Annals of Epidemiology 28 (2018) 316–321

Contents lists available at ScienceDirect

Annals of Epidemiology

journal homepage: www.annalsofepidemiology.org

Original article

Neighborhood disadvantage and racial disparities in colorectal cancer incidence: a population-based study in Louisiana

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ARTICLE INFO

Article history:
Received 20 September 2017
Accepted 9 February 2018
Available online 22 March 2018

Keywords:
Colorectal cancer
Concentrated disadvantage
Disparities
Multilevel modeling
Social epidemiology

ABSTRACT

Purpose: Colorectal cancer (CRC) continues to demonstrate racial disparities in incidence and survival in the United States. This study investigates the role of neighborhood concentrated disadvantage in racial disparities in CRC incidence in Louisiana.
Methods: Louisiana Tumor Registry and U.S. Census data were used to assess the incidence of CRC diagnosed in individuals 35 years and older between 2008 and 2012. Neighborhood concentrated disadvantage index (CDI) was calculated based on the PhenX Toolkit protocol. The incidence of CRC was modeled using multilevel binomial regression with individuals nested within neighborhoods.
Results: Our study included 10,198 cases of CRC. Adjusting for age and sex, CRC risk was 28% higher for blacks than whites (risk ratio [RR] = 1.28; 95% confidence interval [CI] = 1.22–1.33). One SD increase in CDI was associated with 14% increase in risk for whites (RR = 1.14; 95% CI = 1.10–1.18) and 5% increase for blacks (RR = 1.05; 95% CI = 1.02–1.09). After controlling for differential effects of CDI by race, racial disparities were not observed in disadvantaged areas.
Conclusion: CRC incidence increased with neighborhood disadvantage and racial disparities diminished with mounting disadvantage. Our results suggest additional dimensions to racial disparities in CRC outside of neighborhood disadvantage that warrants further research.

Introduction

Colorectal cancer (CRC) is the second leading cause of cancer-related deaths in the United States [1]. CRC incidence is significantly higher in Louisiana than in the United States, for all race-sex groups [1]. In the past 2 decades, CRC incidence has decreased overall, but racial disparities remain, with blacks having greater incidence of CRC and poorer survival than non-Hispanic whites [2].

The World Health Organization's Commission on the Social Determinants of Health recognizes that health disparities arise from the conditions in which people are born, grow, live, work, and age [3]. Social determinants of health encompass the social, economic, political, cultural, and environmental factors that affect a person's health. Social determinants potentially play a principal role in the development and progression of certain cancers. This is partially attributable to the increasing recognition that social stress represents an environmental exposure that affects individual health through metabolic pathways leading to obesity [4–9]. Obesity has been identified as a risk factor for a variety of chronic disease outcomes, including cancer [10].

Neighborhood environment is an important indicator of individual health, independent of individual characteristics, such as income or education [4,11–13]. Adverse neighborhood living environments are associated with conditions that contribute to metabolic dysfunction either directly through social stressors (i.e., lack of resources and crime) or indirectly through neighborhood conditions that promote unhealthy behaviors (i.e., unhealthy

Disclaimer: All statements and views expressed in the submitted article are of the authors' own and not an official position of the institution or funder.
The authors do not have any conflicts of interest to disclose.
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https://doi.org/10.1016/j.annepidem.2018.02.004
1047-2797/

diet and physical inactivity) [14]. With regard to social stressors, studies have found that chronic exposure to disadvantaged neighborhoods has a direct effect on individual health through prolonged activation of the hypothalamic-pituitary-adrenal and sympathetic adrenal axes in a process described as allostasis [15–18]. Allostatic changes are associated with a chronic inflammatory state and metabolic dysfunction. With regard to neighborhood conditions, disadvantaged neighborhoods lack physical characteristics that can promote healthy behavior (e.g., walkability and access to fresh foods), a constraint that also leads to metabolic dysfunction [19–22].

Conventionally, incidence rates for cancer are reported for geographic units larger than the census tract to increase the reliability of calculated rates. Thus, most studies regarding the incidence of cancer are conducted at the county level. However, it is recognized that smaller units are more ideal for characterizing exposures to social determinants in the neighborhood environment (i.e., census tract and block group) because of socioeconomic heterogeneity within counties [23]. Although some researchers use small unit area–based social measures as a proxy for individual status in traditional single-level models, research has shown that this approach can lead to model misspecification, particularly in the realm of health disparities, and that multilevel models are superior [24,25]. However, a common limitation of multilevel studies of social determinants of health is that many data sources lack a sufficient number of individuals nested within neighborhoods to produce a strong multilevel data structure.

Using methods initially proposed by Subramanian et al. [26], we designed a population-based study using cancer registry and U.S. Census population data to investigate the role of neighborhood concentrated disadvantage in the incidence of CRC and the degree this appears to contribute to racial disparities. Two previous studies have used similar methods to examine racial disparities in mortality. In both studies, differential exposure to neighborhoods by race resulted in the misspecification of race in a single-level model. In addition, area poverty explained a significant portion of neighborhood variation in all-cause mortality, which evidenced area poverty as a key contributor to mortality and to racial disparities overall [25,26].

The aim of this study is to investigate potential risk of CRC associated with living in a local environment characterized by concentrated disadvantage and if differential exposure to neighborhood environments contributes to racial disparities. We hypothesize that differential exposure to adverse community environments leads to increased incidence of CRC in disadvantaged and minority residents. Results from this study will shed light on the role of neighborhood environment in disparities in CRC.

Methods

This study involves secondary data analysis, using data from the Louisiana Tumor Registry, a participant of the National Cancer Institute's Surveillance, Epidemiology, and End Results Program, and U.S. Census data. The Louisiana State University Health Sciences Center Institutional Review Board approved this research. Primary invasive colon and rectum cancer cases diagnosed from January 2008 to December 2012 were identified by International Classification of Diseases for Oncology, Third Edition, site codes C180–C189, C199, C209, and C260. Cases with International Classification of Diseases for Oncology, Third Edition, morphology codes 9050–9055, 9140, and 9590–9992 were excluded. Cases of CRC from the Louisiana Tumor Registry were geocoded to 2010 census tracts using the Automated Geospatial Geocoding Interface Environment system, which was developed through a partnership between the North American Association of Central Cancer Registries, Texas A&M University, and the National Cancer Institute as a single, uniform geocoding platform for open use by cancer registries [27]. The geocoding process used street address or zip code +4 at the time of diagnosis, with a success rate above 93%. The population at risk was determined from the 2010 U.S. Census.

In assessing cancer incidence, we address adults 35 years and older, of black or white race alone, diagnosed with at least one primary invasive colorectal tumor during the study period. *In situ* or unknown stage tumors were not included. Age was categorized into four age groups (35–44, 45–54, 55–64, and 65 years and older). Sex was categorized as male or female. Race was grouped as black or white, as defined by the U.S. Census; other races were not included in these analyses due to small group numbers. The total number of possible individual-level demographic risk factor combinations was 16.

An individual's neighborhood environment was measured in terms of socioeconomic disadvantage. Concentrated disadvantage index (CDI) scores for neighborhoods (i.e., census tracts) were calculated based on the PhenX Toolkit protocol, established by a collaboration of the Research Triangle Institute and the National Human Genome Research Institute for the development of consensus measures of phenotypes and exposures across research studies [28]. CDI is a sample-based composite score derived from a principle components analysis of six measures at the census tract level (given as percentages): (1) individuals below the poverty line; (2) households receiving public assistance income; (3) female-headed families; (4) individuals who are unemployed; (5) individuals below the age of 18 years; and (6) individuals who are black. The construct operationalizes urban theory regarding the overconcentration of blacks, children, and female-headed families in economically disadvantaged neighborhoods [29]. In addition to associations with adverse neighborhood conditions such as increased crime, the construct has been linked to metabolic conditions and racial disparities in cancer survival [7,30,31]. We derived CDI using 2008–2012 5-year estimates from the American Community Survey, to align with the study period. The resulting factor explained 58% of the variance present in the original six variables for the state of Louisiana during the study period. Factor loadings for the original variables are provided as supplemental material (Table S1). Factor scores for study census tracts follow a standard normal distribution with a mean of zero and SD of 1.

Louisiana has one thousand one hundred forty-eight 2010 census tracts; there were 19 census tracts with no population, which did not contribute to the analysis. Standard U.S. census tracts typically contain between 2500 and 8000 residents [32]. We excluded eight nonstandard census tracts that had a population less than 500. These tracts had a total of 1190 residents and three incident cases. Because census tracts are designed to be relatively homogenous in terms of socioeconomic characteristics [32], we did not feel it was appropriate to merge the population into other tracts. Finally, we excluded the census tract occupied by the Orleans Parish Prison. The prison had a population of 3089 in 2010 and no incident cases of CRC. After these exclusions, individuals from 1120 Louisiana census tracts remained eligible for the study.

Based on the study design, cases of CRC were aggregated for 16 demographic risk combinations (cells) for each of the 1120 census tracts, which yielded 17,920 possible data cells. The population at risk for age-, sex-, and race-specific cells within each census tract was determined from 2010 U.S. Census population counts, multiplied by 5 to represent person-years at risk. For each data cell, cancer cases and population-years were used to construct a binomial random variable, where the response was given as the number of incident cases out of the person-years at risk. Less than 2% of cells had no at-risk population (person-years) and did not contribute to the analysis. There were 4 incident cases of CRC recorded for these