plans and instruments, contact: Ms. Diane Miller, Scientific Communications Branch, Office of Scientific Affairs, NIAAA, NIH, Willco Building, Suite 409, 6000 Executive Boulevard, Rockville, MD, 20892–7003 or e-mail your request, including your address to: dmiller@willco.niaaa.nih.gov. Ms. Miller can be contacted by telephone at 301–443–3860.

Comments Due Date

Comments regarding this information collection are best assured of having their full effect if received on or before January 25, 2001.

Dated: December 15, 2000.

Stephen Long,

Executive Officer, NIAAA.

[FR Doc. 00–32817 Filed 12–22–00; 8:45 am]

BILLING CODE 4140–01–M

DEPARTMENT OF HEALTH AND HUMAN SERVICES

National Institutes of Health

Government-Owned Inventions; Availability for Licensing

AGENCY: National Institutes of Health, Public Health Service, DHHS.

ACTION: Notice.

SUMMARY: The inventions listed below are owned by agencies of the U.S. Government and are available for licensing in the U.S. in accordance with 35 U.S.C. 207 to achieve expeditious commercialization of results of federally-funded research and development. Foreign patent applications are filed on selected inventions to extend market coverage for companies and may also be available for licensing.

ADDRESSES: Licensing information and copies of the U.S. patent applications listed below may be obtained by writing to the indicated licensing contact at the Office of Technology Transfer, National Institutes of Health, 6011 Executive Boulevard, Suite 325, Rockville, Maryland 20852–3804; telephone: 301/496–7057; fax: 301/402–0220. A signed Confidential Disclosure Agreement will be required to receive copies of the patent applications.

Dombrock Blood Typing

Jeffery L. Miller, Alexander Gubin, Marion E. Reid (NIDDK)

[DHHS Reference No. E–185–00/0 filed 23 Sep 2000]

Licensing Contact: John Rambosek; 301/496–7056 ext. 270; email: rambosej@od.nih.gov.

The Dombrock blood group was first discovered in 1965. It is comprised of five alleles: two common alleles, Do(a+) and Do(b+), and three very rare alleles Gy(a), Hy, and Jo(a) which are essentially different null alleles. The Dombrock blood group system has been estimated to be the fifth most useful blood group marker in Caucasians. Blood typing for this blood group is hard to do, since there is a limited amount of antibodies, and the antigens are tricky to work with. This invention discloses the gene and polymorphisms of that gene that result in the Dombrock blood group antigenicity. Thus this invention provides for the first time a method for reliably typing the human blood supply for the Dombrock blood group antigenicity. The genetic information may also be used to generate antigen-specific antibodies for blood typing. The primary use for the technology is to improve blood typing practices through molecular means and thereby prevent clinical problems (transfusion reactions, etc.) associated with improperly mismatched blood.

Microbial Identification Databases

Jon G. Wilkes, Fatemeh Rafii, Katherine L. Glover, Manuel Holcomb, Cao M. Xiaoxi, John B. Sutherland (FDA)

[DHHS Reference No. E–169–00/0 filed 10 Oct 2000]

Licensing Contact: Dale Berkley; 301/496–7735 ext. 223; e-mail: berkleyd@od.nih.gov.

The invention is a method for assembling a coherent database containing an essentially unlimited number of pyrolysis mass spectra to enable rapid chemotaxonomy of unknown microbial samples. The invention corrects for short and long-term drift of microbial pyrolysis mass spectra by using spectra of similar microbes as internal standards. The invention provides for the first time a practical way to assemble a coherent database containing an essentially unlimited number of pyrolysis mass spectra, where one or more is representative of each relevant strain, and representative of additional strains as they are added to the pool of microbial agents. Microorganisms can be identified using the invention from their fingerprint spectra regardless of the growth medium used to culture the bacteria. This is a result of the discovery that corrections made to the fingerprint spectrum of one type of bacterium to compensate for changes in growth medium may be applied successfully to metabolically similar bacteria. Fingerprint spectra to which the method of the invention may be applied include mass spectra, infrared spectra, chromatograms, NMR spectra and ion-mobility spectra. The present invention is especially useful for the rapid identification of microorganisms, including human pathogens.

Quantifying Gene Relatedness via Nonlinear Prediction of Gene Expression Levels

Dougherty et al. (NHGRI)

[Serial No. 09/595,580 filed 15 Jun 2000]

Licensing Contact: Dale Berkley; 301/496–7735 ext. 223; e-mail: berkleyd@od.nih.gov.

This invention relates to a new way to analyze the function of a newly identified gene. Working together, the genes within a genomic system constitute a control system for modulating gene expression activity and protein production. Regulation within this control system depends on multivariate relations among genes. Therefore, a key window into understanding genomic activity is to quantify the manner in which the expression profile among a set of genes can be used to predict the expression levels of other genes. This invention provides the experimental, statistical, and computational basis for nonlinear and linear multivariate prediction and co-determination among gene expression levels, and it is applied in the context of cDNA microarrays. Using these measures of multi-gene interactivity, it is possible to infer genomic regulatory mechanisms and thereby identify the manner in which genetic malfunction contributes to cancer and developmental anomalies.

Dated: December 14, 2000.

Jack Spiegel,

Director, Division of Technology Development and Transfer, Office of Technology Transfer, National Institutes of Health.

[FR Doc. 00–32814 Filed 12–22–00; 8:45 am]

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