potassium, phosphorous, iron, and zinc. These minerals are the building blocks for our body's tissues and aid in regulating metabolic activity at the cellular level.

Grusak and colleagues found no downward trend in nutritional value of commercially available broccoli. “We know that even though plant breeders and growers have changed and improved upon the way in which broccoli is grown, over the years there has been no change in the mineral quality of broccoli,” said Grusak. “In the future, this information can be a useful guide for future plant breeders so they can maintain this level of mineral quality in new varieties.”

Others who took part in the study include Mark W. Farnham with the USDA/ARS U.S. Vegetable Laboratory, Charleston, South Carolina and Anthony P. Keinath at Clemson University. Funding for this study came from the U.S. Department of Agriculture – Agricultural Research Service.

The full report can be found at https://www.crops.org/publications/cs/abstracts/51/6/2721.
For a significant percentage of children, stomach pain is not just “belly-aching.” It is a serious health issue that can keep them from going to school or enjoying pleasurable activities.

In a first step toward identifying and treating this problem that can affect as many as 20 percent of school-age children, researchers at the USDA/ARS Children’s Nutrition Research Center at Baylor College of Medicine have identified several specific bacteria in children with recurrent abdominal pain and irritable bowel syndrome. A report on their findings appeared in the journal Gastroenterology.

It is the first major report by the Texas Children’s Microbiome Center and Baylor’s Alkek Center for Metagenomics and Microbiome Research, which have been federally funded to understand the links between children’s gastrointestinal diseases and their microbiomes. The microbiome refers to the billions of bacteria, viruses and fungi that normally inhabit the skin, intestines, genitourinary tract and other parts of the human body.

“When we characterized the bacteria that make up the microbiome in the intestines of children with irritable bowel syndrome, we found it was different from what we found in healthy children,” said Dr. Robert Shulman, CNRC researcher and professor of pediatrics – gastroenterology at BCM. “We also found that the severity of their pain and how frequently it occurred was associated with certain types of bacteria. That does not mean necessarily that the bacteria cause the pain, but these children had certain species of bacteria that were less likely to be found in the intestines of healthy children.”

Shulman and his colleagues have long attempted to understand the source of chronic belly pain in children.

“It is a mystery as to what triggers the chronic belly pain of some children,” said Dr. James Versalovic, professor of pathology & immunology at BCM, director of the Texas Children’s Microbiome Center and a corresponding author of the study. “Why do some kids have frequent bouts of pain and why do some have constipation or diarrhea with their belly pain?”

To understand the mysteries of abdominal pain better, Versalovic and his colleagues assembled a profile of the bacteria in the intestines of children with irritable bowel syndrome and compared it to a profile of the bacteria of children who did not suffer from the disorder. Youngsters with irritable bowel syndrome have stomach pain that is associated with changes in their bowel movements—either constipation or diarrhea. A total of 44 children completed the study. Half of the children had irritable bowel syndrome and half did not. Children kept diaries of their abdominal pain and bowel function for two weeks. They also gave a stool sample for microbiome analyses.

Researchers extracted DNA from the samples and determined what types of bacteria were present in the samples. While the total amount of bacteria did not differ between the two groups, the researchers did find differences in the kinds of bacteria. Children with irritable bowel syndrome had more Gammaproteobacteria than the healthy ones. Gammaproteobacteria encompass a wide range of bacteria—some benign and others associated with disease. In particular, the study found a greater proportion of Haemophilus parainfluenzae, Veillonella and Alistipes bacteria in the children with irritable bowel syndrome than those who were healthy. They also found a new organism related to a genus of bacteria called Ruminococcus that was more common in the intestines of children with irritable bowel syndrome.

“The next step is to see if these bacteria can be causing the children’s belly pain and whether we can use this information to devise new treatments that change the gut bacterial composition, including specific nutritional diets, probiotics, or antibiotics,” Versalovic said. Shulman said the findings have many important contributions. With more studies, the scientists will be able to figure out how these bacteria might influence the severity of pain or changes in bowel habits.

(Continued on page 4)
The understanding of the human genome and its impact on health is constantly evolving. Researchers at the USDA/ARS Children’s Nutrition Research Center at Baylor College of Medicine now suggest that studying genetics is not only important in identifying and treating rare genetic conditions, but also in understanding a person’s general health and risk for disease. These researchers propose a unified genetic model for human disease in a recent issue of the journal Cell.

Dr. John Belmont, professor of molecular and human genetics at BCM, and his colleagues noted, as an example, that several genes known to contribute to common diseases such as diabetes, obesity, atherosclerosis and cancer also cause severe genetic diseases in some individuals.

“There are common molecular mechanisms involved in the rare genetic diseases that are also now known to be involved in the common diseases,” Belmont explained.

This finding reinforces what researchers already knew—by studying rare diseases we learn a lot about basic disease mechanisms important to all types of human diseases. However Belmont also notes that the opposite is also true—studying the common diseases also tells us important things about how rare diseases work.

This conclusion allows researchers to set a research agenda in the future of how they will use genetic information to help improve health care.

“These studies tell us we should continue our focus on finding the causes of rare genetic diseases because it is extremely helpful and informative to find those rare and unusual cases. It also gives us an idea of how we should use the genetic information that is coming from studies of common diseases and tells us that we need to go more deeply into the study of those diseases,” Belmont said. “We need to use new methods like complete genome sequencing to study common human diseases because we are going to find not just common genetic variants, but we’ll find rarer variants that are specific to a particular family or even unique to a certain individual that are contributing to that common disease.”

Belmont’s work at the CNRC involves supporting researchers at the Center through genomic research. He applies genetic methods to help researchers understand underlying problems in nutrition. For example, Belmont is collaborating with CNRC researchers in using genetic methods to study severe malnutrition in children and determine why some children have severe and life threatening complications, but others recover quickly.

“This problem has defined explanation for the last 100 years, so we’re hoping and different epigenetic mechanism that may play a role in how the body handles exposures to poor nutrition or an otherwise suboptimal environment in early development,” said Van den Veyver.

Epigenetic mechanisms are established during development to stably regulate how genes are expressed in different tissues. This new finding may point to another layer of epigenetic regulation.

“If you look at the mice, they are healthy,” said Balasa. “They are smaller and leaner. Some of the liver enzymes were significantly lower in the low-protein offspring when compared to controls.”

He and Van den Veyver plan to study the effect of this diet and determine whether other early exposures induce similar changes in other organs of the mice.

Others who took part in this research include Dr. Amarilis Sanchez-Valle (another first author of the report), Dr. Bekim Sadikovic, Dr. Haleh Sangi-Haghpeykar, Jaclyn Bravo, Liang Chen, Dr. Wei Liu, Shu Wen and CNRC researcher, Dr. Marta L. Fiorotto, all of BCM.

Funding for this work came from the U.S. Department of Agriculture, Agriculture Research Service, the National Institute of Arthritis, Musculoskeletal and Skin Diseases and the National Institute of General Medical Sciences.
“It allows us to look at children more objectively. Instead of just relying on children’s or parent’s reports of their symptoms, we can characterize them by the bacteria in their guts,” he said.

Shulman and Versalovic hope to expand the study, encompassing a wider group of children with chronic belly pain. In the future, being able to determine what kind of belly pain a child has by the character of the bacteria in the gut may make treatments easier.

“Two children who appear to have the same type of chronic belly pain may actually need two different treatments,” said Shulman.

Those who wish to enroll in the expanded study should call 713-798-0381.

Others who took part in this research include Delphine M. Saulnier, Kevin Riehle, Toni-Ann Mistretta, Maria-Alejandra Diaz, Sabeen Raza, Erica M. Weidler, Xiang Qin, Cristian Coarfa, Aleksandar Milosavljevic, Joseph F. Petrosino, Sarah Highlander, Richard Gibbs, all of BCM, and Debamita Mandal and Susan V. Lynch of the University of California San Francisco. Saulnier is now with NIZO, Ede, The Netherlands. Many of the BCM researchers are also affiliated with Texas Children’s Hospital. Petrosino is director of the Alkek Center for Metagenomics and Microbiome Research at BCM.

Funding for this work came from the National Institute of Diabetes, Digestive and Kidney Disease, the National Human Genome Research Institute, the National Institute of Nursing Research, the Daffy’s Foundation, and the Rainin Foundation.