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A Quest for a Custom-Made Mesenchymal Stem Cell in the Treatment of Inflammatory Diseases

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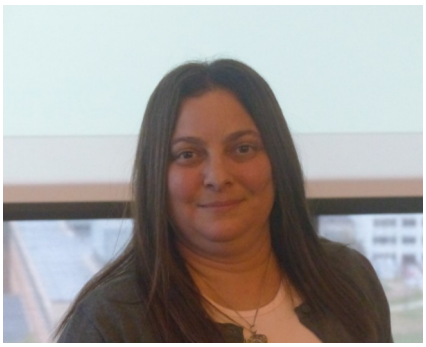

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Articles can be submitted electronically to *invivo@mec.cuny.edu* or mailed as a printed copy (preferably with a diskette that contains the file) to the Editorial Board at Medgar Evers College. All submissions should be formatted double spaced with 1 inch margins. The title of the article, the full names of each author, their academic affiliations and addresses, and the name of the person to whom correspondence should be sent must be given. As a rule, full length articles should include a brief abstract and be divided into the following sections: introduction, materials and methods, results, discussion, acknowledgments and references. Reviews and short communications can be arranged differently. References should be identified in the text by using numerical superscripts in consecutive order. In the reference section, references should be arranged in the order that they appeared in the text using the following format: last name, initials., year of publication. title of article, journal volume number: page numbers. (eg. - [1]Hassan, M. and V. Herbert, 2000. Colon Cancer. *In Vivo* **32:** 3 - 8). For books the order should be last name, initial, year of publication, title of book in italics, publisher and city, and page number referred to. (eg. - Prosser, C.L., 1973. *Comparative Animal Physiology*, Saunders Co., Philadelphia, p 59.). Abbreviations and technical jargon should be avoided. Tables and figures should be submitted on separate pages with the desired locations in the text indicated in the margins.

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A Quest for a Custom-Made Mesenchymal Stem Cell in the Treatment of Inflammatory Diseases. Natalie Fernandez, Caroline Winters, Maria Barandica, Abi Ocava, Michael Delsignore, Kristina Coppola and Jodi Evans, Molloy College, Rockville Centre, NY.

Mesenchymal stem cells (MSC) are multipotent cells that can differentiate into adipocytes, osteoblasts and chondrocytes. These cells are widely studied in tissue regeneration and for their therapeutic effects in inflammatory disease. MSC interact with cells of the innate and adaptive immunity to promote or suppress the inflammatory response. MSC from the bone marrow (D1 MSC) decrease inflammatory responses by lowering macrophage (Mϕ) secretion of soluble factors such as nitric oxide (NO), interleukin-12 (IL-12) and tumor necrosis factor--α (TNF-α). Aorta-derived MSC (mAo MSC) support the macrophage inflammatory response by contributing to NO secretion and enhancing secretion of TNF-α by Mϕ. Previous studies have isolated and enriched MSC populations using one or two specific cell surface markers and subsequently tested their functional properties in the regulation of immune cells. In this study we took a different approach. Using two populations of MSC with opposing immune regulatory function, we examined differences in their MSC-associated gene expression using PCR array. We sought to identify sets of MSC-associated genes that correlate with either suppression or support of the Mϕ inflammatory response. Our results revealed that the mAo MSC express genes that potentiate chondrogenic differentiation, while the D1 MSC express genes that potentiate adipogenic and osteogenic differentiation. Our unique approach identified MSC populations that have greater propensity to develop into osteogenic and adipogenic lineages are immunosuppressive, while those with greater propensity to develop into chondrocytes are immuno-supportive. We have identified lineage potential as a way to select MSC populations for use in cell-based therapies of inflammatory disease.

A Study of Marine Biology in the New York/New Jersey Harbor Estuary: A Multi-Pronged Approach. D'Angelo Fletcher[1], William Echavarria[1], Nazish Nawaz[1], Mauricio Gonzalez[2], and Kathleen A. Nolan[1], [1]St. Francis College, Brooklyn, NY, and [2]Harbor School, Governor's Island, NY.

Water quality sampling, seining, and restoration ecology are three of the ways that we have been studying and analyzing various waters of the New York/New Jersey Harbor estuary (Hudson and East Rivers, Fire Island, Fort Tilden, and Orchard Beach). Water has been tested for various parameters, including pH, salinity, dissolved oxygen (DO), nitrates, phosphates, and others. These water samples were compared and contrasted with water collected from places such as Maine and Vermont. We seined with school groups in the East and Hudson Rivers. We assisted with a restoration project that is currently underway at the esplanade on the East River near 125th street in New York City, and are helping draft an environmental impact statement for this project. We participated in New York State Department of Environmental Conservation projects such as The Great Fish Count (in which texting pictures for ID to exports was incorporated for the first time) and a Day in the Life of the Hudson River in an effort to contribute to a monitoring of the estuary databases. In preparation for the latter event, we participated in an invertebrate identification workshop at the Great Kills National Park in Staten Island. This holistic approach of sampling mixed with education should enhance our motivation to learn and discern more about the New York/New Jersey Harbor Estuary and other waterways.

Using Next Generation Sequencing Technology to Elucidate the Microorganism Diversity in Different Water Sites in Brooklyn. Fabiola Fontaine[1], Jeremy Seto[1] and Davida S. Smyth[1,2], [1]New York City College of Technology, Brooklyn, NY and [2]Mercy College, Dobbs Ferry, NY.

There is much interest in examining the effects of human activities on water sites in urban areas. Many studies have utilized classical microbiology techniques to examine the abundance of microbes in the water. More recently, next generation sequencing has been used to examine prevalence of microbes in a variety of sites and has led to great insights. Our project is examining three sites in Brooklyn, one with little human activity, Greenwood Cemetery and two with extensive human activity, Newtown Creek and the Gowanus canal. To date, examination of the three sites in Brooklyn, Green-Wood Cemetery has been performed using 16S rRNA sequencing. Within each site multiple samples were taken. Visual surveys of the biodiversity were done as well as taking into account the location of human activities such as sewage outflows. The flora and fauna were assessed. Water samples were filtered through 0.2um and 0.45 um filters and the DNA extracted. Extracted DNA was sent to a company for PCR amplification and DNA sequencing. The results have been analyzed using QIIME, STAMP and PiCRUST. Significant differences in the samples from the sites were observed both from site to site and from season to season. Several notable organisms were identified that could be used as potential makers for the health of the water bodies. Our future work will examine samples from the remaining seasons. We hope that our project will generate data that could be used to develop non-culture based methods of testing water quality.