

Whole genome-sequencing uncovers new genetic cause for osteoporosis

Using one of the world's most extensive genetics data sets, the most recent collaborative effort of the Genetic Factors of Osteoporosis (GEFOS) Consortium has identified a gene with the strongest effect on the risk of osteoporosis and fracture

Embargo: Rotterdam, September 14, 2015 17:00 h CET – Using extensive genetic data derived from the UK10K project (a large sequencing project), an international team of researchers from the Genetic Factors of Osteoporosis (GEFOS) Consortium (<http://www.gefos.org/>) have identified a genetic variant near the gene EN1, displaying the strongest effect on bone mineral density (BMD) and fracture found to date. The findings, of this effort led among others by researchers from McGill University in Montreal, Canada and the Erasmus University Medical Center Rotterdam, in The Netherlands, are published today in the prestigious journal Nature.

Osteoporosis is a common disease that will lead to fractures in between one-third and one-half of all women over the course of their lives. Because osteoporosis becomes more severe with age, it is becoming more prevalent with the overall aging of the population. Current compounds are not free of severe adverse effects nor are they effective for the whole population. In addition, no curative therapies for osteoporosis are available. Steps further improving this situation have been accomplished by this collaborative effort.

This particular study stands as proof of principle that uncommon genetic variants can have a significant impact on common diseases. “The effect of this infrequent genetic variant, which has never before been linked to osteoporosis in humans, is up to four times as large as that observed for most common variants identified for BMD and fracture and so far,” stated Dr. Brent Richards, an Associate Professor of Medicine at McGill University, and senior last author of this effort.

“While the discovery of the EN1 gene does not essentially modify the way we assess the individual risk of patients, it does opens up new horizons for the development of drugs which reverse the disease” adds Fernando Rivadeneira, Associate Professor of Musculoskeletal Genomics from Erasmus MC in the Netherlands and co-senior last author of this paper.

This study also represents an initial realization of the hope to translate discoveries from genetic sequencing technology into palpable contributions to human health: “Having walked a very successful path identifying hundreds of genetic determinants underlying disease using the genome-wide association approach, it is thrilling to see that the application of sequencing technology has already started to provide novel genetic underpinnings of a complex disease like osteoporosis” says André Uitterlinden, Professor of Complex Genetics also at Erasmus MC.

“Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture” by Zheng et al, *Nature*, on-line September 14, 2015.