Advance Discovery

Learn from the experiences and outcomes of every patient with cancer.

Improved clinical outcomes and the future of patient care depend on learning from the experiences of every cancer patient. CancerLinQ Discovery® sits at the forefront of real-world cancer research, providing access to harmonized, codified, and curated sets of aggregated, de-identified real-world patient data representing the diverse pool of over 6 million patients in the CancerLinQ® network. This powerful database can then be used to uncover unseen patterns in patient characteristics and unlock actionable insights—shaping the future of cancer care.

Since June 2020, CancerLinQ Discovery has been more broadly available to the academic, nonprofit and government research communities. Visit https://www.cancerlinq.org/solutions/researchers to learn more.

- Compare the effectiveness and value of alternative treatment options
- Study the use of cancer treatments in populations typically excluded from clinical trials to generate new knowledge to improve patient care
- Deliver insights to inform and continuously improve practice guidelines and quality measures
CancerLinQ was built with the vision of being able to learn from the experiences of every patient with cancer, and the CancerLinQ team is dedicated to bringing the power of real-world oncology data and advanced analytics to improve cancer care and research. But what exactly are "real-world data" and "real-world evidence," and what is the relevance in 2022 for oncology care and research? Real-world data (RWD) refers to data collected outside conventional clinical trials from a wide range of sources including electronic health records, disease registries, claims databases, genomic repositories, and wearable patient-monitoring devices. Real-world evidence (RWE) was defined by the FDA in a 2018 guidance as "the clinical evidence regarding the usage and potential benefits or risks of a medical product derived from analysis of RWD." Real-world data can be collected both prospectively and retrospectively at the point of routine care. When the intent of data collection is research, purposeful prospective collection of RWD can accommodate experimental designs similar to those employed in conventional clinical trials while offering unique benefits that include generating results with an appropriate balance between internal and external validity. Conventional RCTs are typically optimized for internal validity by imposing strict definitions for endpoints and study procedures in a narrowly eligible patient population. Conventional RCTs are often expensive and slow to accrue, with control arms that can become obsolete with shifts in the standard of care. Furthermore, barriers to clinical trial participation coupled with narrow eligibility criteria typically lead to enrolling patients that are younger, healthier, and less diverse than population averages. In contrast, RWD reflects “what does work,” it has strong external validity, and it captures data on patients commonly encountered in day-to-day practice that may be under-represented in conventional RCTs. However, RWD’s challenges include the fact that it is subject to bias especially data missing not-at-random, assessments and outcome measures are not standardized, and heterogeneity in the subject population may obscure any treatment effect. Conventional RCTs and RWD currently complement each other; both are needed for modern oncology care. In the past decade, remarkable advances in the understanding of the molecular basis of cancer have led to the development of multiple new targeted agents and immunotherapy drugs which are revolutionizing treatment. However, these agents are being tested in the small number of adults with cancer who actually enroll in clinical trials, and the populations studied are neither clinically nor ethnically
representative of patients typically encountered in most practice settings. To help unlock this valuable RWD and inform care, in 2017, CancerLinQ launched CancerLinQ Discovery®, now one of the largest real-world oncology research data sets in the world, incorporating harmonized, curated, and de-identified data from the millions of patients whose providers are a part of the CancerLinQ network. CancerLinQ Discovery has made it possible for researchers to learn from the experiences of patients throughout the CancerLinQ network, dramatically shifting oncology research, including investigations supporting the development of precision therapeutics, to include data from a diverse network of rural, community, academic, and health system care settings, with data extracted from 13 different electronic health record systems and other data sources. CancerLinQ Discovery data has been used by researchers across the oncology ecosystem to advance oncology knowledge and ultimately to improve patient care and the development of better anticancer therapies. Past publications have addressed such diverse topics as the characterization of telehealth use at the end-of-life during the COVID pandemic; the real-world clinical outcomes of patients with BRCA-mutated, HER-2 negative metastatic breast cancer; and using machine learning techniques to predict cardiac adverse events in patients with non-small cell lung cancer, melanoma, and renal cell carcinoma receiving checkpoint inhibitors. All publications using CancerLinQ data can be found on our website at https://www.cancerlinq.org/scientific-publications.

In the last several years, RWD has been incorporated in FDA decisions for the approval and label expansions of several oncology-specific agents. Oncologists can use RWD to guide individual treatment decisions, particularly in areas where traditional clinical practice guidelines are insufficient to address the complexity of a patient’s clinical scenario. In addition, RWD, when collected prospectively, can support an expanded range of use cases such as prospective registries and pragmatic clinical trials, to inform oncologists about important questions such as sequencing of therapies and the effectiveness and safety profile of approved therapies in special populations excluded from traditional clinical trials, such as those with poor performance status, organ dysfunction, and older adults. CancerLinQ is working to incorporate RWD in its product roadmap which will be made available to our subscribing practices. Two examples include the Patient Journey/Patient Match prototype application which will be demoed during this Annual Meeting and our recently announced collaboration with Atropos Health which will make available on a pilot basis a “Prognostogram” digital consult for providers to quickly access RWE generated from millions of past patient encounters to guide care for their patients. Most importantly, CancerLinQ remains committed to working to improve health equity for patients historically under- and unrepresented in clinical trials by being broadly representative of practice types and patient populations throughout the US and by delivering tools and services to oncologists and researchers to overcome these traditional barriers.

We encourage you to review this 2022 Scientific Evidence Guide to learn more about some of the important research using CancerLinQ data that is being presented at this meeting. For more information about joining CancerLinQ or accessing our research datasets, visit cancerlinq.org.
Key Findings
Natural language processing-optimized case selection for real-world evidence studies. Koskimaki et al. | Abstract #1556 | Poster #149

BACKGROUND:

Much information describing a patient’s cancer treatment remains in unstructured text in electronic health records and is not recorded in discrete data fields. Accurate data completeness is essential for quality care improvement and research studies on de-identified patient records. Accessing this high-value content often requires manual and extensive curation review.

RESULTS:

NLP methods improved cohort identification. Successfully returned cases using the NLP method ranged from 75.2% to 96.5% over more general case selection criteria based on limited structured data. For all cohorts combined, 84.2% of the cases sent out for NLP curation were returned with curated content (see table). Each cohort contained a range of NLP-derived elements for curators to further review. In comparison, more general case selection criteria yielded a total of 3,878 cases returned out of 41,186 lung cancer cases sent for curation, for a success rate of only 9.6%.

CONCLUSION:

NLP-driven case selection of six distinct, complex lung cohorts resulted in an order of magnitude improvement in eligibility over candidate selection using structured EHR data alone. This study demonstrates NLP-assisted approaches can significantly improve efficiency in curating unstructured health data.

NLP-assisted cohort selection for the six pre-specified lung cancer cohorts.

<table>
<thead>
<tr>
<th>COHORT</th>
<th>COHORT DESCRIPTION</th>
<th>NUMBER OF CASES AVAILABLE FROM NLP-ASSISTED IDENTIFICATION METHODS</th>
<th>NUMBER OF CASES SENT TO TEMPUS AND CONCERTAI FOR CURATION</th>
<th>NUMBER OF CASES RETURNED TO CANCERLINQ WITH CURATED CONTENT</th>
<th>PERCENT OF SUCCESSFULLY CURATED CASES</th>
</tr>
</thead>
<tbody>
<tr>
<td>1A</td>
<td>NSCLC, stage I, II, III, EGFR+, complete resection</td>
<td>408</td>
<td>408</td>
<td>341</td>
<td>83.6%</td>
</tr>
<tr>
<td>1B</td>
<td>NSCLC, non-squamous, stage I, II, III, EGFR wild type/unknown, complete resection</td>
<td>4313</td>
<td>1500</td>
<td>1285</td>
<td>85.7%</td>
</tr>
<tr>
<td>2A</td>
<td>NSCLC, stage III, unresectable, curative radiation to the chest total dose &gt;= 50 Gy, did receive Imfinzi</td>
<td>852</td>
<td>620</td>
<td>466</td>
<td>75.2%</td>
</tr>
<tr>
<td>2A</td>
<td>NSCLC, stage III, unresectable, curative radiation to the chest total dose &gt;= 50 Gy, did not receive Imfinzi</td>
<td>3050</td>
<td>750</td>
<td>724</td>
<td>96.5%</td>
</tr>
<tr>
<td>3</td>
<td>SCLC, received Imfinzi or Tecentriq</td>
<td>559</td>
<td>500</td>
<td>402</td>
<td>80.4%</td>
</tr>
<tr>
<td>4</td>
<td>NSCLC, received Tagrisso as first line treatment</td>
<td>971</td>
<td>812</td>
<td>647</td>
<td>79.7%</td>
</tr>
<tr>
<td>Total:</td>
<td></td>
<td>10153</td>
<td>4590</td>
<td>3865</td>
<td></td>
</tr>
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</table>
Associations between biomarker testing and characteristics of patients with metastatic non–small cell lung cancer (mNSCLC): An analysis of CancerLinQ Discovery (CLQD) data.

Mileham et. al. | Abstract #9127 | Poster #113

**BACKGROUND:**
Guidelines have evolved from 2011-2019; there are now 23 approved therapies targeting various predictive biomarkers in mNSCLC. 2021 NCCN Guidelines advocate for a minimum of ALK, EGFR, BRAF, METex14, NTRK1/2/3, RET, KRAS, and ROS1 testing before determining a treatment regimen. The study objective was to estimate the association between the presence of biomarker testing and smoking status, age, sex, race, ethnicity, histology, and diagnosis year in patients with mNSCLC.

**RESULTS:**
- Testing rates increased from 31.5% in 2011 to a peak of 62.3% in 2017. Patients with a smoking history were half as likely to receive testing than patients without a smoking history (OR = 0.50, 95% CI: 0.41, 0.60); patients with unknown smoking history were 0.66 times as likely (95% CI: 0.52, 0.84).
- Females were more likely to be tested than males (OR = 1.19, 95% CI: 1.07, 1.32). After adjusting for other covariates, Asian patients were 1.51 times more likely to be tested than patients of other races (95% CI: 1.05, 2.17); Hispanic patients were 1.33 times more likely to be tested than patients without Hispanic ethnicity (95% CI: 0.99, 1.78). The odds of receiving biomarker testing were 6x greater for patients with non-squamous mNSCLC versus squamous mNSCLC.

**CONCLUSION:**
Our data demonstrate annual increases in testing rates, reflecting guideline changes. However, in this cohort of patients with mNSCLC, biomarker testing was more likely for non-squamous mNSCLC patients, females, Asians, Hispanics, or those who did not have a history of smoking. Patient characteristics should no longer factor into obtaining biomarker testing. Non-discriminant, broad panel-based reflex molecular testing in mNSCLC can reduce treatment choice ambiguity and enhance patient opportunities.

8,704 Patients from 31 practices were eligible.

1.51 Asian patients were 1.51 times more likely to be tested than patients of other races.

1.33 Hispanic patients were 1.33 times more likely to be tested than patients without Hispanic ethnicity.

6x The odds of receiving biomarker testing were 6x greater for patients with non-squamous mNSCLC versus squamous mNSCLC.

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Molecular testing and patterns of treatment in patients with NSCLC: An IASLC analysis of ASCO CancerLinQ Discovery Data³.

Behera et. al. | Abstract #9128 | Poster #114

BACKGROUND:

Precision medicine has resulted in improved outcomes for non-small cell lung cancer (NSCLC); while molecular testing is considered critical for guiding treatment decisions for advanced stage NSCLC, adoption of testing in routine practice is variable. We analyzed the factors contributing to molecular testing and treatment patterns in patients with lung cancer.

RESULTS:

37,925 NSCLC patients with stage IV disease were analyzed

- 22% of all NSCLC patients had molecular testing results.
- 49% of adenocarcinoma patients had molecular testing results available.
- 47% were treated with chemotherapy in the stage IV group.
- 16% were treated with immunotherapy in the stage IV group.
- 3% were treated with targeted therapy in the stage IV group.

Patient characteristics: median age 65 years, 51% male, 68% white, 33.5% adenocarcinoma.

Approximately 22% of all NSCLC patients had molecular testing results. In adenocarcinoma patients, 49% had molecular testing results available. In the stage IV group, 47% were treated with chemotherapy, 16% with immunotherapy and 3% with targeted therapy. On multivariable analysis, females were more likely to have molecular testing compared to males [(OR: 1.29 (1.22-1.37); p < 0.001]. Compared to White patients, Black patients were less likely to have molecular testing [OR: 0.89 (0.81-0.97); p = 0.009] and Asians were more likely to undergo testing [OR: 2.22 (1.79-2.75); p < 0.001]. Hispanic patients were more likely to undergo molecular testing compared to non-Hispanics [OR:1.24 (1.02-1.52); p = 0.03]. Additionally, treatment with immunotherapy [OR: 1.86 (1.72-2.01); p < 0.001] and targeted therapy [OR: 2.29 (2.00-2.64); p < 0.001] were associated with significantly higher likelihood of having molecular testing. These results were also confirmed on a subgroup analysis of adenocarcinoma patients.

CONCLUSION:

In this analysis of a US-based real-world dataset of stage IV NSCLC patients, White race and female sex are associated with higher likelihood of having molecular test performed. The percentage of patients undergoing testing remains sub-optimal.

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The survival benefit of anti-HER2 treatment in the management of small (T1mic, T1a, T1b, T1c), node-negative HER2+ breast cancer.  

Johnson et. al. | Abstract #532 | Poster #304

**BACKGROUND:**

Limited compelling prospective and retrospective data regarding the added benefit of anti-HER2 therapy in the management of small, node-negative HER2-positive breast cancer (HER2+BC) exists, in part due to differences in outcome reporting, unmatched analyses, and a lack of head-to-head comparisons. As a result, national guideline committees find themselves unable to confidently recommend anti-HER2 therapy and clinicians are left to exercise clinical judgement on whether the use of anti-HER2 therapy should be considered for such patients.

**RESULTS:**

1,206 Patients met inclusion criteria

779 patients received trastuzumab with or without chemotherapy

We found a statistically significant improvement in both iDFS (HR 0.73, p = 0.01) and OS (HR 0.63, p = 0.027) on univariate analysis for those receiving anti-HER2 therapy. Similarly on multivariate analysis, iDFS (HR 0.75, p = 0.030) and OS (HR 0.61, p = 0.029) were improved in those who received therapy, regardless of tumor size.

Our three-arm univariate analysis involving no treatment (n = 427), trastuzumab monotherapy (n = 169), and combination therapy (n = 578) found that iDFS was significantly improved for both treatment arms compared to observation alone (p = 0.006), whereas OS trended towards significance in the treatment arms but did not reach this target (p = 0.061). No significant difference was noted between treatment arms.

**CONCLUSION:**

Our analysis found a statistically significant improvement in iDFS and OS when patients with small, node negative, HER2+BC received adjuvant anti-HER2 therapy with or without chemotherapy as compared to observation. From our univariate three-arm comparison, it appears that trastuzumab provides the majority of benefit to patients in terms of DFS, but this result is exploratory. Further investigation is warranted, including meta-analyses to better characterize the degree of benefit seen with anti-HER2 treatment. For now, this data adds to evidence suggesting added benefit with therapy over observation.
**RESULTS:**

Amongst the 160,888 patients with regional/metastatic prostate cancer, only 1.5% patients were enrolled in a clinical trial (n = 2,368).

For the entire cohort, clinical trial enrollment correlated with higher survival (HR: 1.19; p < 0.001) and lower survival for AAM men (HR: 0.85; p < 0.001) compared to white men after adjusting for other covariates.

On multivariable analysis, patients with worse ECOG performance status were associated with lower odds of clinical trial enrollment (p < 0.001). Relative to white patients, African-American men (AAM) also had lower odds of clinical trial enrollment (OR: 0.67; p < 0.001). For the entire cohort, clinical trial enrollment correlated with higher survival (HR: 1.19; p < 0.001) and lower survival for AAM men (HR: 0.85; p < 0.001) compared to white men after adjusting for other covariates. In the subgroup analysis of patients enrolled in clinical trials, AAM demonstrated similar survival to white patients (HR: 0.96; p = 0.95).

**BACKGROUND:**

Clinical trials can provide access to novel systemic agents and possible improved survival for men diagnosed with regional and metastatic prostate cancer. Although clinical trials should be accessible to all patient populations, racial disparities to enrollment of clinical trials and its outcomes remain an important unknown outcome. Herein, we sought to elucidate the racial disparities in clinical trial enrollment and survival amongst advanced prostate cancer patients from a large community-based medical oncology consortium.

**CONCLUSION:**

Although African-American men with regional/metastatic prostate cancer face barriers to clinical trial enrollment, racial disparities in survival appear to resolve for patients who enroll in clinical trials. Increased attention is needed to address barriers to communication and access to clinical trials.

**Diagnosed with advanced prostate cancer: A population-based cohort from national oncology practices.**

Kim et. al. | Abstract #5087 | Poster #270

BACKGROUND:

Patients with node-negative non-small cell lung cancer (NSCLC) whose tumors are completely resected account for approximately 17% of all patients with lung cancer, and disease recurrence occurs in approximately 1 in 5 of these patients. The lack of consensus on factors associated with risk of disease recurrence among node-negative NSCLC patients is a significant barrier to applying precision medicine strategies in this patient population. Clustering similar patients based on distances between various features of data is an emerging topic in precision medicine. Patient similarity networks represent a new model for clustering patients based on heterogeneous data, whereby any data type is converted into a similarity network by defining a similarity measure. The objective of this study was to examine the utility of patient similarity networks to identify NSCLC patients at higher risk of adverse outcomes.

RESULTS:

![83%](image1)

Patients in the network community enriched for renal disease and congestive heart failure have an increased risk of mortality.

![37%](image2)

Patients in the network community enriched for pulmonary disease have an increased risk of mortality.

![14%](image3)

After adjusting for comorbidity network community, male patients have an increased risk of mortality.

In the adjusted analyses, patients in the network community enriched for renal disease and congestive heart failure had an 83% increased risk of mortality (95% CI = 1.39-2.41). Patients in the network community enriched for pulmonary disease had a 37% increased risk of mortality (95% CI = 1.06-1.74) yet a lower risk of recurrence (HR = 0.5, 95% CI = 0.34-0.75). After adjusting for comorbidity network community, male patients had a 14% increased risk of mortality (95% CI = 1.02-1.28) and a 21% increased risk of recurrence (95% CI = 1.05-1.40) and black patients had a lower mortality risk (HR = 0.71, 95% CI = 0.58-0.86).

CONCLUSION:

Future studies applying patient similar networks to integrate additional diverse and high dimensional data types may afford more clarity in assigning risk of adverse outcomes.
**RESULTS:**

The prostate cancer cohort (#1) had 151,261 patients, of which 99,152 (65.6%) were attributed to sites. The percentage of Black patients being treated at the top ten sites ranged from 33.0% to 66.4%, with a median of 45.2% (see table). All ten sites had participated in an interventional cancer trial, and eight had participated in prostate cancer trials. Half of them were community, and half were academic sites. The abiraterone cohort (#2) had 1,267 patients, of which 1,174 (92.7%) were attributed to sites. Among the top ten sites the Black patient percentages ranged from 23.8% to 85.7%, with a median of 39.3%.

**CONCLUSION:**

In an analysis of 17 recent FDA drug registration trials for prostate cancer, Black trial participation ranged from only 1.4% to 6.2%, with a median of 3.0%. In contrast, Black patients being treated at the top sites in our data ranged from 33.0% to 66.4%, with a median of 45.2% (cohort #1). The percentages for the abiraterone cohort (#2) were similar, suggesting that even after applying trial criteria the Black patient percentages remain in the double-digits at top sites. Our results demonstrate that informed trial site selection could have a substantial positive impact on minority patient recruitment.
Identifying genetic factors of response and resistance to CDK4/6 inhibitors in metastatic HR+/HER2-breast cancer using real-world data.

Agrawal et al. | Abstract #1064 | Poster #442

**BACKGROUND:**

CDK4/6 inhibitors plus endocrine therapy are approved for treatment of HR+/HER2- metastatic breast cancer (MBC) and have shown to provide a significant progression free survival benefit over endocrine therapy alone. But not all patients benefit from this treatment and some develop resistance over time. The molecular mechanisms governing this resistance are poorly understood. We have developed a real world dataset that includes data elements from structured EMR tables as well as deeply curated unstructured data from BC patients (ConcertAI Genome360 BC Dataset) who have been treated with CDK4/6 inhibitors and have undergone DNA sequencing to identify somatic mutations. We have leveraged this linked clinical-genomics dataset to identify genetic drivers of resistance and response to CDK4/6 inhibitors.

**RESULTS:**

We identified 7 potential segments (similar groups of genes) which predicted response or resistance to CDK4/6 inhibitors. Here we present data on 3 such segments which are closely related. Loss of function mutations in RB1 were enriched in the non-responder population ($Z$ value = 2.33; $p$ value = 0.026; $N = 31$). This is consistent with previously reported findings. In addition, amplifications and gain of function mutations in MYC and associated genes were also significantly enriched in the non-responder population ($Z$ value = 2.71; $P$ value = 0.01; $N = 44$). Interestingly, loss of function mutations in TSC1/2 genes which are downstream of MYC were predictors of good response to CDK4/6 inhibitors ($Z$ value = 2.19; $P$ value = 0.036; $N = 30$), strengthening the role of the parallel MYC signaling pathway in resistance to CDK4/6 inhibitors.

**CONCLUSION:**

Using our Genome360 BC Dataset, we have identified genetic markers affecting response to CDK4/6 inhibitors. In addition to the known role of RB1 in resistance to CDK4/6 inhibitors, the MYC signaling pathway emerged as a strong candidate. Based on these results, patients with mutations in these pathways may benefit from addition of mTOR or PKL1 inhibitors to CDK4/6 inhibitors to overcome resistance and prolong their effect.
Evaluating the impact of performance status criteria on minority eligibility for oncology clinical trials.

**BACKGROUND:**
Restrictive criteria contribute to low enrollment in clinical trials. These criteria can also amplify health disparities by reducing the racial and ethnic diversity of the cohort. Many studies show that minority patients exhibit worse Eastern Cooperative Oncology Group (ECOG) performance status than white patients. Based on clinical trial data, some researchers have hypothesized that relaxing the ECOG criterion in clinical trial criteria could improve the diversity of the cohort. However, little research exists to measure ECOG’s impact on minority eligibility. Using Real-World Data (RWD), we evaluate whether relaxing the ECOG criterion monotonically increases the racial diversity of the cohort in oncology clinical trials.

**RESULTS:**
Relaxation in ECOG status led to no uniform change in the racial diversity of patients across the 16 trials. The limited changes we did observe were not statistically significant.

**CONCLUSION:**
Our findings suggest that improving diversity will require more than just relaxing ECOG restrictions, and a multi-faceted approach may be needed. Future research exploring the relationship between ECOG and diversity should control for potential confounders like age, gender, and comorbidities using multivariable models. Such research needs to also account for patients with unknown race and ECOG, which represented large parts of our study population. Such research could elucidate whether the phenomenon observed in the general population—that minority patients tend to have worse performance status than whites—holds true in the sub-population of oncology patients.

**Racial distribution of two representative clinical trials with varying ECOG values.**

<table>
<thead>
<tr>
<th>TRIAL</th>
<th>ECOG</th>
<th>INDICATION</th>
<th>COHORT SIZE</th>
<th>WHITE %</th>
<th>UNKNOWN %</th>
<th>NON-WHITE %</th>
</tr>
</thead>
<tbody>
<tr>
<td>BEYOND</td>
<td>≤ 4</td>
<td>Non-Small Cell Lung Cancer (NSCLC)</td>
<td>4341</td>
<td>60.45</td>
<td>28.54</td>
<td>11.01</td>
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<tr>
<td>BEYOND</td>
<td>≤ 3</td>
<td>NSCLC</td>
<td>4192</td>
<td>60.62</td>
<td>28.53</td>
<td>10.85</td>
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<tr>
<td>BEYOND</td>
<td>≤ 2</td>
<td>NSCLC</td>
<td>3279</td>
<td>60.26</td>
<td>28.67</td>
<td>11.07</td>
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<tr>
<td>BEYOND</td>
<td>≤ 1</td>
<td>NSCLC</td>
<td>2020</td>
<td>60.94</td>
<td>27.38</td>
<td>11.68</td>
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<tr>
<td>BEYOND</td>
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<td>NSCLC</td>
<td>626</td>
<td>62.78</td>
<td>25.72</td>
<td>11.5</td>
</tr>
<tr>
<td>CARTITUDE-5</td>
<td>≤ 4</td>
<td>Multiple Myeloma (MM)</td>
<td>3564</td>
<td>60.77</td>
<td>14.56</td>
<td>24.67</td>
</tr>
<tr>
<td>CARTITUDE-5</td>
<td>≤ 3</td>
<td>MM</td>
<td>3501</td>
<td>60.7</td>
<td>14.65</td>
<td>24.65</td>
</tr>
<tr>
<td>CARTITUDE-5</td>
<td>≤ 2</td>
<td>MM</td>
<td>3204</td>
<td>60.74</td>
<td>14.64</td>
<td>24.62</td>
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<td>CARTITUDE-5</td>
<td>≤ 1</td>
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<td>60.9</td>
<td>14.66</td>
<td>24.44</td>
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<td>MM</td>
<td>1081</td>
<td>62.44</td>
<td>14.99</td>
<td>22.57</td>
</tr>
</tbody>
</table>
Machine learning modeling of real-world primary resistance and hyperprogression in immune checkpoint inhibitor (ICI) treated advanced non-small cell lung cancer (aNSCLC) patients.10

Das et. al. | Abstract #e21127

BACKGROUND:
Many ICI-eligible patients display primary resistance (1º-res), with some experiencing hyperprogressive disease (HPD). Machine learning (ML) on real-world data (RWD) can improve our clinical and mechanistic understanding related to ICI response.

RESULTS:
The clinical model was superior at predicting HPD; the CG model was better at predicting 1º-res (AUROC = 0.67 for both). Total metastases (≥ 2) and lower levels of hemoglobin (HGB), and lymphocytes, higher ALP were risk factors for both HPD and 1º-res. Elevated WBC and bilirubin, higher heart rate, lower body temperature, and history of anti-inflammatory medications were risk factors for HPD. Non-ICI-based regimens, low TMB, lower PD-L1 expression, and mutations in EGFR or KEAP1 were risk factors for 1º-res. Mutation in KRAS was protective of 1º-res. In addition to PD-L1 and TMB, the models identified prior lung radiation, smokers, higher baseline comorbidities, and positive MMR status as predictive of lower risk of 1º-res from ICI but not in CT. STK11 mutation was predictive of higher risk of 1º-res from ICI vs. CT. Non-adenocarcinoma histology was predictive of higher risk of HPD from ICI vs. CT.

CONCLUSION:
ML on RWD generated evidence to support both established and emerging prognostic and predictive markers for ICI response.
Disparities in timely treatment among lung cancer patients\textsuperscript{11}.

BACKGROUND:
NSCLC is the leading cause of cancer-related deaths in the US. There are no federal standardized guidelines regarding timely treatment (TT) of NSCLC care and little is known regarding the sociodemographic differences in TT of anticancer therapies among NSCLC patients. This is particularly notable among Black Americans, who are less likely to receive lung cancer screening, more likely to be diagnosed with advanced or metastatic NSCLC, and less likely to receive NCCN-concordant targeted therapy relative to their white counterparts. The objective of this retrospective study is to assess racial differences in TT and related outcomes among patients with advanced or metastatic NSCLC (aNSCLC).

RESULTS:

79.1\% of Black aNSCLC patients did not receive TT. Descriptive analyses revealed 79.1\% of Black aNSCLC patients did not receive TT, as compared to 71.4\% of White aNSCLC patients. When controlling for associated confounding factors, Black aNSCLC patients had a 21.4\% less chance of receiving TT as compared to White patients, and the same was evident from the predicted probabilities of TT for Black vs. White aNSCLC patients. When evaluating institutional setting type, 76.1\% of community hospitals provided TT vs. 61.3\% of academic centers.

<table>
<thead>
<tr>
<th>BASELINE CHARACTERISTIC</th>
<th>PROPORTION WITH TT</th>
<th>ODDS RATIO</th>
</tr>
</thead>
<tbody>
<tr>
<td>Black (vs. White)</td>
<td>20.9% (28.6%)</td>
<td>0.786</td>
</tr>
<tr>
<td>Community (vs. Academic)</td>
<td>38.7% (23.9%)</td>
<td>1.83</td>
</tr>
</tbody>
</table>

CONCLUSION:
This real-world study shows Black aNSCLC patients were associated with treatment delay. While present findings suggest improving access to effective screening and timely access to NCCN-concordant targeted therapies may be used as a means through which to lessen NSCLC disparities, further investigation is required to assess how it may improve overall outcomes for minorities.
Comparison of DNA sequencing, immunohistochemistry, and in-situ hybridization techniques to determine HER2 status in metastatic breast cancer patients. 

Lal et al. | Abstract #e13045

**BACKGROUND:**

Limited studies exist comparing methods for HER2 status determination using real-world data (RWD). Results of metastatic breast cancer (MBC) patients with Next Generation Sequencing (NGS) within the ConcertAI Genome360 dataset with DNA sequencing were compared to the standard immunohistochemistry (IHC) or in-situ hybridization (ISH) or both IHC and ISH for HER2 status.

**CONCLUSION:**

RWD indicate a relatively high level of match rate among DNA sequencing, IHC, and ISH results in MBC patients. However, 13-20% of the combinations did not match. For these patients, mechanisms to reach consensus need to be explored to determine optimal treatments.

**RESULTS:**

The study sample included 252 patients (99% female, mean age [SD] of 62 [11.93]) with 382 test combinations as follows: 220 (58%) with DNA sequencing and IHC results, 127 (33%) with DNA sequencing and ISH results, and 35 (9%) with DNA sequencing and IHC and ISH results. Of the 220 combinations with DNA sequencing and IHC results, 15 were uniformly considered HER2+, 160 HER2-, and 1 equivocal, while 44 differed in the results, resulting in 80% match rate. Of the 127 combinations with DNA sequencing and ISH results, 14 were HER2+ and 96 HER2-, while 17 differed, resulting in 87% match rate. Of the 35 combinations with DNA sequencing and IHC and ISH, 3 were HER2+ and 26 were HER2-, while 6 differed, resulting in 83% match rate.
CancerLinQ® is a health technology venture focused on advancing cancer care quality and research. Launched in 2014, CancerLinQ’s vision is to enable the goal of truly learning from every patient with cancer. CancerLinQ accomplishes this by securely compiling, harmonizing, and analyzing vast amounts of electronic cancer data on such factors as patient and tumor characteristics, treatments, clinical outcomes, and long-term side effects. This real-world data is derived from the everyday care experiences of the more than 6.5 million patients seen in the 100+ cancer centers and oncology practices across the US that participate in the CancerLinQ network. Using sophisticated technology, data processing, and advanced analytics, CancerLinQ can identify trends and associations between myriad variables, thereby enabling physicians and researchers to test new hypotheses and rapidly apply those conclusions to improve care in real-world settings.