The Human Microbiome Project is a large genetic survey, launched in 2007 by the National Institutes of Health. Its purpose is to shed scientific light on the diverse types of microorganisms that inhabit various locations on the healthy human body and that live in harmony with it. Researchers from 80 universities and scientific institutions collaborated to map these various organisms that are so critical for human survival.

The June 13, 2012 on-line issue of *Nature* reported on some of this research, in particular the structure, function, and diversity of these microorganisms. Body areas of the 242 healthy US volunteers (129 male, 113 female) that were sampled included 15 sites in men, and 18 in women. Up to three samples were collected from each volunteer at locations such as mouth, nose, skin, lower intestines (stool), and vaginal areas in women. In all nearly 5,000 samples were utilized for this phase of the Project.

The genetic blueprint, or DNA, was analyzed and "sequenced" meaning that specific sections known as ribosomal RNA, that are specific to microbes, were identified and characterized through a process called polymerase chain reaction. To further characterize these microbes, researchers looked at certain metabolic functions, such as energy production, digestion of fats, proteins and carbohydrates in the gut, also synthesis of enzymes, vitamins, and anti-inflammatory compounds. From this work, researchers calculated that more than 10,000 microbial species inhabit the human ecosystem, contributing some 8 million protein-coding genes, of which 81-99% have been identified so far.

Researchers discovered that the distribution of metabolic activities performed by microbes matters more than the species providing them. For example, digestion of fats remains constant in our intestines yet may be performed by different bacteria over time, and from person to person. It was also found that variation in microbiota metabolism correlated in varying degrees with ethnicity (Asian, Black, Mexican, Puerto Rican, White), age, gender, BMI, and vaginal pH. For example, bacterial-mediated histidine production on the tongue was more pronounced in Asians, and age had a profound effect on variation in metabolic pathways in the skin, whereas BMI showed little association at all with any microbiotic variables.

The diversity of microbes, that is the type and relative abundance, was found to vary considerably from one body location to another. For example, oral and stool samples were especially diverse whereas vaginal sites were more limited. But within a given location, the richness of diversity was similar between individuals, that is they showed similar organisms at similar sites. Furthermore it was found that skin location on a given individual did not show as much diversity as between individuals.

Microorganisms are divided into genus, species and strains, similarly to the divisions and categories in the plant and animal kingdoms. In terms of this taxonomic diversity, vaginal samples displayed limited variation in genus yet greater diversity in species. In terms of relative abundance, there was considerable variation in streptococcus species and strains in oral samples from all subjects in the study. That the function of individual

strains varies between subjects, such as coding for different enzyme synthesis, despite a common location on the body, suggests human genetic variation as a determining factor.

Results reported in the *Nature* article support the contention that a healthy human microbiome establishes an equilibrium on a healthy individual. This research also revealed a unique, genetic microbial blue print for each person in the study, regardless of degree of diversity from one bodily location to another or between individuals at a given site. It also suggests that in cases of similarity in pattern across the entire human microbiome, for example with high-risk pathogens, common human genetic traits may be responsible.

Until the Human Microbiome Project, only a few hundred microbial species had been isolated from the human body. Why is the new knowledge generated by this Project important? Because it will enable future understanding into how this living, microscopic mass changes due to diet and environment as its human host experiences changes in health and disease. This extensive sampling paves the way for future study that may investigate how human immunity and genetics influence patterns of microbial diversity, how these patterns found in inhabitants of the US compare to other areas of the world, and how intentional manipulation of human microbiota may optimize an individual's unique physiology. As such, this Project has partnered with several other research institutions to gain further understanding on the role these microorganisms play in areas such as allergies and infectious diseases, arthritis and skin disorders, cancer, diabetes, and digestive, dental, and kidneys disease.