Health Disparities in High-Risk Lung Cancer Families and Their Association with Smoking, Environmental Exposures, and Other Etiological Factors

Grace Brandhurst, Angelle Bencaz, Sarah North, Ellen Jaeger, and Diptasri Mandal Ph.D
LSUHSC Department of Genetics

LSU Health NEW ORLEANS School of Medicine

NIH NATIONAL CANCER INSTITUTE

LSUHSC • MOFFITT SPIRIT-CHD Southeast Partnership for Improving Research & Training in Cancer Health Disparities

Introduction

- Lung cancer (LC) is by far the leading cause of cancer-related deaths worldwide.
- LC survival has only improved marginally over the last decades with the five-year survival rate (18.6 percent) for LC being lower than most other leading cancer sites. [1]
- Although tobacco smoking has been identified as the major risk factor for LC, studies have shown there is a genetic component involved in the development of the disease.
- Hereditary predisposition has been observed in many LC cases, indicating that family history is a relevant risk factor.
- African Americans (AAs) have a higher incidence rate and lower survival rate for LC in comparison to all other racial and ethnic groups in the United States.
- Furthermore, in AAs the age-adjusted incidence rate for LC is about 32% higher than European Americans (EAs).[2]
- Sex-based disparities in LC have shifted in the past decades. Despite having lower rates of tobacco use among females compared to males, women now have an increased risk for developing LC.
- There are several histological subtypes of LC. Non-small cell lung cancer (NSCLC) accounts for most new diagnoses of LC and includes large cell carcinoma, squamous cell carcinoma, and adenocarcinoma. Incidence rates among males and females of AA and EA ancestry vary with histology of LC.
- Lung cancer is a complex disease caused by a sequence of many gene-environment interactions.

1. U.S. National Institute Of Health, National Cancer Institute. SEER Cancer Statistics Review, 1975–2015.
2. Ryan BM. Lung cancer health disparities. Carcinogenesis. 2018;39(6):741-751.

Objective

The goal of our study is to characterize genetic, clinical, and environmental risk factors among individuals of EA and AA ancestry from the high-risk families with LC that could hold important clinical value to address LC disease disparity.

Methods

- Study participants with LC were recruited from a network of 30 hospitals from Louisiana along with multiple states across the country.
- Study participants with at least two confirmed cases of primary LC within the family were eligible. Participants were divided into two subgroups: Familial (≥2 LC cases/family) and Hereditary LC (HLC families) (≥3 affected LC cases/ family).
- Medical and pathology reports were obtained from hospitals along with demographic and environmental data from the families.
- A total of 192 study participants (157 EA and 35 AA) from both familial and HLC families from the years 1992 through 2021 were used in this study
- Data abstracted from the pathology, clinical reports, and study questionnaire was entered into spreadsheets and analyzed.
- Histology of LC diagnosis and clinical reports on mutation analysis were documented.

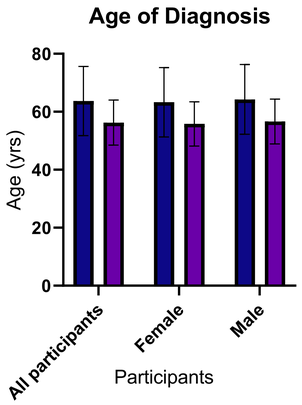

Figure 1: Average age of diagnosis in LC participants of EA and AA ancestry. Average age of diagnosis being 63.7 years old for EA and 56.3 years old for AA. The average age of diagnosis was found to be significantly different between the EA and AA populations (P value <0.0001).

Results

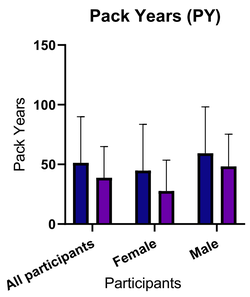

Figure 2: Average pack years in LC participants of EA and AA ancestry. Average pack years for EAs is 51.3 years and 38.8 years for AA. The pack years were found to be significantly different between the EA and AA populations (P value= 0.0177).

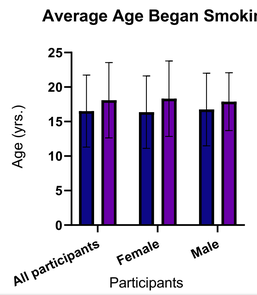

Figure 3: Average "Age Began Smoking" in LC participants of EA and AA ancestry. Average age for EA being 16.5 years old and 18.1 years old for AA. The average age began smoking was found to be significantly different between EA and AA populations (P value = 0.0226).

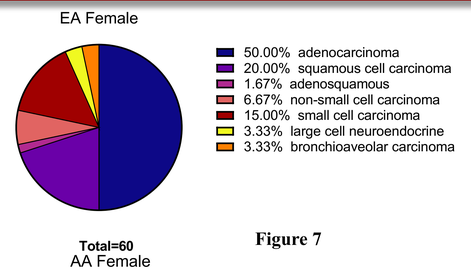

Figure 7

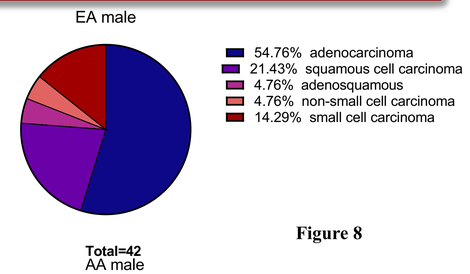

Figure 8

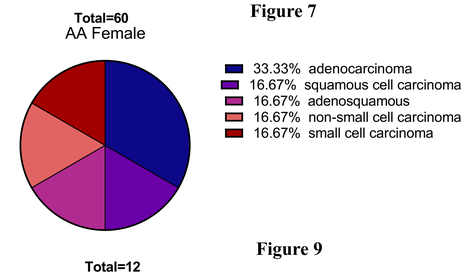

Figure 9

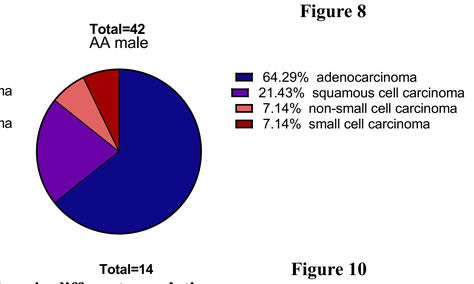

Figure 10

Figures 7-10: Percentage of each histology in different populations

Chart 1: Other Etiological Factors

PY for each Histology	adenocarcinoma	squamous	adenosquamous	non-small cell*	small cell
European American	33.09	49.80	62.50	45.75	55.85
African American	33.87	49.33	22.25	29.00	52.67
Town Population	**less than 20,000**	**20,000 - 49,999**	**50,000-249,999**	**250,000-500,000**	
European American	46.88%	16.67%	25.00%	11.46%	
African American	62.50%	0%	12.50%	25.00%	
Ever Drink?	**EA Yes**	**EA No**	**AA Yes**	**AA No**	
	74.77%	25.23%	66.67%	33.33%	
	Never Smoker	**Smoker**	**Excessive Smoker**		
Female	19.61%	55.88%	24.51%		
Male	13.41%	58.54%	28.05%		
Years Smoked	Female	Male			
	32.47	37.68			
BMI	**EA Average**	**AA Average**			
	27.08	26.56			

*participants with "non-small cell" listed as their histology have not had their subtype identified

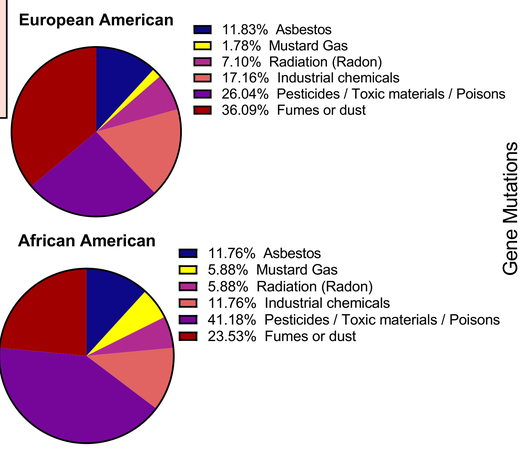

Figure 4-5: Percentage of exposure to environmental hazards among people of EA and AA ancestry

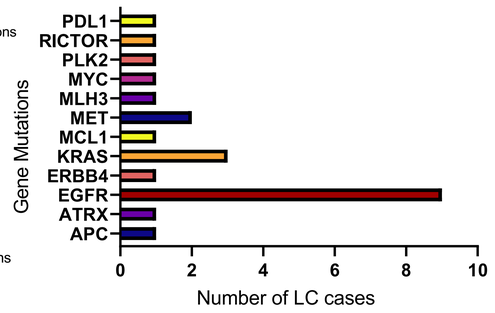

Figure 6: Positive Gene Mutations. All study participants with pathology reports containing mutation analyses are of EA ancestry.

Discussion & Conclusions

- While AAs smoke fewer pack years and begin smoking later in life, they are developing LC at an earlier age.
- Most of the study participants with LC were diagnosed with adenocarcinoma irrespective of the number of pack-years for cigarette use.
- Differences in etiological factors between AA and EA populations did not precisely define a reason for these disparities.
- Not all people with these risk factors develop lung cancer, which indicates the rising significance of studying genetic factors in contribution to the development of lung cancer.
- While this study has identified racial and gender disparities in LC, additional efforts are needed to prevent these disparities in the years to come.
- One of the main challenges we face when studying LC is the complexity of the disease. Lung cancer generally has a poor prognosis, with over half of people with lung cancer dying within one year of being diagnosed.
- Other limitations of this study include a small sample size for AAs. Additionally, while LC health disparities are highest among AAs, it is imperative to emphasize that disparities exist among many populations in the United States. Given that much of the data in this study comes from participants of AA and EA ancestry, they were the primary subject of this study. Nevertheless, in the future to correct this it is critical that we recruit a diverse set of study participants from all populations.
- Similarly, a larger enrollment of AAs in our study may be able to help identify novel susceptibility loci in this population.
- Lastly, it is imperative that we better characterize the biological factors that influence the development of lung cancer in the female population so as to achieve more personalized practices for the prevention and management of this disease.
- Additional analysis is ongoing using next-generation sequencing. Genetic, clinical and pathological characterization in association with risk factors from high-risk families with EA and AA ancestry will provide us with a better understanding behind the disproportionate distribution of incidence and survival for LC in the AA population.

Acknowledgements

We express our gratitude to the study participants, the collaborating hospitals, and the physicians. This work is funded by the National Institutes of Health (NIH): HHSN26820100007C (Mandal), HHSN268201700012C (Mandal), 75N92020C00001 (Mandal), and 3U01CA076293-10S1 (Amos).

This research project was supported by the National Institutes of Health (NIH), National Cancer Institute (NCI).