The molecular signature of loneliness

September 13 2007

People who experience chronically high levels of loneliness show gene-expression patterns that differ markedly from those of people who don't feel lonely, according to a new molecular analysis in the online open access journal *Genome Biology*.

The findings suggest that feelings of social isolation are linked to alterations in immune system activity, which result in increased inflammatory signalling within the body. This is the first study to show an alteration in genome-wide transcriptional activity linked to a social epidemiological risk factor. It provides a molecular framework for understanding why social factors are linked to an increased risk of diseases where inflammation is thought to be a factor, such as heart disease, infection and cancer.

It is already known that a person's social environment can affect their health, with those who are socially isolated suffering from higher all-cause mortality, and higher rates of cancer, infection and heart disease. Researchers are trying to determine whether these adverse health consequences result from of reduced social resources (e.g., physical or economic assistance) or from the biological impact of social isolation on the function of the human body. "What this study shows us," said lead author Dr. Steven Cole, of the University of California Los Angeles (UCLA) School of Medicine, "is that the biological impact of social isolation reaches down into some of our most basic internal processes - the activity of our genes."

In their study, Dr. Cole and colleagues at UCLA and the University of

Chicago used DNA microarrays to survey the activity of all known human genes in white blood cells from 14 individuals in the Chicago Health, Aging and Social Relations Study. Six participants scored in the top 15% of the UCLA Loneliness Scale (a widely used measure of loneliness that was developed in the 1970s), the others scored in the bottom 15%. The researchers found 209 transcripts were differentially expressed between the two groups, with 78 being overexpressed and 131 underexpressed. "The leukocyte transcriptome appears to be remodelled in chronically lonely individuals," said Dr. Cole.

Genes overexpressed in high-lonely individuals included many involved in immune system activation and inflammation. However, several key gene sets were underexpressed, including those involved in antiviral responses and antibody production. Bioinformatics analyses identified some of the biological signalling pathways that shaped these differences in gene expression, including reduced activity of the anti-inflammatory glucocorticoid pathway and the pro-inflammatory NF-"B/Rel pathway. "These findings provide molecular targets for our efforts to block the adverse health effects of social isolation," said Dr. Cole.

"In this study, changes in immune cell gene expression were specifically linked to the subjective experience of social distance," said Dr. Cole. "The differences we observed were independent of other known risk factors for inflammation, such as health status, age, weight, and medication use. The changes were even independent of the objective size of a person's social network. What counts, at the level of gene expression, is not how many people you know, it's how many you feel really close to over time." In the future, the transcriptional fingerprint identified by Cole and colleagues might become useful as a 'biomarker' to monitor interventions designed to reduce the impact of loneliness on health.

Source: BioMed Central