suitable CRADA collaborator has not been selected.

FOR FURTHER INFORMATION CONTACT: Queries and capability statements should be addressed to William C. Ronnenberg, JD, M.I.P., Office of Technology Development, National Institute of Allergy and Infectious Diseases, 6610 Rockledge Drive, Room 4071, MSC 6606, Bethesda, MD 20892–6606 (Zip Code for Courier: 20817), telephone 301–451–3522, fax: 301–402–7123, e-mail: *wronnenberg@niaid.nih.gov.*

SUPPLEMENTARY INFORMATION: With the increased availability of detailed proteomic data, the main obstacle to developing realistic software-based simulation models of cellular signaling processes is the technical difficulty of transforming complex biological models into quantitative simulations. Biological models typically describe cellular signaling processes in terms of bimolecular interactions or the interaction between specific sites on two proteins. These bimolecular interactions can be integrated by available software into diagrammatic representations of signaling pathways. However, these descriptions are generally qualitative and are not useful for a quantitative understanding of the underlying biological systems. For quantitative representations of biological models, the current approach is to ask theorists (mathematicians, physicists, etc.) to transform these qualitative models into sets of equations or automata rules that roughly reflect the properties of the original model. The resulting descriptions of complex biological models are frequently inadequate because the theorist involved lacks an understanding of biological details or the resulting mathematical descriptions are over-simplified.

The goals of the proposed CRADA are to integrate an existing software program for the simulation of multi-scale, cellular, biological models with protein database interfaces and to improve the software's graphical user interface. NIAID has developed, in part, software that simulates reaction networks of all possible molecular interactions in biological systems based on user inputs. The current development stage of the software combines several unique features, such as a graphical interface for the definition and simulation of cell biological models spanning the scale from bi-molecular interactions to the behavior of cell populations. Its internal algorithms for the integration of the partial differential equations governing the spatio-temporal behavior of the simulated biological system use state-of-the-art approaches to deal with very large reaction networks and the stiffness of the equations.

Simulations created with the software take into account the differential behavior of cytosolic and membrane-bound complexes as well as transmembrane signaling events and generates the equivalent of a set of partial differential equations describing the spatio-temporal dynamics of the system. The graphical user interface of the software allows the user to define bi-molecular interactions, enzymatic transformations, (initial) spatial distribution of the components of cellular biochemistry and the location of cells within extracellular spatial compartments. Based on the initial distribution of molecules and cells defined by the user the software then simulates the behavior of the system providing a range of different graphical and tabular representations of the system's evolving state. At any time during the simulations, the user can add components (cells, molecules) and query the detailed biochemical state of cells (localized concentrations of signaling components) and investigate how these correlate with the cells' behavior.

The capability statement must address, with specificity, each of the following selection criteria:

(1) A demonstration of expertise and experience in the areas of design and coding of biological software with an extensive GUI component, as well as the development of supporting documentation;

(2) A demonstration of and a willingness to commit reasonable and adequate resources (including facilities, equipment, and personnel) the development of this technology;

(3) A demonstration of the expertise and ability to commercially develop, produce, sell, and provide user support for similar technologies; and

(4) Ability to provide adequate and sustained funding for CRADA activities.

Dated: June 2, 2006.

Michael R. Mowatt,

Director, Office of Technology Development, National Institute of Allergy and Infectious Diseases, National Institutes of Health.

[FR Doc. E6–9301 Filed 6–13–06; 8:45 am]

BILLING CODE 4140–01–P

DEPARTMENT OF HEALTH AND HUMAN SERVICES

National Institutes of Health

Government-Owned Inventions; Availability for Licensing

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

ACTION: Notice.

SUMMARY: The inventions listed below are owned by an agency 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.

Generation of Regulatory T Cells for Immunotherapy

Description of Technology: Abnormalities in immunoregulation are responsible for a wide variety of disorders such as autoimmune disease, chronic inflammatory diseases, and allergic diseases. These diseases include systemic lupus erythematosus, rheumatoid arthritis, type I diabetes mellitus, inflammatory bowel disease, multiple sclerosis, Crohn's disease and asthma. The defining event for induction of an immune-mediated disorder is the loss of T cell tolerance to self-antigens, which is provided by regulatory T cells. Traditional methods for treating immune-mediated disorders involve the use of steroids or other immunosuppressive drugs, which have significant undesirable side effects.

This invention provides methods for generating regulatory T cells by culturing CD4+CD25 − T cells with autologous antigen-presenting cells (APCs) in the presence of the Th2 cytokines interleukin-4 (IL-4) and/or interleukin-13 (IL-13). Immunotherapy via this mechanism is anticipated to have a large number of potential therapeutic applications. Methods are also provided for treatment of

autoimmune disease or inflammation in a subject by administration of an IL-4 agonist, as well as methods of treating cancer by administration of an IL-4 antagonist.

Applications: Therapeutic method for treatment of autoimmune disease or inflammation; Therapeutic method to prevent graft rejection in a transplant recipient; Therapeutic method for treatment of cancer; Diagnostic test for efficacy of an IL-4 antagonist in cancer treatment.

Development Status: Early stage.

Inventors: Peter E. Lipsky (NIAMS) *et al.*

Publication: A Skapenko *et al.,* ''The IL-4 receptor alpha-chain-binding cytokines, IL-4 and IL-13, induce forkhead box P3-expressing CD25+CD4+ regulatory T cells from CD25 − CD4+ precursors,'' J Immunol. (2005 Nov 1) 175(9):6107–6116.

Patent Status: U.S. Provisional Application No. 60/728,475 filed 19 Oct 2005 (HHS Reference No. E–010–2005/1–US–01).

Licensing Status: This technology is available for exclusive, co-exclusive, or nonexclusive licensing.

Licensing Contact: Marlene K. Astor, JD, MS, MIP; 301/435–4426; *ms482m@nih.gov.*

Collaborative Research Opportunity: The NIAMS, Autoimmunity Branch, is seeking statements of capability or interest from parties interested in collaborative research to further develop, evaluate, or commercialize a process for the generation of regulatory T cells for immunotherapy. Please contact Dr. Peter E Lipsky at 301/594–0596 or *lipskyp@mail.nih.gov* for more information.

Method Evolved for Recognition of Thrombophilia (MERT): Clinical Predictive Genetic Test for Venous Thrombosis

Description of Technology: Venous thrombosis (VT) is one of the leading causes of mortality and morbidity resulting in approximately 300,000 hospitalizations and 50,000 fatalities per year in the United States with an incidence of 141 per 100,000 African-Americans, 104 per 100,000 Caucasians and 21 per 100,000 Asian/Pacific Islanders. However, it is an avoidable disease if effective preventive measures such as early thromboprophylaxis are instituted.

It is highly beneficial to estimate individual thrombotic risk to aid in development of individualized risk-adapted prophylaxis.

Venous thrombosis is a multifactorial disorder and occurs as an outcome of a combination of environmental and genetic risk factors. In addition to well-established venous thrombosis associated acquired or environmental factors such as surgery, use of oral contraceptives and/or hormone replacement therapy, trauma, bone fractures, prolonged immobilization, advanced age, previous thrombosis history, malignancy and pregnancy, genetic predisposition via a number of variably penetrant genetic mutations or polymorphisms impart an increased risk for venous thrombosis.

In pregnant women, inherited thrombophilia can greatly increase the risk of adverse pregnancy outcomes such as miscarriages, intrauterine growth restriction, preeclampsia, placental abruption, or stillbirth as well as thrombosis during the recovery period after childbirth.

In addition to the differences in the prevalence of venous thrombosis among ethnic groups, there are accumulating data revealing differences in genetic determinants among ethnic groups such as differences in susceptibility associated genes and even in sequence alterations of the same gene. Furthermore some of the mutations and polymorphisms are mainly restricted to the specific populations. Such examples are FV Leiden, prothrombin G20210A polymorphisms. Whereas FV Leiden and prothrombin G0210A polymorphisms are the most prevalent risk factors for venous thrombosis in Caucasians, the patients from ethic populations other than Caucasians exhibit no or very rare FV Leiden or prothrombin G20210A polymorphisms.

This invention describes a highly-predictive genetic test to identify individuals with increased risk for venous thrombosis. It comprises a rapid, accurate and affordable genetic screen, utilizing genomic DNA microarray technology consisting of a combination of venous thrombosis associated mutations and polymorphisms that is applicable to diverse ethnic populations. Eight genes (antithrombin III, PC, PS, fibrinogen, factor V, prothrombin (factor II), MTHFR and ACE) are screened for the 143 known venous thrombosis-associated recurrent mutations and polymorphisms. This multi-gene test increases the predictive power for detection of genetic susceptibility to thrombosis over 20-fold compared to single-gene analysis, in multiple ethnic populations.

Applications: (1) Rapid, cost-effective predictive test kit to identify asymptomatic individuals at risk for venous thrombosis in diverse ethnic populations; (2) Rapid, cost-effective predictive test kit to identify pregnant women at risk for thrombophilia-associated adverse pregnancy outcomes such as miscarriage, intrauterine growth restriction, preeclampsia, placental abruption, or stillbirth as well as postpartum thrombosis; (3) Provides reduction of the yearly incidence of venous thrombosis by early identification of individuals at inherited risk, allowing protection before they develop symptoms by instituting effective preventive measures, such as early thromboprophylaxis or even decisions such as avoiding the use of oral contraceptives or hormone replacement therapy; (4) Provides advantages over currently available plasma-based thrombophilia screening panel by avoiding underdetermination of anticoagulant protein deficient individuals or by avoiding high rates of false positivity; (5) Allows individualized management and anticoagulation treatment of patients according to inherited thrombophilia status.

Market: (1) Individuals before or during exposure to situations that increase the risk of venous thrombosis, such as surgery, use of oral contraceptives and/or hormone replacement therapy, trauma, bone fractures, prolonged immobilization, long air journeys, advanced age, malignancy, or combinations thereof; (2) Pregnant women, or women who plan to become pregnant, as inherited thrombophilia is a significant risk factor for adverse pregnancy outcomes such as miscarriage, intrauterine growth restriction, preeclampsia, placental abruption, stillbirth and postpartum thrombotic events.

Development Status: Validation stage.

Inventors: Cigdem F. Dogulu, Owen M. Rennert, and Wai-Yee Chan (NICHD).

Patent Status: PCT Application No. PCT/US2005/01419 filed 14 Jan 2005, which published as WO 2005/071114A1 on 04 Aug 2005 (HHS Reference No. E–282–2003/0–PCT–02).

Licensing Status: Available for licensing.

Licensing Contact: Fatima Sayyid, M.H.P.M.; 301/435–4521; *sayyidf@mail.nih.gov.*

Dated: June 8, 2006.

David R. Sadowski,

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

[FR Doc. E6–9302 Filed 6–13–06; 8:45 am]

BILLING CODE 4140–01–P