

Characterizing Genetic Mutations in Familial Lung Cancer: Insights & Implications

Carley Kronlage, Angelle Bencaz MSPH, and Diptasri Mandal PhD
LSUHSC Department of Genetics



Introduction

Background:

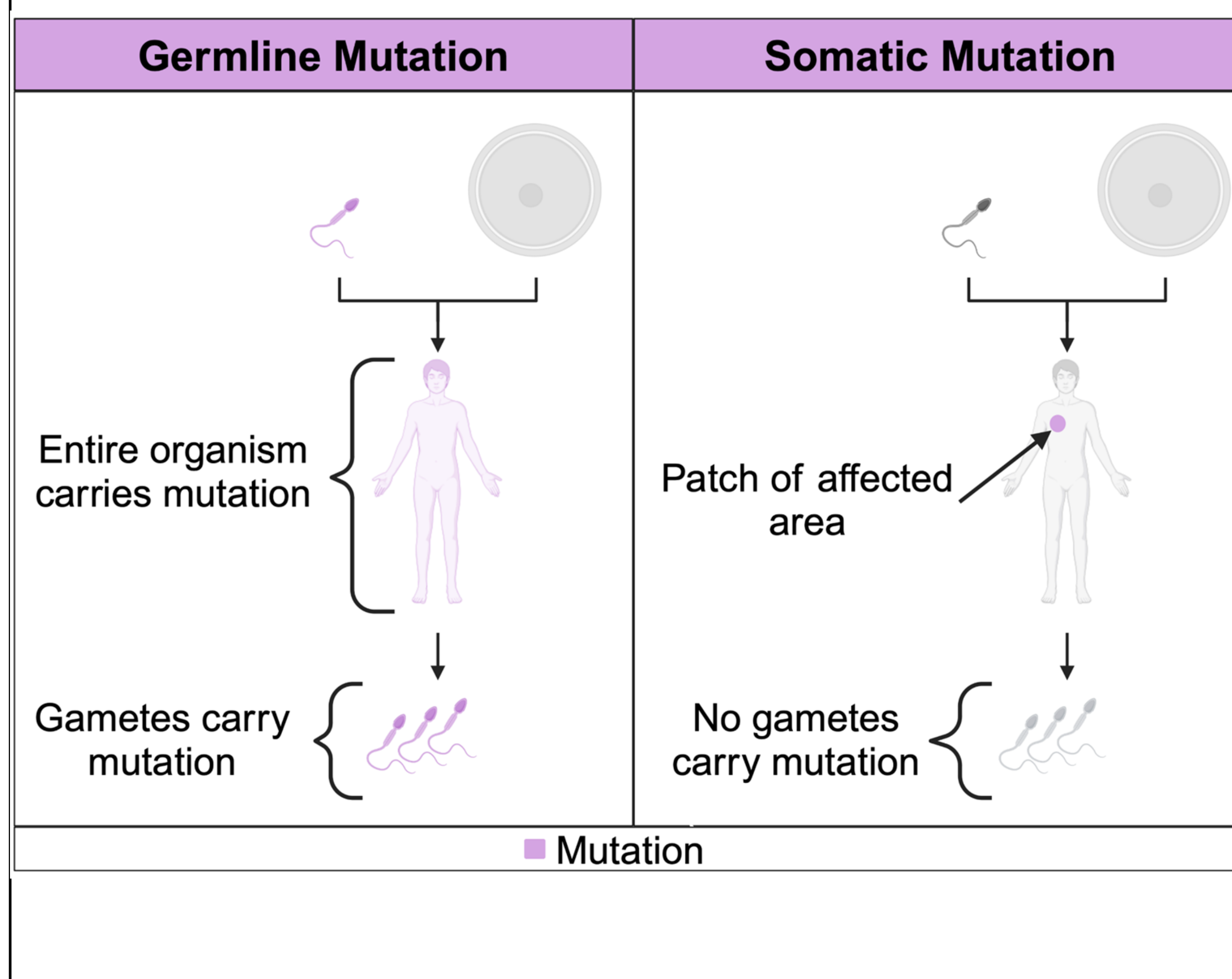
- Lung Cancer (LC) is the leading cause of cancer-related deaths worldwide
- First-degree relatives of LC patients have a 1.51 times higher risk of developing LC
- Less than 20% of smokers develop LC
 - ↳ suggests that genetics play a key role
- Difficult to pinpoint a list of specific genetic mutations that cause LC
 - ↳ Caused by a combination of both genetic and environmental risk factors
 - ↳ Multiple genes are responsible
- Identifying genetic mutations aids in determining the best treatment options
 - ↳ Precision Medicine (PM): specific drugs can target specific genetic mutations
 - ↳ PM can help LC patients avoid generalized harmful treatments like chemotherapy

Gaps:

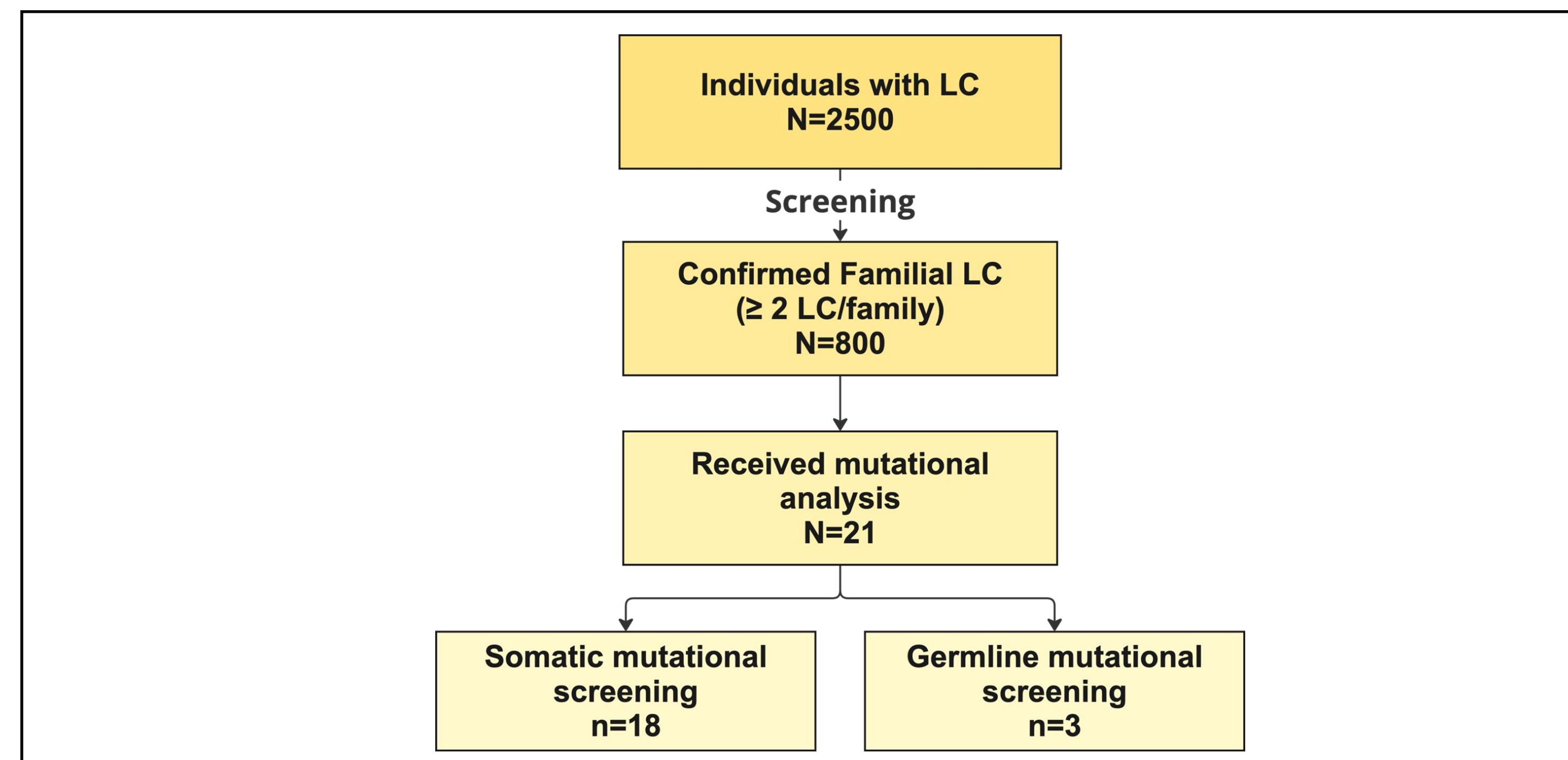
- Identified genetic mutations linked to LC susceptibility need further validation
- More research is required to confirm findings across different populations

Objective:

- Characterize genetic mutations in familial LC cases

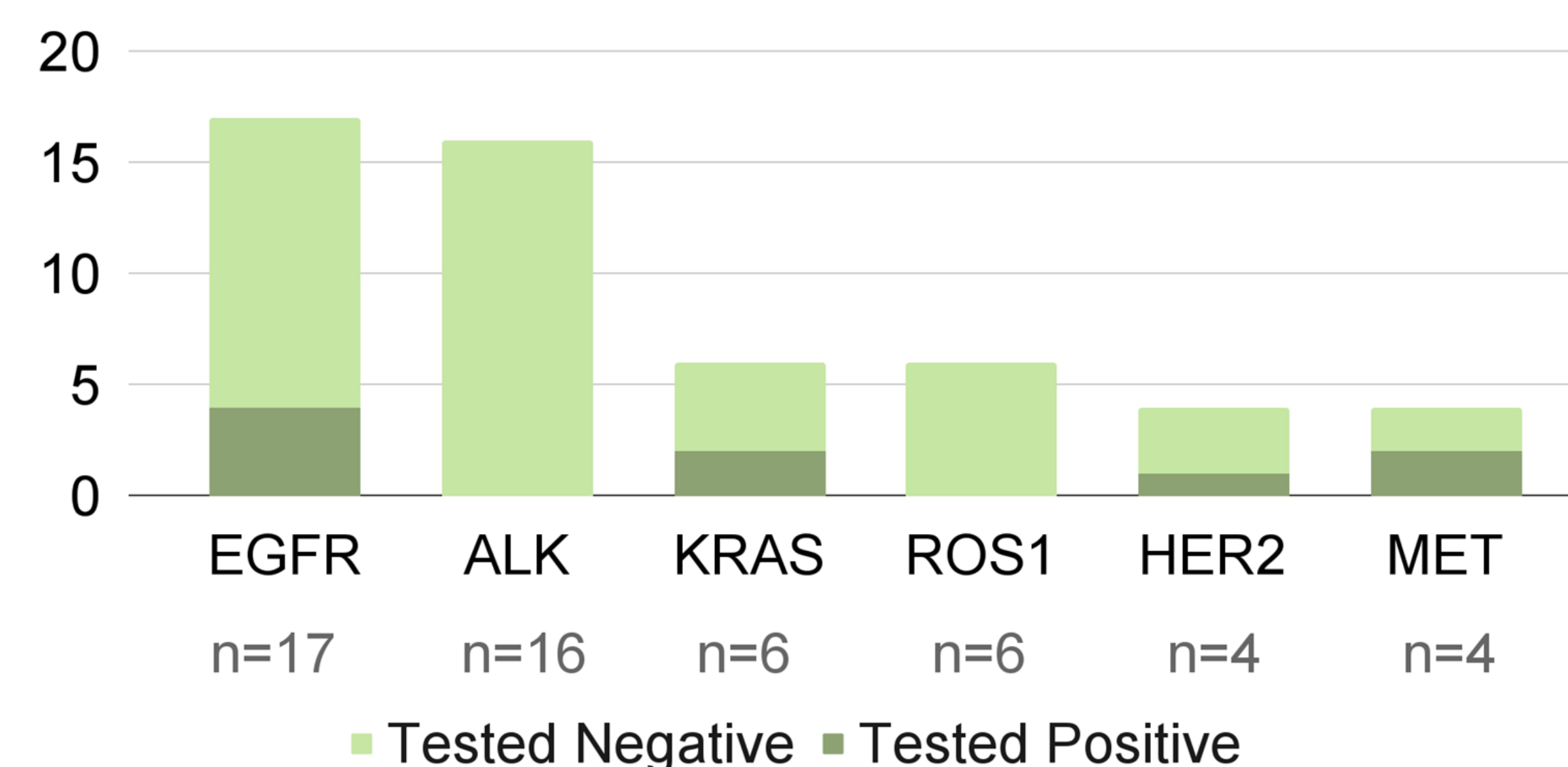


Methods



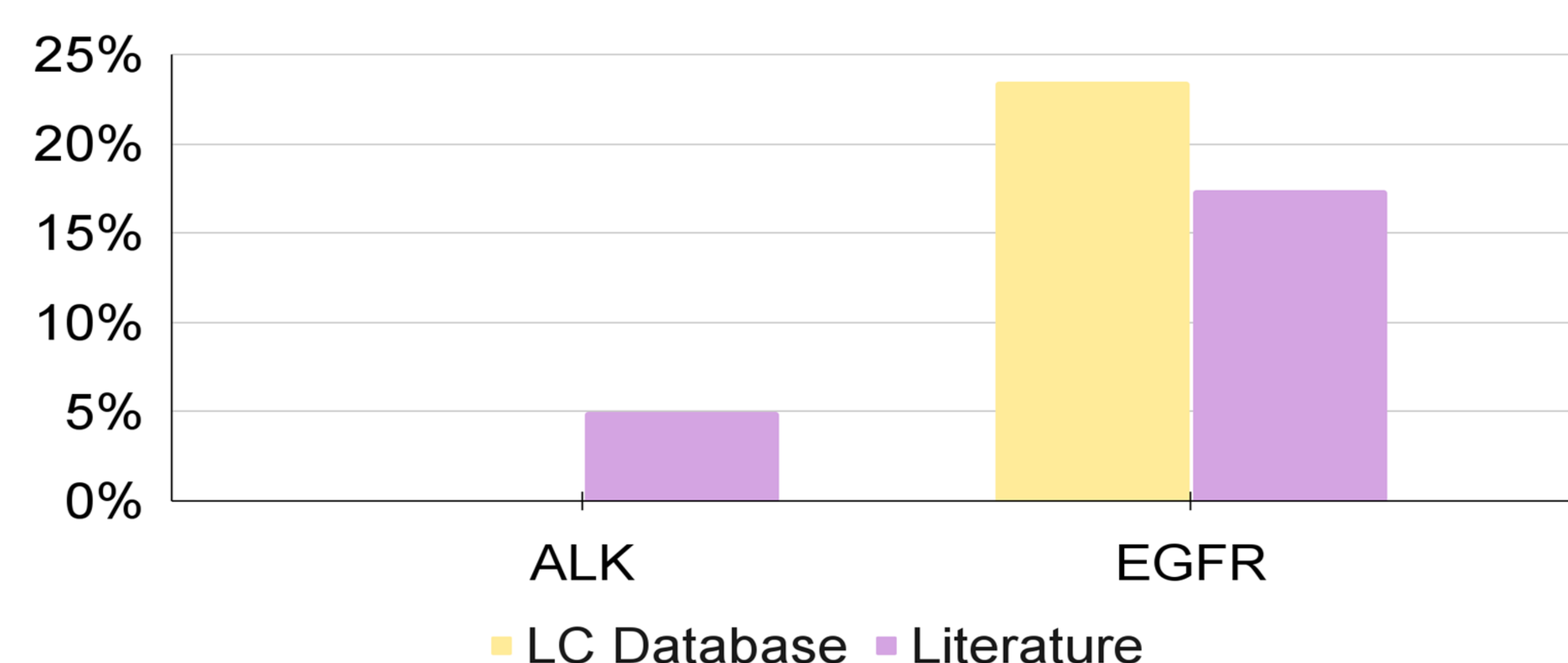
Results

Proportion of Individuals who Tested Positive for a Gene Mutation



Individuals	Mutation Type	Age of Diagnosis	Relatives with LC	Histology	Smoking History
# 1	EGFR	55	5	adenocarcinoma	S(ex)
# 2	EGFR	62	4	squamous cell	S(ex)
# 3	EGFR	51	5	adenocarcinoma	N
# 4	KRAS	62	9	adenocarcinoma	S(ex)
# 5	KRAS	75	2	adenocarcinoma	S(ex)
# 6	MET	87	2	adenosquamous carcinoma	N
# 7	MET	63	3	adenocarcinoma	S(ex)

Distribution of EGFR & ALK Gene Mutations



Conclusions & Future Directions

Interpretations of Results

- Prevalence of the EGFR and ALK gene mutations amongst study participants varied by about 5% each from what they were reported to be in literature
- Those with EGFR mutation
 - ↳ Higher number of relatives with LC
 - ↳ Earlier age of onset
 - ↳ Different types of mutations were observed: exon 19 deletion, exon 20 insertion, and p.T790M mutation
- No participants tested positive for the ALK mutation despite being one of the most common genes tested for

Limitations

- No standard screening panels for mutational analysis
- Only included Caucasians
- Only 21 participants had mutational analysis

Future Directions

- How PM can be applied in the presence of multiple genetic mutations
- Whether somatic or germline mutations of a gene more commonly occur
- How the presence of certain gene mutations affects LC prognosis
- Average age of LC onset in patients with a germline mutation
- Common genetic mutations in never smokers
- How patients can possess certain germline mutations but never develop LC

Acknowledgements

We express our gratitude to the study participants, the collaborating hospitals, and the physicians. This work is funded by the National Heart, Lung, and Blood Institute (NHLBI)/National Institutes of Health (NIH): HHSN268201200007C and 3U01CA076293-10S1.