

Youngstown State University

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Frontiers

SCHOOL OF GRADUATE STUDIES AND RESEARCH

Enhancing Rehabilitation for Stroke Survivors

According to the American Stroke Association, at least 800,000 people have strokes every year in the United States. Every forty seconds, someone has a stroke. Formerly thought of as only happening to the elderly, stroke survivors' profiles are getting younger every year. More people in their sixties and even fifties are suffering strokes as they try to maintain jobs and support their families. This change in the profile of stroke patients causes increased concerns for their rehabilitation needs. All persons who suffer a stroke need some form of rehabilitation therapy to assist them with recovery.

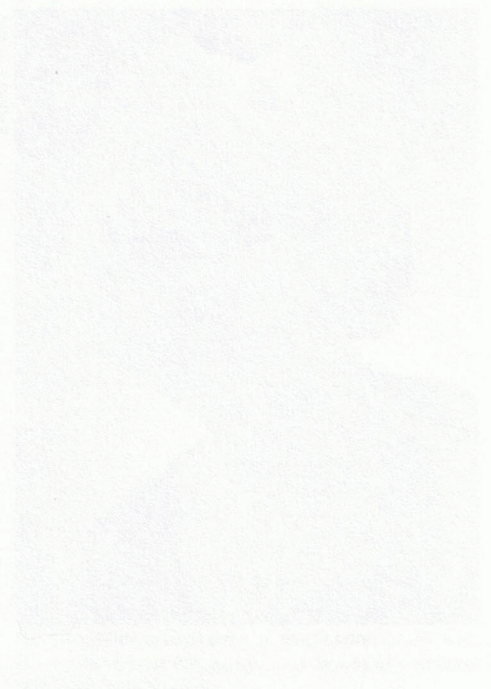
Because of this need, Dr. Nancy Landgraf, professor of physical therapy at YSU and senior research professor of research in the School of Graduate Studies at the University of Pittsburgh, is leading a new study which seeks to improve rehabilitation outcomes for stroke survivors. The study is a part from the National Institutes of Health, funded by the University of Pittsburgh. Landgraf plans to

offer, "because we know these patients can have deficits in cognition, which hinders sport and recovery, long-term memory, cognitive ability, motor planning, and processing difficult thoughts."

says Dr. Landgraf, "it is not just the physical recovery that is important, but also the cognitive recovery."

The study is a part of the National Institutes of Health's Chronic Disease Management and Prevention Research Program.

The study will focus on the rehabilitation outcomes of stroke survivors. According to Dr. Landgraf, rehabilitation outcomes will also be improved if patients are better able to participate, follow



Cutting-Edge Research with Bioinformatics

Plants and fungi are playing a vital role in the latest research on biofuel technology at YSU. This research is being led in part by biology professor, Dr. Xiangjia (Jack) Min, with assistance from his graduate research student Gengkon Lum. Dr. Min recently received a research grant from the Ohio Plant Biotechnology Consortium for the development of a database containing the protein sequences and relative information of plant secretomes.

Secretomes are proteins synthesized within a cell that are used outside the cell, i.e. in extracellular space. Secreted proteins “play important biological roles in cell wall structure, cellular communication, and the host-pathogen relationships” (Lum and Min, 2011). How these secretomes are used, their abilities, and their implications for biofuel technology have been the focus of Dr. Min’s research for many years. At his former university in Canada, Dr. Min helped analyze how secreted proteins could break down into fuel the leftover pulp, branches, and wood from the lumber industry. Instead of being left for compost, the particles can be harnessed as an alternative fuel source and reduce pollutants left by the industry.

Trained as a biologist before joining the YSU faculty in 2008, Dr. Min has been able to carry over his previous work on biofuel gene/enzyme technology into his current research on fungal and plant secretomes, which has transformed into an interdisciplinary field called “secretomics,” a sub-discipline of “bioinformatics.” Bioinformatics is “a combination of biology

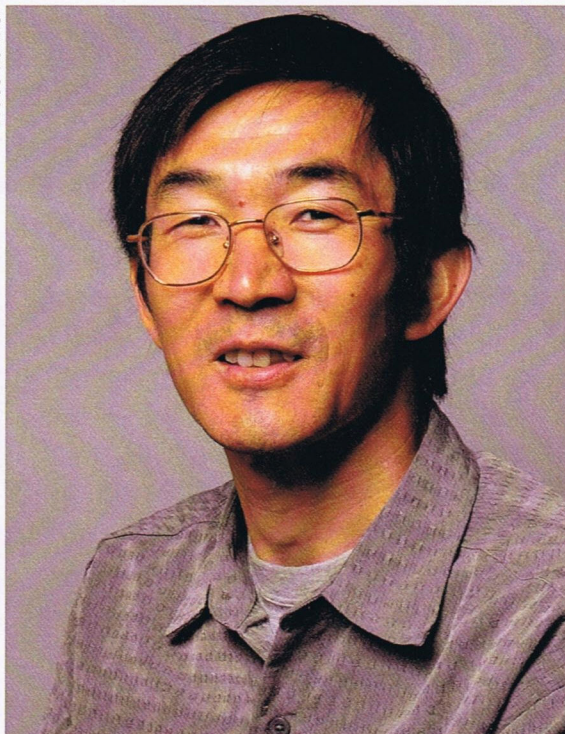
and computer science,” says Dr. Min. “Basically we use computer information technology to analyze biological information.” Dr. Min says that bioinformatics, a relatively new term, was developed in the late 1990s at the start of the human genome project. “At that time, the computational technologies moved

very quickly so we now have better computing than twenty years ago,” says Dr. Min. “At the same time, the sequencing technology improved so we can sequence entire genomes for the organisms of our interests. Now we can sequence bacteria, plants, fungi and human genomes. There was so much data generated by machines at that time that computer technology was applied, and this new field called bioinformatics was developed. My own research just transferred to this computer technology.” Computer programs help predict which proteins can be secreted. “For fungal research and plant research, we can identify these secreted

enzymes which have great potential as catalysts for biofuel production,” says Dr. Min.

Because of this application of computer technology to the field of biology, Dr. Min writes grants for graduate students to assist him with his research projects. Dr. Min’s current research assistant is Gengkon Lum, a second year graduate student with undergraduate work in chemistry, biochemistry and computer science, who has collaborated with Dr. Min to publish two research papers in peer-reviewed journals and one book chapter that has already been accepted. In addition, Lum is taking the algorithms developed

Bruce Palmer



Dr. Min's research has potential long-term benefits for both humans and animals.

by Dr. Min for predicting secretomes and proteins and inputting them into a database which would be accessible online for researchers around the world. For this online project, Lum says, "We are basically getting data from collected databases here in the United States, Europe, and Japan, which have collections of known proteins and other proteins that are being researched. Once we collect these proteins and their data, we analyze them for our specific purposes, one of them to predict if the protein is secreted or not." Running these predictive tests on the computer save the high costs of running physical tests in a wet lab. "You can run predictive tests on these proteins using computer algorithms," says Lum, "because each of these amino acids have certain shapes, and you can combine them in certain orders and make certain shapes. The functions of the proteins are based on the shapes of the proteins."

Analyzing and understanding secreted proteins have beneficial implications for human and disease research in the future. Lum is currently working on the plant secretome database (a database on fungi has been completed already) and mentions what occasionally happens with diseases in humans. "Proteins that are translated from DNA have a certain sequence, but sometimes in the translation the sequence is changed; a lot of diseases arise from a missed translation caused by gene (DNA) mutation." Lum says Dr. Min is writing proposals for further research. "We did a fungi database already and we're working on the plant one this year," says Lum. "[Dr. Min] wants to do one for animals and for humans later on."

Dr. Min spoke about the additional topics he's planning to propose. "We are trying to expand the project from fungi and plants to humans and animals," says Dr. Min. "Being able to predict the destination of proteins being secreted from cells makes it possible to identify these proteins as biomarkers for some



Second-year graduate student Gengkon Lum assists Dr. Min with the creation of plant and fungal secretome databases.

diseases like cancer. The application potential of this type of research could provide a tool for disease diagnosis."

For Dr. Min's current research project, however, the use of computer technology will specifically identify more effective enzymes to help convert materials into biofuels, such as cellulose (organic matter leftover after harvesting) to ethanol. The completed database project on fungal species has already had almost 2,000 hits (since release in February of this year) from researchers asking for data, many from other countries. Dr. Min's research on biofuel production, along with his other research projects, includes much international collaboration and publishing. In his career, Dr. Min has published approximately twenty-nine papers through collaboration with students and other professionals in his field. He believes that the work being done in his lab is "leading internationally" in this particular area of research and is proud of the contribution his department is making to biofuel production.

For more information on Dr. Min's research, along with a list of professional publications, visit:
<http://proteomics.ysu.edu>.