension by the now well known technique of isoelectric focusing and by molecular weight in the second dimension by discontinuous SDS electrophoresis. Garrels, J.I., "Two-dimensional Gel Electrophoresis and Computer

Analysis of Proteins Synthesized By Clonal Cell Lines", Journal of Biological Chemistry, Vol. 254, No. 16, 7961-7977 (1979), used a two dimensional gel electrophoresis system to study the pattern of protein synthesis in nerve cells and glial cells. Garrels conducted a comparative analysis of data from multiple samples to correlate the presence of particular proteins with specific functions. Computerized scanning equipment was used to scan a section of the gel fluorogram, detect the spots and integrate their densities. The information was stored and plotted according to intensity in each of several different scans.

Urwin, V.E. and Jackson, P., "A multiple High-resolution Mini Two-dimensional Polyacrylamide Gel Electrophoresis System: Imaging Two-dimensional Gels Using A Cooled Charge-Coupled Device After Staining With Silver Or Labeling With Fluorophore", Analytical Biochemistry 195:30-37 (1991) describes a technique wherein several isoelectric focusing (IEF) gels were used to separate proteins by charge, then loaded onto a gradient slab gel such that the IEF gels were positioned end to end along the top of the slab gel. The gels were then electrophoresed. The resulting protein spots were visualized either by staining the second dimensional slab gel with silver or by fluorescent labeling following the isoelectric focusing step. Labeling must take place after the first electrophoresis, i.e., the isoelectric focusing because the presence of the fluorescein label on the protein changes the isoelectric point of the protein when subjected to electrophoresis. In addition, the label attaches to a sulfur on the protein forming an unstable bond which would tend to break during isoelectric focusing if the label is attached prior to the electrophoresis step. An article by Santaren, J. et al., "Identification of Drosophila Wing Imaginal Disc

Proteins by Two-Dimensional Gel Analysis and Microsequencing", Experimental Cell Research 206: 220-226 (1993), describes the use of high resolution two dimensional gel electrophoresis to identify proteins in *Drosophila melanogaster*. The dry gel was exposed to X-ray film for five days. The developed X-ray film is analyzed by a computer to determine the differences in the samples.

Two dimensional gel electrophoresis has been a powerful tool for resolving complex mixtures of proteins. The differences between the proteins, however, can be subtle. Imperfections in the gel can interfere with accurate observations. In order to minimize the imperfections, the gels provided in commercially available electrophoresis systems are prepared with exacting precision. Even with meticulous controls, no two gels are identical. The gels may differ one from the other in pH gradients or uniformity. In addition, the electrophoresis conditions from one run to the next may be different. Computer software has been developed for automated alignment of different gels. However, all of the software packages are based on linear expansion or contraction of one or both of the dimensions on two dimensional gels. The software cannot adjust for local distortions in the gels.

An object of the present invention is to eliminate problems associated with gel distortions of different samples associated with electrophoresis of cell samples. Other objects of the present invention will become apparent from the following description thereof.

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BRIEF SUMMARY OF THE INVENTION

According to one embodiment of the present invention there is provided a method of comparing multiple samples of cell extract containing a plurality of components comprising:

preparing at least two samples of cell extract from at least two different groups of cells;

exposing each said sample of said cell extract to a different one of a set of matched luminescent dyes to covalently bind the dye to the cell extract to label the cell extract, each dye within said set of dyes being capable of covalently binding to the cell extract and having generally the same ionic and pH characteristics as all other dyes within said set of dyes and emitting light at a wavelength sufficiently different from all other dyes within said set of dyes to present a different colored light;

mixing said samples of labeled cell extract to form a mixture;

electrophoresing said mixture to separate the components within the cell extract; and

detecting the difference in fluorescence intensity in the separated labeled components by luminescence detection.

According to another embodiment of the present invention there is provided a method for detecting differences in the protein components of at least two different samples, the components having binding sites thereon, the method comprising:

preparing extracts of each said sample;

adding a different luminescent dye to each separate sample of extract, each luminescent dye being capable of covalently binding to protein and having generally the same ionic and pH characteristics but differing from the other luminescent dyes

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added to the samples of extract in the wavelength at which each such dye emits light so that each dye fluoresces a different color;

incubating the extract with the dye added thereto for a period of time sufficient for forming a covalent bond between the dye and a plurality of the binding sites on the components of the extract;

then mixing the extract samples together to form a mixture;

electrophoresing the mixture on a single gel to separate the components of the extract by differences in charge and mass; and

detecting the presence of differences in the components of the mixture of cell extract by detecting differences in the color of fluorescence emitted from different regions of the gel.

According to another embodiment of the present invention there is provided a kit for use in detecting the presence of differences in the protein content of at least two different samples comprising:

a matched set of luminescent dyes, each dye within said set being capable of covalently binding to protein and having generally the same ionic and pH characteristics but differing from the other dyes within said set of dyes in the wavelength at which each such dye emits light so that each dye fluoresces a different color when excited.

Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integers or steps.

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DESCRIPTION OF THE DRAWINGS

FIG. 1 is a schematic diagram of the process of the present invention;

FIGS. 2a and 2b are images of proteins labeled with a preferred matched pair of labels of the present invention run on a single SDS polyacrylamide gel;

FIG. 3 is an image of a portion of a two dimensional gel loaded with two different samples of bacterial extract, one IPTG-induced and the other uninduced, labeled with a different one of the dyes of

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the matched pair of dyes according to the process of the present invention; and,

FIG. 4 is an image of a portion of a two dimensional gel loaded with two different samples of bacterial extract, one having exogenously added carbonic anhydrase and one without carbonic anhydrase, each labeled with a different one of the dyes of the matched pair of dyes according to the process of the present invention.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

The process of the present invention employs a matched set of dyes wherein each dye in the set is generally equal to the other dyes in ionic and pH characteristics, and chemical reactivity for covalent attachment to proteins, yet fluoresces at a different wavelength, thereby exhibiting a different color luminescence when viewed. The dyes are preferably roughly equal in molecular weight, but need not be. Each one of the dyes within the matched set of dyes is used to label proteins in a different one of a set of different samples of cell extract so that each cell extract sample is labeled with a different dye within the set of dyes. After labeling, the extracts are mixed and electrophoresed in the same gel, either by one or two dimensional electrophoresis.

With reference to the schematic diagram of Figure 1, a first cell extract is prepared by known techniques from a first group of cells (1), then labeled with the first dye of a matched pair of dyes, such as propyl Cyanine (3)-NHS. A second cell extract is prepared by known techniques from a second group of cells (2) then labeled with the second dye of the matched pair of dyes, such as methyl - Cyanine (5)-NHS. The structures and methods of preparation of the cyanine (3) and (5) dyes are described below. To label the cell extract mixture, the reactive form of the dye and the protein

extract are incubated in a suitable container, such as a test tube (3) for a period of time sufficient to allow for the formation of a covalent bond between the reactive form of the dye and potential attachment or binding sites on the proteins in the extract. The period of time is generally from 15 to 30 minutes, depending on the temperature. The temperature range is generally from about 0°C to 25°C. The reaction between the dye and the proteins may be quenched after a sufficient percentage of available binding sites on the protein molecule are covalently bound to the dye. Any suitable known quenching material may be used.

The first and second group of cells (1,2) can be any two sets of cells the protein content of which one wishes to compare or contrast. For example, the first group of cells can be the wild-type, or normal, cells, and the second group of cells can be mutant cells from the same species. Alternatively, the first group of cells can be normal cells and the second group can be cancerous cells from the same individual. Cells from the same individual at different stages of development or different phases of the cell cycle can be used also. The cells from a developing embryo, from the ventral furrow of *Drosophila melanogaster*, for example, can be harvested as the first group of cells and cells that develop adjacent to the ventral furrow cells can be harvested as the second group of cells. The differences in protein composition between cells of the same type from different species can also be the subject of study by the process of the present invention. In addition, the process of the present invention can be used to monitor how cells respond to a variety of stimuli or drugs. All of the events that might alter cell behavior as expressed through protein changes can be detected without the need and expense of high precision 2D PAGE systems. Those skilled in the art will recognize that the proteins for comparison may

also be derived from biological fluids, such as serum, urine, or spinal fluid.

The labeled samples are mixed and, as illustrated in FIG. 1, applied in measured aliquots to one gel (4), then preferably subjected to 2D PAGE. One dimensional SDS electrophoresis can be used instead of 2D PAGE. The procedures for running one dimensional and two dimensional electrophoresis are well known to those skilled in the art.

Proteins that the two cell groups have in common form coincident spots (6). The ratio of the fluorescent intensity between identical proteins from either group will be constant for the vast majority of proteins. Proteins that the two groups do not have in common (8, 9) will migrate independently. Thus, a protein that is unique or of different relative concentration to one group will have a different ratio of fluorescence intensity from the majority of protein spots, and will produce a color specific for one or the other of the protein extracts, depending on the label used. For example, the proteins that are in the first sample may be labeled red, while the second group is labeled blue. Under conditions where exactly equal amounts of protein from each group is mixed together and run on the same gel the ratio of fluorescence intensity will be one for the majority of proteins. Those proteins that are distinct to one or the other group will have a fluorescence intensity ratio less than or greater than one, depending on the order or ratioing.

The gel can be analyzed by a two wavelength fluorescence scanner, by a fluorescent microscope or by any known means for detecting fluorescence. Gel analysis can be completely automated by means of computer aided identification of protein differences. Using an electronic detection system such as a laser scanning system with a photo multiplier tube or a

charged-coupled device (CCD) camera and a white light source, two electronic images are made of the wet gel using different known filter sets to accommodate the different spectral characteristics of the labels. One image views fluorescence of the first dye using a first filter appropriate to filter out all light except that emitted at the wavelength of the first dye and the other image views fluorescence of the second dye using a second filter, appropriate to filter out all light except that emitted at the wavelength of the second dye. Exposure is about 5 to 500 seconds. The differences in the samples can be identified, either during electrophoresis or in less than 1/2 hour following electrophoresis. Several software packages are commercially available which will either subtract the first image from the second to identify spots that are different, or, alternatively, the images may be divided to leave only the spots not common to both images. In subtracting the images, like spots will cancel each other, leaving only those that are different. In ratio analysis, like spots will provide a value of one. Differences will result in values greater than one less than one.

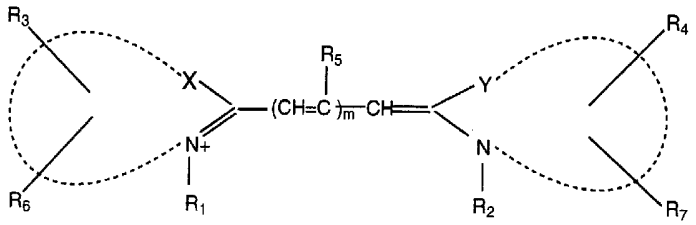
In conventional analysis, a control is run with known proteins for the cell type being studied. The known spots on the sample gel have to be identified and marked, compared to the control and the second gel to determine differences between the two gels. In the present invention, there is only one gel so no marking is necessary. In addition, the software used on conventional processes for alignment of different gels prior to comparing and contrasting protein differences does not correct for local distortions and inconsistencies between two or more gels. The process of the present invention eliminates the need for such correction because the extracts for all samples to be

tested are mixed and run on the same gel. Any gel distortions are experienced equally by each sample.

Selection and synthesis of the matched set of dyes is important. In the process of the present invention, the fluorescent dyes are covalently coupled to proteins, preferably via lysine residues of the proteins, but coupling may also be to sulfhydryl or carboxylic acid groups in the proteins. Regulation of the pH of proteins to force attachment of labels at one amino acid residue to the exclusion of other amino acids is a well known technique, as set forth in R. Baker, Organic Chemistry of Biological Components, (Prentice Hall, pub. 1971). For analysis of proteins, a plurality of attachment sites are labeled. The optimum percentage of attachment sites labeled will depend on the dyes chosen. When the preferred dyes specifically discussed hereinbelow are used, preferably no more than 2% of the attachment sites and more preferably, slightly less than 1%, are labeled, to avoid rendering the protein insoluble. Thus, where a typical protein is composed of about 7% lysines, there will be less than one modified amino acid per one thousand. A typical protein is composed of about 450 amino acids. When lysine is the attachment site, the covalent linkage destroys the positive charge of the primary amine of the lysine. Because isoelectric focusing depends on charge, it is important to compensate for the charge loss. A basic residue should remain basic. Changing the pKa of one residue per protein by as much as 3 can be tolerated, provided the basicity or acidity of the modified residue, as the case may be, is not altered. Dyes like rhodamine and fluorescein are not suitable because of the difference in charge.

The first group of dyes evaluated were the fluorescent cyanine dyes described in Mujumdar, R.B. et al., "Cyanine dye labeling reagents containing

isothiocyanate groups", Cytometry 10:11-19 (1989) and Waggoner et al., U.S. Patent No. 5,268,486 entitled "Method for labeling and detecting materials employing arylsulfonate cyanine dyes" issued in 1993 and incorporated herein by reference. The cyanine dyes have the following general structure,

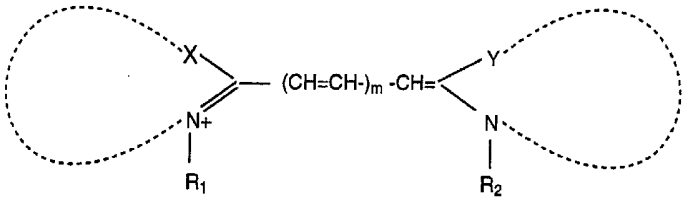


where X and Y can be O, S or $(CH_3)_2$-C, m is an integer from 1 to 3 and at least one of R_1, R_2, R_3, R_4, R_5, R_6 or R_7 is a reactive group which reacts with amino, hydroxy or sulfhydryl nucleophiles. The dotted lines represent the carbon atoms necessary for the formation of the cyanine dye, preferably for the carbon atoms forming three fused rings having 5 to 6 atoms in each ring. R_3, R_4, R_6 and R_7 are attached to the rings. The reactive moiety can be any known reactive group. Reactive groups that may be attached directly or indirectly to the chromophore to form R_1, R_2, R_3, R_4, R_5, R_6 or R_7 groups may include reactive moieties such as groups containing isothiocyanate, isocyanate, monochlorotriazine, dichlorotriazine, mono- or di-halogen substituted pyridine, mono- or di-halogen substituted diazine, maleimide, aziridine, sulfonyl halide, acid halide, hydroxysuccinimide ester, hydroxysulfosuccinimide ester, imido ester, hydrazine, azidonitrophenyl, azide, 3-(2-pyridyl dithio)-proprionamide, glyoxal and aldehyde.

The cyanine dyes described in the Waggoner et al. patent were the fluorophors of choice because of their intrinsic positive charge. The cyanines attach to the protein via the activated ester of hexanoic acid. While the coupling destroys the charge of the lysine side chain, the intrinsic charge in the dye compensates. It in effect moves the charge away from the protein molecule but maintains the same overall charge within the sample to be electrophoresed. In the cyanine dye molecule, two functionalized indole rings are connected via a polyene linker. The spectral characteristics of cyanine dyes can be easily modulated by simply changing the length of the linker between the indole rings of the dye. A longer or shorter linker length will result in fluorescence at different wavelengths and thus, different colors. However, changing the length of the linker changes the molecular mass of the dye. Since electrophoresis depends also on the mass of the proteins, the effect of the dye on a protein's mass can also be of concern. Because the proteins are labeled before electrophoresing, the mass of the dye attached to the protein must not significantly alter the relative differences in the molecular weights of the various proteins in the extracts. Molecular weight is not critical, however, because only a relatively small number of sites on the protein are labeled. As indicated above, preferably less than 1%, up to about 2% of the possible attachment sites on the proteins are labeled. If more are labeled, maintaining generally equal molecular weights for the dyes within the set of matched dyes becomes a greater concern.

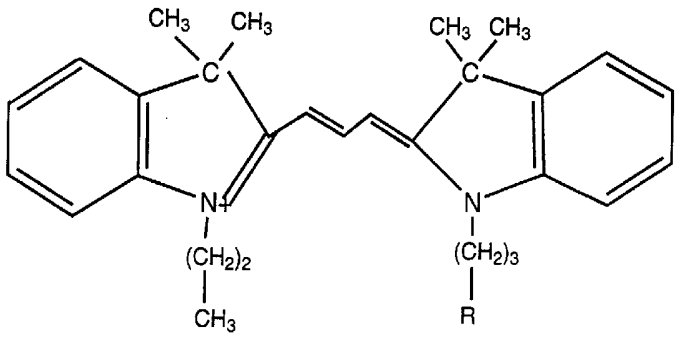
The difference in molecular weight caused by changing the linker length in the fluorescent cyanine dyes can be compensated for by modulating the size of an aliphatic chain R_1 or R_2, attached to one of the dye's indole rings. One of R_1 or R_2 must be a reactive

group. These design constraints led to the modification of the cyanines and the development of a dye of the general formula

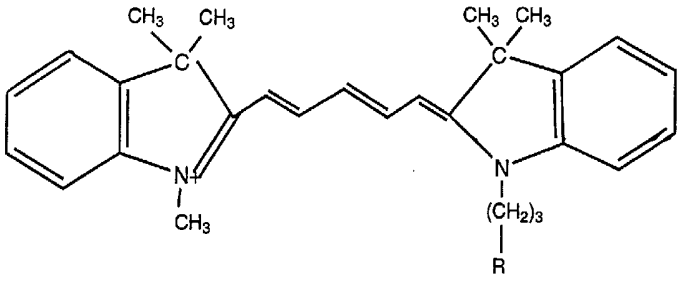


wherein X and Y equal S, O, or CH_3-C-CH_3, m is an integer from 1 to 3 and either R_1 or R_2 is a reactive group capable of covalently binding to the protein in the cell extract, such as the reactive groups described above for the unmodified cyanine dyes. The dotted lines represent 1, 2 or 3 fused rings having 5 or 6 carbon atoms in each ring. Each side should balance the other side.

An example of a matched pair of dyes developed according to the general formula follows:



(Propyl Cyanine-NHS) which fluoresces red and,



(Methyl Cyanine 5-NHS) which fluoresces far red in the spectrum wherein R is a reactive group. As stated above, O or S or a combination thereof can be placed in the X and Y positions in place of $(CH_3)_2C$-.

The cyanine dyes are one choice for the matched set of dyes of the present invention. Other dye compounds may be used in place of the cyanines, such as dipyrromethene boron difluoride dyes, the derivatized 4,4-difluoro-4-bora-3a,4a,-diaza-S-indacene dyes, described in U.S. Patent No. 4,774,339 to Haugland et al. and incorporated herein by reference, which are sold by Molecular Probes, Inc. under the trademark BODIPY®. The BODIPY® dyes, which have no net charge, are covalently linked to lysine side chains using an activated n-hydroxysuccinimidyl ester which forms an amide bond. The result is the loss of the lysine positive charge. Therefore, a positively charged linker group is used in the matched dyes of the invention to replace the lost primary amine with the linker's tertiary amine. The procedures for making BODIPY® dyes are described in U.S. Patent No. 4,774,339. Addition of the positively charged linker is by techniques well known to those skilled in the

art. A linker can be designed with three functional groups; (1) to react with the BODIPY®-NHS ester, (2) to carry the desired charge, and (3) to be activated so that the BODIPY®-linker construct will react with specific amino acid residues of the proteins in the extract.

The major considerations for the matched set of dyes are the maintenance of charge and distinct and different spectral characteristics. Any neutral dyes with a positive linker or any positively charged dyes, preferably each having a +1 charge, that otherwise satisfy the requirements described herein can serve as the dyes in the matched set of dyes of the present invention. Roughly equal molecular weight in the samples of labeled protein is desirable, but as explained above, not critical. The intrinsic positive charge of cyanine dyes is advantageously used in the preferred embodiment to replace the positive charge of lysine. The pK_a of cyanines and lysine are rather different; however, conditions were selected for dye:protein ratio to be less than one. This low level of labeling ensures that there will be negligible changes in the protein's migration on two-dimensional electrophoresis gels. Dyes may be used which match the pK_a of lysine more closely. Alternately, dyes that modify other amino acid residues may be used, provided the amino acid's ionic characteristics are preserved by the modification. Instead of a lysine, the attachment site on the protein may be a sulfhydryl or carboxylic group. When a sulfhydryl group is the attachment site on the protein, the corresponding attachment site on the dye is an iodoalkyl group. When a carboxylic acid group is the attachment site on the protein, the corresponding attachment site on the dye is a chloroketone or a carbodiimide.

It is anticipated that the method of the present invention also can be used to detect the presence of

different nucleic acids in different samples. The charge of nucleic acids is very negative. The addition of the dye does not therefore alter the overall charge in nucleic acids so the choice of the matched set of dyes does not have to compensate for charge loss when nucleic acid analysis is contemplated. To facilitate attachment of the dye, nucleic acids can be modified to have a free amino acid coming from the nucleic acid nucleus by techniques known to those skilled in the art. A lysine would be suitable in this instance also.

EXAMPLE 1

Synthesis of the dyes (Methyl Cyanine 5 and Propyl Cyanine 3):

1. Synthesis of indole derivatives (common to both dyes):

4.8 g (30 mmoles) of 2,3,3-trimethyl-(3H)-indole and 35 mmoles of the desired bromoalkyl reagent (6-bromohexanoic acid or 1-bromopropane) in 40 ml of 1,2-dichlorobenzene were heated to 110°C under nitrogen gas and stirred overnight with refluxing. The product (acid indole, methyl indole, or propyl indole) precipitated as an orangish gum. The supernatant was decanted and the gum was washed several times with ethyl ether. This intermediate was used as is.

2. Cyanine (3) (Cy-3) intermediate:

1.5 g (7.5 mmoles) of propyl indole was added to 1.6 g (7.6 mmoles) of N-N' diphenyl formamidine in 20 ml glacial acetic acid and was refluxed for 4 hrs. The solvent was removed under vacuum leaving a deep orange syrup. This intermediate was used as is.

2a. Cyanine (5) (Cy5) intermediate:

The synthesis of the Cy-5 intermediate is the same as the synthesis of the Cy-3 intermediate in step 2 of the dye synthesis except that 2-methylene-1,3,3-trimethylindoline was used instead of propyl indole and the linker was malonaldehyde dianil. The gummy, bluish intermediate was washed twice with ethyl ether.

3. Cy-3:

2.5 ml of triethylamine and 1.8 ml of anhydrous Ac_2O were added to the intermediate from step 2., and the mixture was boiled for 5 minutes. 1.70 g (5.0 mmoles) of acid indole was added and the mixture was refluxed for two hours. The solvent was removed under vacuum and the products were dissolved in 10 ml of EtOH.

3a. Cy-5:

The preparation of Cy-5 is the same as that of Cy-3 except that the intermediate from step 2a. was used instead of the intermediate from step 2.

4. Purification of the products from steps 3. and 3a.:

Methyl Cy-5 and propyl Cy-3 were separated from contaminating side products by running flash chromatography with a silica gel solid phase and 40% MeOH in dichloromethane as the mobile phase.

5. Activation of carboxyl groups:

The carboxylic acid moiety of each dye was converted into an N-hydroxysuccinimidyl ester by dissolving a quantity of purified material in 5 ml of dry dimethylformamidine (DMF). 1.5 equivalents of N-N' disuccinimidyl carbonate (DSC) was added with 0.1 ml dry pyridine/100mg dye. The reaction was refluxed at 60°C for 90 minutes under nitrogen.

EXAMPLE 2

Protein Labeling:

1. Bacterial culture:

Initial experiments were performed on E. coli that expressed the chimeric GAL4VP16 protein under the control of the lac promoter as described in Chasman, D.I. et al., "Activation of yeast polymerase II transcription by Herpesvirus VP16 and GAL4 derivatives in vitro", Molecular Cell Biology 9:4746-4749 (1989). Two cultures of bacteria were grown to an OD_{600} of 0.7 at 37°C. in 125 ml of standard LB medium containing 50 µg/ml ampicillin. Isophenylthiogalactopyranoside

(IPTG), a non-hydrolyzable analog of lactose, was added to one culture at a final concentration of 1 mM. Both cultures were incubated for an additional 2.5 hours.

2. Protein isolation for two-dimensional gel electrophoresis:

Isolation of protein was as follows. The bacteria was isolated by centrifugation. Each bacterial pellet was washed with sonication buffer containing 5 mM Hepes KOH pH 8.4, 5 mM $Mg(OA_c)2$. The pellet was resuspended in sonication buffer containing 50 µg/ml RNase to a final volume of 100 µl. This was then sonicated in ice until the solution was clear, usually several minutes. DNase was added to 50 µg/ml and the sample was incubated for 30 min at 0°C. Solid urea and CHAPS were added to a final concentration of 8 M and 5% respectively. The sample was taken off the ice and 1 volume of lysis buffer added. The sample was either labeled immediately or stored at -80°C.

3. Protein labeling:

Propyl Cy-3-NHS was added to the first sample and Methyl Cy-5-NHS was added to the second sample of cell extract at a concentration of 2 nmole of dye/50 µg of protein. The dye stock solution was typically 2 mM in dimethyl formamide. The reaction was incubated at 0°C for 30 minutes. Incubation times may vary from about 15 to about 30 minutes, depending on the temperature and the type of cells being studied. Incubation can be for 15 minutes when the temperature is about 25°C. The temperature should not be above that which will cause the proteins to be degraded. The labeled sample was immediately subjected to isoelectric focusing or stored at -80°C.

4. Protein isolation and labeling for SDS-gel electrophoresis:

Bacteria were grown and isolated by sonication as in step 2. of the protein labeling procedure, except RNase or DNase was not added. The cell extract was directly

labeled as in step 3 of the protein labeling procedure. SDS, glycerol, Tris HCl pH 6.8, and bromophenol blue were added to bring the final concentrations to 1%, 10%, 64 mM, and 5 µg/ml, respectively. The sample was then placed in a boiling water bath for 2 minutes and then subjected to electrophoresis.

5. Determination of dye to protein ratio:

In order to prevent solubility problems with labeled proteins, conditions were chosen to only label 1-2% of the lysines in the cell extract. This is based on the assumption that 7% of an average protein's amino acids are lysine. The first step in determining the dye to protein ratio was the removal of free dye by adsorption to SM-2 beads (Bio-Rad). The protein concentration was determined by $OD_{260/280}$. The dye content was determined by OD548 and OD650 for Propyl Cy-3 and Methyl Cy-5, respectively (ϵ=100,000 for both dyes).

EXAMPLE 3

Gel Electrophoresis:

1. Two-dimensional electrophoresis:

High resolution two-dimensional gel electrophoresis was carried out by well known techniques.

2. SDS polyacrylamide gel electrophoresis:

SDS polyacrylamide gel electrophoresis was carried out by known techniques.

EXAMPLE 4

Fluorescence Gel Imaging:

At the end of electrophoresis, the gels were soaked in a solution of 25% methanol and 7% acetic acid. The fluorescently labeled proteins in the gel were imaged in the following manner. Gels were placed on a surface of anodized aluminum and irradiated at an incident angle of 60° with a 300 W halogen lamp housed in a slide projector. The light exiting the projector was passed through 1' diameter bandpass filters (Chroma Technologies, Brattleboro VT), 545 ± 10 nm and 635 ± 15 nm for Cy-3 and Cy-5, respectively. The images were collected on a cooled, CCD camera (Photometrics Inc., Tucson AZ) fitted with a 50 mm lens (Nikon) and a double bandpass emission filter (Chroma Technologies, Brattleboro VT), 587.5 ± 17.5 nm and 695 ± 30 nm for Cy-3 and Cy-5, respectively. The CCD camera was controlled by a Macintosh II si computer running Photometrics camera controller software. Image integration time ranged from tenths of seconds to several minutes. The excitation filters were housed in a filter wheel attached to the projector. Two successive images were recorded with irradiation from the two filters without moving the gel.

EXAMPLE 5

Image processing:

The image files were transferred to a Personal Iris 4D/35 (Silicon Graphics Inc., Mountain View CA). The image files were then processed using the

DeltaVision™ software (Applied Precision, Mercer Island WA). The two schemes were used to determine the differences between the differently labeled samples on the gel:

1. Subtraction:

Each image can be considered as a grid-like array of pixel intensities. These arrays of values can be manipulated by a number of arithmetic operations. Here one image was subtracted from the other. Because the two samples loaded onto the gel were not perfectly balanced for overall fluorescence, one image was multiplied by a balancing constant. This factor was determined arbitrarily so that the number of differences between the samples were kept small.

2. Ratio Imaging:

Here one image was divided by the other. Before this operation was performed the images were first normalized to a common intensity range. This was done by setting the minimum and maximum pixel values of each image to zero and an arbitrarily large value, 4095, the maximum possible output value of the CCD camera employed. Intermediate pixel values were scaled linearly between these values. One image was then divided by the other. A balancing factor was also used here to keep the mean quotient at one. Regions of difference were those with a quotient greater than one.

EXAMPLE 6

1. Difference SDS gel electrophoresis of induced GAL4VP16 expression in bacteria:

Figure 2 shows images of Propyl Cy-3 and Methyl Cy-5 labeled proteins run on a single SDS polyacrylamide gel.

Lanes 1-3 show Cy-3 labeled protein. The samples loaded in there lanes were:

Lane 1. Propyl Cy-3 labeled IPTG-induced bacterial extract.

Lane 2. Propyl Cy-3 labeled IPTG-induced bacterial extract plus Methyl Cy-5 labeled uninduced extract.

Lane 3. Propyl Cy-3 labeled purified GAL4VP16 protein.

Lanes 4-6 show Cy-5 labeled protein. The samples loaded in there lanes were:

Lane 4. Propyl Cy-3 labeled IPTG-induced bacterial extract.

Lane 5. Propyl Cy-3 labeled IPTG-induced bacterial extract plus Methyl Cy-5 labeled uninduced extract.

Lane 6 Propyl Cy-3 labeled purified GAL4VP16 protein.

Only Lane 5 showed Cy-5 fluorescence.

Lanes 7 and 8 show the subtracted product of Lane 2 - Lane 5 and Lane 3 - Lane 6, respectively. The arrows point to the position of GAL4VP16 as confirmed by the position of the purified GAL4VP16 band in lane 8. The identity of the upper bands is not known. However, there are several proteins that are known to be induced by IPTG, including β-galactosidase.

Lanes 9-11 show Cy-5 labeled protein. The samples loaded in these lanes were:

Lane 9. Methyl Cy-5 labeled IPTG-induced bacterial extract.

Lane 10. Methyl Cy-5 labeled IPTG-induced bacterial extract plus Propyl Cy-3 labeled uninduced extract.

Lane 11. Methyl Cy-5 labeled purified GAL4VP16 protein.

Lanes 12-15 show Cy-5 labeled protein. The samples loaded in there lanes were:

Lane 12. Methyl Cy-5 labeled IPTG-induced bacterial extract.

Lane 13. Methyl Cy-5 labeled IPTG-induced bacterial extract plus Propyl Cy-3 labeled uninduced extract.

Lane 14. Methyl Cy-5 labeled purified GAL4VP16 protein.

Only Lanes 12-15 all showed some Cy-3 fluorescence. This is due to slight crossover between the bandpass filters. This causes Cy-5 labeled material to appear when excited by Cy-3 light. The converse is not seen. Cy-3 material is not visualized by Cy-5 excitation light. There are two ways to eliminate the crossover effects: design better bandpass filters or computationally remove the Cy-5 contribution to the Cy-3 image by knowing the crossover constant.

Lanes 15 and 16 show the subtracted product of Lane 2 - Lane 5 and Lane 3 - Lane 6, respectively. The arrows point to the position of GAL4VP16 as confirmed by the position of the purified GAL4VP16 band in Lane 8. The identity of the upper bands is not known. However, there are several proteins that are known to be induced by IPTG, including β-galactosidase.

2. Difference two-dimensional gel electrophoresis of induced GAL4VP16 expression in bacteria:

Figure 3 shows images of a portion of a two-dimension gel loaded with Propyl Cy-3 labeled IPTG-induced bacterial extract plus Methyl Cy-5 labeled uninduced extract.

Panel A. Images taken with Cy-3 excitation light showing the IPTG-induced proteins.

Panel B. Images taken with Cy-5 excitation light showing the uninduced proteins.

Panel C. Ratio of the Cy-3 image divided by the Cy-5 image.

Panel D. Overlay of the image in Panel C, colored red, and placed on top of the image from Panel B, colored blue.

3. Difference two-dimensional gel electrophoresis of bacteria extract with exogenously added protein: Figure 4 shows images of a portion of a two-dimension gel loaded with Propyl Cy-3 labeled bacterial extract that had exogenously added carbonic anhydrase plus Methyl Cy-5 labeled extract without the added carbonic anhydrase.

Panel A. Image taken with Cy-3 excitation light showing the bacterial proteins plus carbonic anhydrase.

Panel B. Images taken with Cy-5 excitation light showing the bacterial proteins alone.

Panel C. Ratio of the Cy-3 image divided by the Cy-5 image.

Panel D. Overlay of the image in Panel C, colored red, and placed on top of the image from Panel B, colored blue.

The process of the present invention provides a simple and inexpensive way to analyze the differences in protein content of different cells. The process eliminates problems which can occur using two separate gels which must be separately electrophoresed. The matched dyes used to label the different cell extracts allow simultaneous electrophoresis of two or more different samples of cell extract in a single gel. While the invention has been described with reference to two samples of cell extract and a matched pair of dyes, those skilled in the art will appreciate that more than two samples may be simultaneously tested using an equal number of matched dyes. As long as the spectral characteristics of the dyes can be manipulated to provide fluorescence at a number of different wavelengths resulting in visually distinct images and the pH and ionic characteristics of the dyes can be generally equalized to compensate for changes made to the protein by virtue of covalent bonding to the dye, multiple dyes can be used.

What we claim is:

1. A method of comparing multiple samples of cell extract containing a plurality of components comprising:

preparing at least two samples of cell extract from at least two different groups of cells;

exposing each said sample of said cell extract to a different one of a set of matched luminescent dyes to covalently bind the dye to the cell extract to label the cell extract, each dye within said set of dyes being capable of covalently binding to the cell extract and having generally the same ionic and pH characteristics as all other dyes within said set of dyes and emitting light at a wavelength sufficiently different from all other dyes within said set of dyes to present a different colored light;

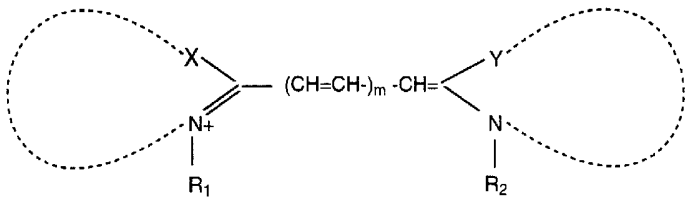
mixing said samples of labeled cell extract to form a mixture;

electrophoresing said mixture to separate the components within the cell extract; and

detecting the difference in fluorescence intensity in the separated labeled components by luminescence detection.

2. The method of claim 1 wherein said set of matched luminescent dyes carry a +1 charge.

3. The method of claim 1 wherein said set of matched luminescent dyes are cyanine dyes having the following structure:



wherein the dotted lines each represent carbon atoms necessary for the formation of said dye, X and Y are selected from the group consisting of S, O or CH_3-CH-CH_3, m is an integer from 1 to 3, one of R_1 and R_2 is a reactive group and the other is an alkyl.

4. The method of claim 1 wherein said reactive group is selected from the group consisting of an isothiocyanate, $(CH_2)_4COOH$ and $(CH_2)_4CON$-hydroxysuccinimidyl ester.

5. The method of claim 1 wherein said set of matched luminescent dyes are neutral dyes bound to the cell extract by a positively charged linker group.

6. The method of claim 1 wherein said set of matched luminescent dyes are derivatives of dipyrromethene boron difluoride dyes having positively charged linker groups to bind the dye to the cell extract.

7. The method of claim 1 wherein said cell extract comprises proteins and said dyes covalently bind to lysines in the proteins.

8. The method of claim 1 wherein said cell extract comprises proteins and said dyes covalently bind to sulfhydryl groups on the proteins.

9. The method of claim 1 wherein said cell extract comprises proteins and said dyes covalently bind to carboxylic acid groups on the proteins.

10. The method of claim 1 further comprising, prior to mixing said samples, the step of quenching the reaction which binds the dyes to the binding sites on the cell extract to prevent further binding.

11. A method for detecting differences in the protein components of at least two different samples, the components having binding sites thereon, the method comprising:

preparing extracts of each said sample;

adding a different luminescent dye to each separate sample of extract, each luminescent dye being

capable of covalently binding to protein and having generally the same ionic and pH characteristics but differing from the other luminescent dyes added to the samples of extract in the wavelength at which each such dye emits light so that each dye fluoresces a different color;

incubating the extract with the dye added thereto for a period of time sufficient for forming a covalent bond between the dye and a plurality of the binding sites on the components of the extract;

then mixing the extract samples together to form a mixture;

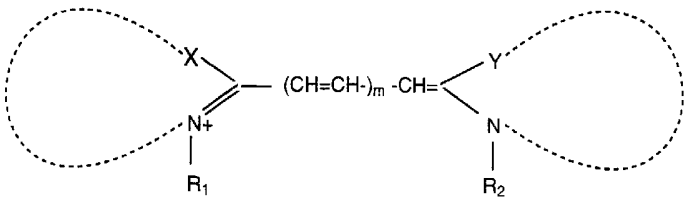
electrophoresing the mixture on a single gel to separate the components of the extract by differences in charge and mass; and

detecting the presence of differences in the components of the mixture of cell extract by detecting differences in the color of fluorescence emitted from different regions of the gel.

12. The method of claim 11 wherein the step of detecting differences in emitted color is by fluorescent microscopy.

13. The method of claim 11 wherein the step of detecting differences in emitted color is by electronic imaging.

14. The method of claim 11 wherein said set of matched luminescent dyes are cyanine dyes having the following structure:



wherein the dotted lines each represent carbon atoms necessary for the formation of said dye, X and Y are selected from the group consisting of O, S and CH_3-C-CH_3, m is an integer from 1 to 3, one of R_1 and R_2 is a reactive group and the other is an alkyl.

15. The method of claim 14 wherein said reactive group is selected from the group consisting of and isothiocyanate, $(CH_2)_4COOH$ and $(CH_2)_4CON$-hydroxysuccinimidyl ester.

16. The method of claim 11 wherein said set of matched luminescent dyes are derivatives of dipyrromethene boron difluoride dyes having positively charged linker groups to bind the dye to the extract.

17. The method of claim 11 wherein the binding sites are selected from the group consisting of lysine, carboxylic acid and sulfhydryl groups.

18. The method of claim 11 wherein the binding sites are one of a moiety selected from the group consisting of lysine, carboxylic acid and sulfhydryl groups.

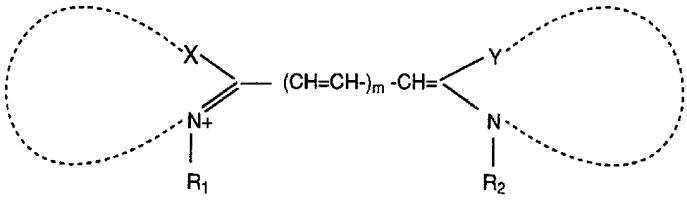
19. A kit for use in detecting the presence of differences in the protein content of at least two different samples comprising:

a matched set of luminescent dyes, each dye within said set being capable of covalently binding to protein and having generally the same ionic and pH characteristics but differing from the other dyes within said set of dyes in the wavelength at which each such dye emits light so that each dye fluoresces a different color when excited.

20. The kit recited in claim 19 further comprising at least one electrophoresis gel.

21. The kit recited in claim 19 further comprising materials to quench the labeling reaction between the dyes and protein in samples tested.

22. The kit recited in claim 19 wherein the luminescent dyes are cyanine dyes having the following structure:



wherein the dotted lines each represent carbon atoms necessary for the formation of one said dye, X and Y are selected from the group consisting of S, O, and CH_3-CH-CH_3, m is an integer from 1 to 3, one of R_1 and R_2 is a reactive group and the other is an alkyl, and wherein m differs for different dyes within said set of dyes and, optionally, the length of the alkyl differs for different dyes within said set of dyes to generally match the overall molecular weights of the different dyes within said set of dyes.

23. The kit recited in claim 19 wherein the luminescent dyes are derivatives of dipyrromethene boron difluoride dyes having positively charged linker groups to bind the dye to the extract.

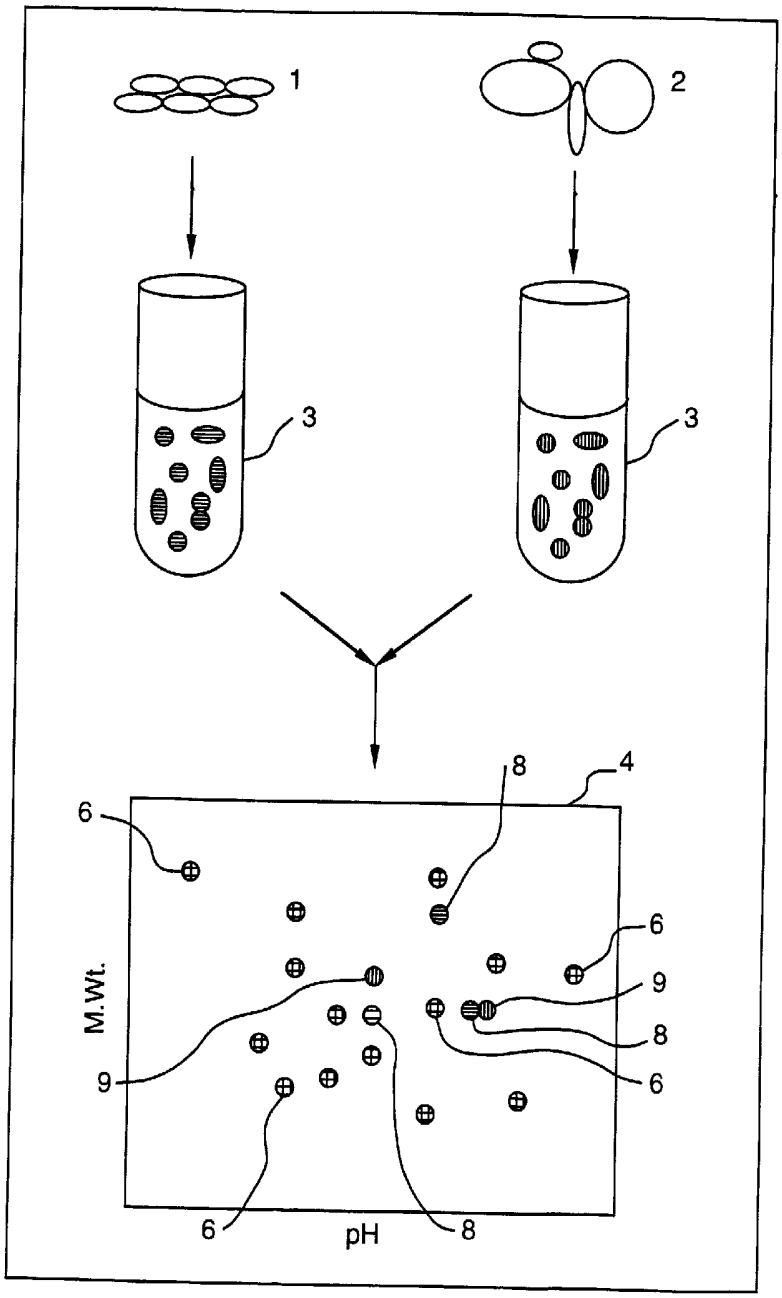


FIG. 1

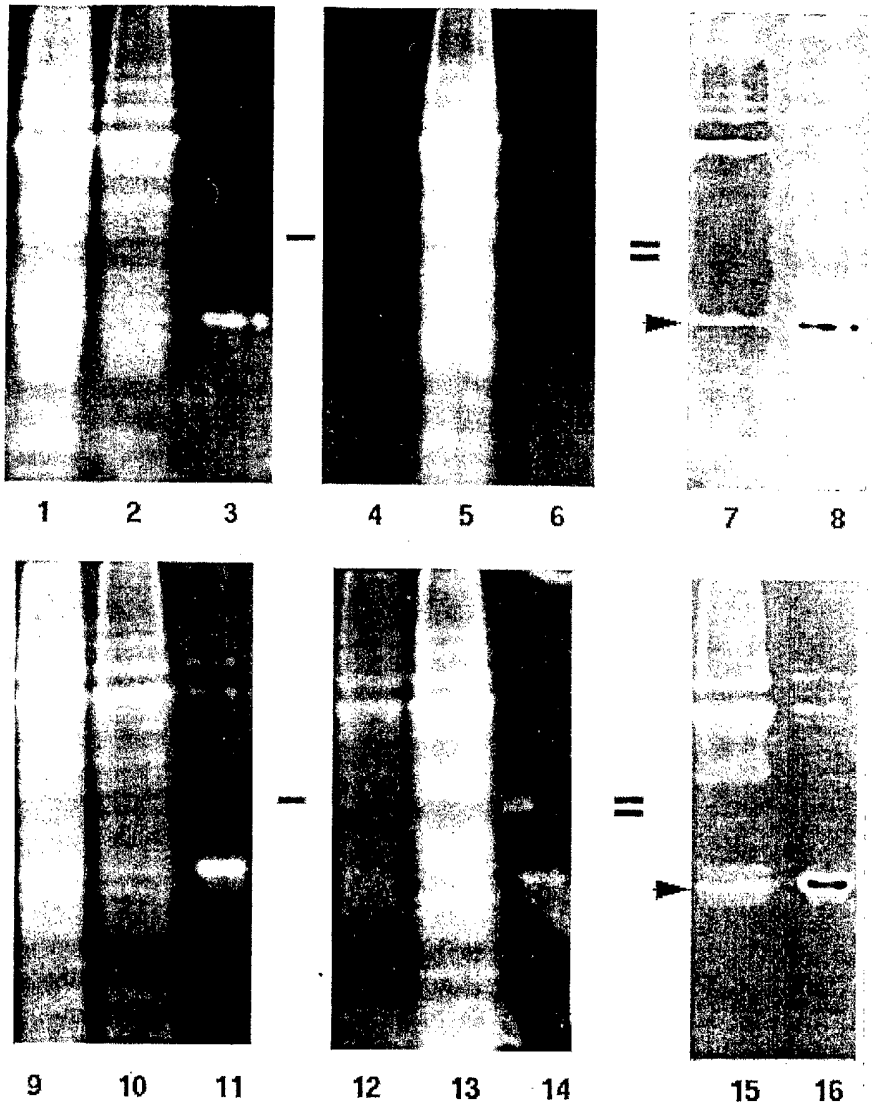


FIG. 2

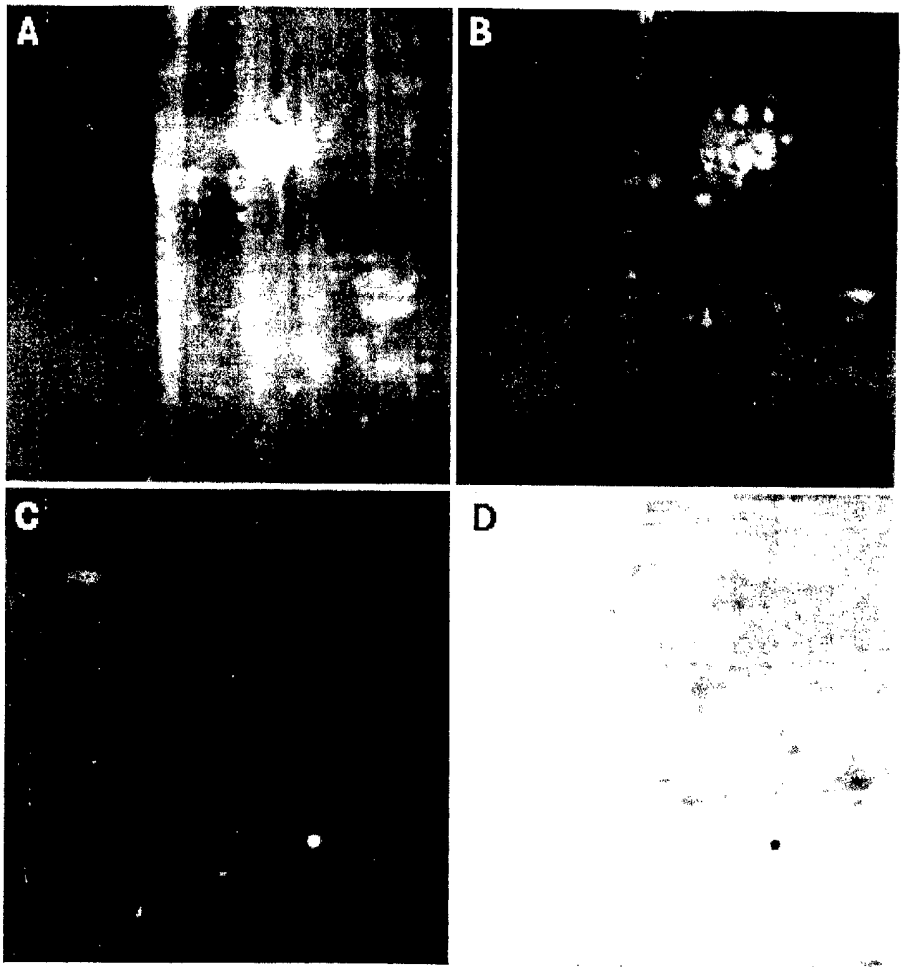


FIG. 3

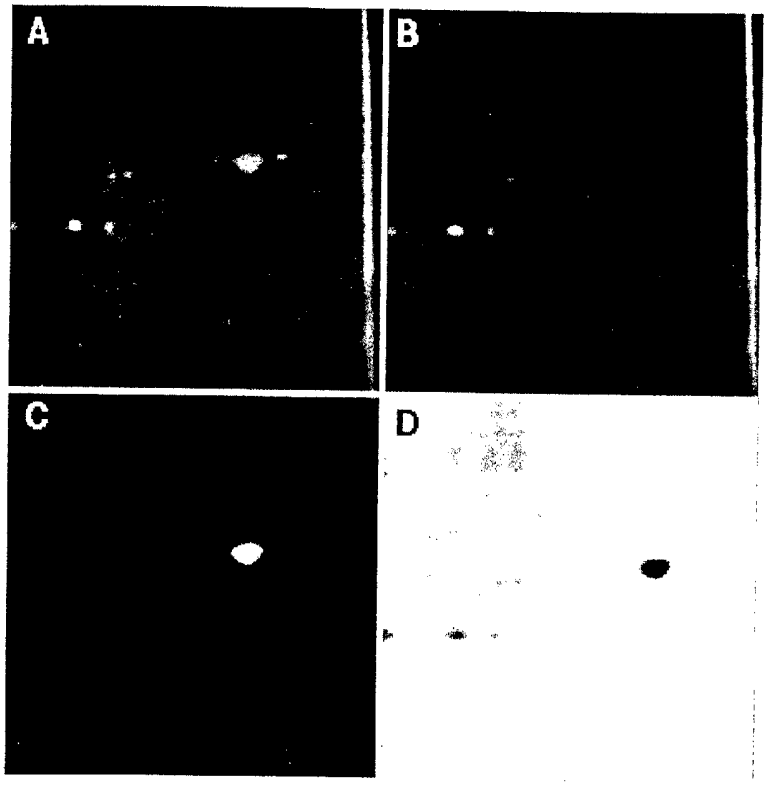


FIG. 4