The Effects of Socioeconomic Status, Race, and Immigration on Inflammatory Levels in the United States: An Analyses Using Quantile Regressions

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EXTENDED ABSTRACT
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Introduction

There has been interest recently in attempting to understand the biological pathways through which socioeconomic status and other social experiences exert their influence on health. One important area of inquiry into the links between social factors and biological outcomes is that of inflammatory activity. High levels of inflammation are thought be to be a risk factor in the development and progression of cardiovascular disease (Danesh *et al*, 1999) and possibly other chronic conditions including diabetes (Duncan *et al*, 2003) and Alzheimer's Disease. Disparities in cardiovascular disease related mortality across socioeconomic class and race continues to persist in the United States. Inflammatory activity may be a key mechanism through which we can measure and understand how socioeconomic status, race, and other social experiences can lead to disparities in chronic conditions.

Theoretical Focus

Socioeconomic status and race are associated with many factors that can influence inflammatory activity. Markers of inflammation have been shown to be sensitive to social factors (Jousilahti *et al*, 2003; Bravata *et al*, 2005). A number of causal exposures can be implicated but the relative importance of these factors in generating disparities across sub-groups is still unclear. Psychosocial effects may play an important role. Research in this area has tended to focus on central nervous system and endocrine responses to environmental stress. Physiological evidence suggests that inflammatory levels are responsive to central nervous system activation, specifically the hypothalamic-pituitary-adrenal axis (Zhou *et al*, 1993).

Exposure to infectious agents may also play a role in generating disparities. The level of pathogen exposure is related to inflammatory levels, and these exposures could differ along socioeconomic and racial groups given the importance of nutrition and sanitation in determining infectious susceptability. Another important cause of disparities may arise from lifestyle differences. Both smoking (Mendall *et al*, 1996) and obesity (Pradhan *et al*, 2001) are associated with inflammatory activity and differ across population sub-groups.

This paper examines differences in levels of C-reactive protein across population sub-groups in the United States by using both ordinary least squares and quantile regression techniques. C-reactive protein is an acute phase protein and non-specific marker of inflammatory activity. C-reactive protein levels have been found to be an independent predictor of cardiovascular disease (Pai *et al*, 2004). It has also been found to vary significantly across social class, although previous studies have shown inconsistent results. Wu et al (2002) found a weak negative association of C-reactive protein with both educational attainment and an index of poverty (whereby those who were poorer tended to have higher levels of circulating C-reactive protein). In a British sample, Danesh et al (1999) found no consistent association between C-reactive protein levels and different indicators of social class after controlling for numerous lifestyle factors.

Alley (2005) reported that differences in C-reactive protein levels across socioeconomic groups were only detectable at the highest levels of the distribution of C-reactive protein (>10 mg/L). This finding suggests that individuals with the highest inflammatory load may be more sensitive to socioeconomic status than individuals who are at lower levels of inflammatory activity.

To our knowledge no study has examined inflammatory levels in immigrant groups in the United States. For example, foreign-born Hispanics seem to have better adult health outcomes as compared with non-Hispanic Whites despite their lower socioeconomic position. Whether this advantage is also reflected in inflammatory load is unknown. There exists a positive relationship between pathogen exposure and C-reactive protein levels (Zhu *et al*, 2000). Foreign-born persons (especially those from tropical countries) may carry a higher inflammatory burden because of pathogen exposure that occurred before they left their home country.

Most previous studies have tended to rely on ordinary least squares or logistic regression techniques for estimating effects. This paper will utilize quantile regression models, which may be more appropriate for analyzing biological data due to violations of underlying assumptions of the classical linear model. Many biological phenomena exhibit heteroskedastic tendencies since it is difficult to adequately capture all relevant predictor variables. Quantile models can incorporate changes in variation of the dependent variable across dimensions of the predictor variables. In fact, changes in the variance of the dependent variable would often indicate that the slope of the conditional quantile lines would differ (e.g. the slope of the 75^{th} percentile would be different from that of the median). Therefore, quantile models can provide a more complete picture of the causal relationships among variables by including estimates of the rates of change at different parts of the dependent variable's distribution.

Research Questions

Key questions that are addressed in this paper include the following:

(1) Do inflammatory levels differ across key demographic variables such as socioeconomic status, race, and immigration status in the United States after controlling for important lifestyle covariates?

(2) Do the effects of these social factors differ across quantiles of the distribution? The use of quantile regression models will allow us to estimate effects at different levels within the C-reactive protein distribution. Therefore, the models will enable us to examine more precisely whether individuals who are in the upper tail are more sensitive to social and environmental influences than individuals in other parts of the distribution as suggested by previous research.

Data

Data from the National Health and Nutrition Examination Survey (NHANES) 1999-2002 were used in these analyses. NHANES is a population-based, cross-sectional survey of the non-institutionalized population of the United States. The overall sample size was 21,004. C-reactive protein levels were obtained in 15,903 participants who were ages 3 and over. The mean level of C-reactive protein was 3.58 mg/L (SD: 7.95 mg/L). NHANES data are publicly available.

Methodology

Ordinary least squares and quantile regression models were developed using serum C-reactive protein levels as the outcome variable. Independent covariates included age, sex, race, poverty status, education level, immigration status, body mass index, reports of recent infection, and smoking status. Heterogeneity in variance was tested using Cook-Weisberg tests for heteroskedasticity in selected models. Quantile regression models were developed at selected increments between the 10^{th} percentile and the 90^{th} percentile inclusive.

Findings

Selected results show the following:

- Ordinary least squares regression models showed that with reference to non-Hispanic Whites, both non-Hispanic Blacks and Mexican Americans had significantly higher levels of C-reactive protein (β=.114, P<.001 for Blacks; β=.192, P<.001 for Mexican Americans). The dependent variable, C-reactive protein was logarithmically transformed in these analyses.

- Ordinary least squares regression models showed that immigration status (foreign born vs. native born) was not statistically significant. In addition, poverty status as measured by the poverty income ratio as defined by the U.S. Census) was significant, although results were inconsistent across ordinary least squares regression models. Our results suggested that an increase in income lowered levels of C-reactive protein net of other covariates. For adults age 25 and over, those with some college had lower levels of C-reactive protein as compared with those who had not completed high school.

- Quantile regression models generally confirmed results from the ordinary least squares models with some exceptions. Our findings showed that those who were foreign born had significantly lower levels of C-reactive protein as compared to those who were native born across the 25^{th}, 50^{th}, and 75^{th} percentiles in a model which included all ages. We did not detect significant differences between Mexican Americans and non-Hispanic Whites in some quantile models. The reason for the discrepancy between these findings in the qauntile models and the findings in the ordinary least squares regression model is unclear at this time.

- A most noteworthy finding is that the effects of gender, race, immigration status, and poverty status tended to be dependent on the quantile being measured. This is succinctly depicted in Figure 1 (below), which shows that for these four variables the coefficient tends to deviate away from zero with increasing quantiles (i.e. the effects of the independent variables are much more pronounced at the upper tails of the C-reactive protein distributions).

Discussion & Conclusion

The results of these analyses generally confirm previous reports of an effect of socioeconomic status and race on C-reactive protein levels after controlling for important covariates such as body fat and recent infectious exposure. However, these effects are not consistent across all of the models developed. Results from the quantile regression models clearly point to the fact that the effects of a number of important demographic variables are dependent on the quantile of the C-reactive protein distribution being modeled. This finding has not been reported in the literature previously and is important to our understanding of the relationship between social experiences and biological outcomes.

Immigration status did not seem to have a consistent effect on inflammatory levels. Countervailing forces may be at work. Those immigrants from poorer tropical environments may have had increased pathogen exposure than those born in the United States. This would tend to raise their inflammatory burden. On the other hand, immigrants to the United States may also be a selected group who are on average healthier than their counterparts at home (the so-called healthy migrant hypothesis) (Palloni & Morenoff, 2001). This would tend to lower their average inflammatory load as compared to non-immigrants who would be less selected.

Theoretical rationale underpinning the finding that inflammation may be most sensitive to social factors at the upper tail of the distribution has not been articulated. One possibility is that those in the upper tail of the C-reactive protein distribution are already quite ill (e.g. advanced cardiovascular disease, autoimmune dysfunction) and that their constitution is more labile to the effects of social and psychological stress. Also, there is a genetic component to inflammatory activity (MacGregor *et al*, 2004). Those who may have lower levels of inflammatory activity may possess a genotype that is more protective against external influences.

This paper highlights the fact that non-traditional techniques such as quantile regression methods are useful to more completely describe the interrelationship between social factors and biological outcomes. We argue that social factors such as socioeconomic status and race are important predictors of immune system function net of other covariates yet the effects may be inconsistent across populations. A more complete characterization of these relationships through further research may prove illuminative to the understanding of the disparities in mortality at the older ages.

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Figure 1: Y-axis is the coefficient (β) for the selected variables. Dashed line represents coefficient (β) for median (50th percentile) quantile regression