ASCO Annual Meeting

SCIENTIFIC EVIDENCE *Guide*

CancerLinQ Discovery®

2023

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ADVANCE DISCOVERY

LEARNING FROM *every patient* WITH CANCER.

Improved clinical outcomes and the future of patient care depend on learning from the experiences of every patient with cancer. 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 6.5 million patients in the CancerLinQ® network.

This powerful database can be used to uncover unseen patterns in patient characteristics and unlock actionable insights—***to advance precision oncology for better quality of care and accelerate cancer research.***

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 Discovery is available to the academic, non-profit, government, and life sciences research communities. Visit ***cancerlinq.org/solutions/researchers*** to learn more.

FOREWORD

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 advanced analytics and the power of real-world data (RWD) to improve cancer care and research. In 2017, CancerLinQ launched CancerLinQ Discovery®, now one of the largest sources of oncology RWD in the world. Since then, CancerLinQ Discovery data has been used extensively by researchers across the oncology ecosystem to advance knowledge and to improve patient care and the development of better anticancer therapies (see our scientific publications page at ***cancerlinq.org/scientific-publications***).

We are pleased to present this 2023 CancerLinQ Discovery Scientific Evidence Guide highlighting some of the important research using CancerLinQ data from the 2023 ASCO Annual Meeting. These include studies characterizing the tumor characteristics and treatment outcomes of patients with lung cancer, breast cancer, bladder cancer, gynecologic malignancies, and multiple myeloma, among others.

Some of the novel and diverse topics covered include: using generative AI to identify patients for trials; developing machine learning models to predict the risk of brain metastases for patients with early-stage non-small-cell lung cancer; identifying clinical predictors for shortened survival in patients experiencing severe adverse events following immunotherapy; and characterizing real-world outcomes in patients with metastatic triple-negative breast cancer treated with sacituzumab govitecan-hziy.

For more information about joining the CancerLinQ practice network or accessing CancerLinQ Discovery research datasets, visit ***www.cancerlinq.org***.

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Chief Medical Science Officer

CANCERLINQ *Abstracts*

Association between severe adverse event management and overall survival in patients treated with immune checkpoint inhibitor with advanced non–small-cell lung cancer[1]

NAIDOO ET. AL. | ABSTRACT #6604 | POSTER #96

BACKGROUND

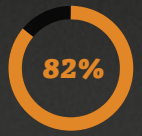
The impact of severe adverse event (sAE) management (mgmt) on clinical outcomes in cancer patients (pts) receiving immune checkpoint inhibitor (ICI) therapy has not been fully examined. We aimed to evaluate the association between mgmt of sAEs and overall survival (OS) in pts receiving ICIs for advanced non-small cell lung cancer (aNSCLC).

CONCLUSIONS

Pts with sAEs first managed with hospital admission or sAE treatment had shorter OS than those with no sAEs. No difference was observed for sAEs first managed with anti-cancer treatment interruptions. Findings suggest early treatment interruption for sAEs does not impact OS.

RESULTS

8.2 Months
Median [Q1-Q3] follow-up duration from ICI initiation



Most pts had advanced disease at initial diagnosis

84 Days
Median [Q1-Q3] time from ICI initiation to first sAE

Started ICI in first line

3,211 pts were identified (median [IQR] age 67 [13] years, 55.1% male). The most common ICI regimens in the first 3 lines were nivolumab (29.5%) and pembrolizumab + carboplatin + pemetrexed (29.1%). 8.6% of pts had at least one sAE, most often diarrhea (3.5%). Mgmt actions any time after first sAE included anti-cancer treatment interruptions [dose reduction (4.0%), hold (20.6%), discontinuation (2.2%)], sAE treatment [corticosteroids (71.8%), immunosuppressive drugs (2.5%)], hospital admission [hospitalization (57.4%), emergency department visit (24.6%)], and other/unknown (4.3%). Overall, median [95% CI] OS was 13.6 [12.6-14.6] months. Compared with pts with no sAEs, pts with sAEs whose earliest mgmt action was hospital admission (N=155) or sAE treatment (N=71) had a higher risk of all-cause mortality (adjusted HR [95% CI] 1.61 [1.38-1.88] and 1.53 [1.22-1.91], respectively). Pts with sAEs first managed with anti-cancer treatment interruptions (N=39) had similar risk of all-cause mortality (0.91 [0.66-1.25]) compared with pts with no sAEs.

The RESECT study: Factors associated with overall survival (OS) and relapse-free survival (RFS) among patients with stages I–III resected NSCLC without known EGFR mutations[2]

GRAY ET. AL. | ABSTRACT #8541 | POSTER #168

BACKGROUND

Approximately one-third of patients with Stages I–III resected non-small-cell lung cancer (NSCLC) do not survive 5 years from diagnosis. This retrospective observational study analyzed factors associated with OS and real-world (rw) RFS among Stage I–III NSCLC patients before the introduction of immuno-oncology (IO) treatment.

RESULTS

In the multivariable analyses (in which no Stage I patients with neoadjuvant or perioperative treatment were included), factors associated with both OS and rwRFS ($p<0.05$) were disease stage, race, ethnicity, year of diagnosis, ECOG performance status, and neoadjuvant treatment. Factors associated with OS ($p<0.05$), but not rwRFS, were age, sex, time from diagnosis to surgery, and type of surgery. Factors associated with rwRFS ($p<0.05$), but not OS, were geographic region, nodal status, and adjuvant treatment in Stage II and III patients but not Stage I patients.

CONCLUSIONS

This study identified several risk factors associated with OS and rwRFS, many of which are known. Notably, in this analysis, neoadjuvant treatment was associated with both improved OS and rwRFS in Stage II–III patients and was not evaluable in Stage I patients. However, adjuvant treatment was only associated with improved rwRFS, and only in Stage II–III patients. Based on these findings, there remains an unmet need for Stage I–III NSCLC patients. The recent introduction of IO treatment in this setting may help improve patient outcomes.

Site of metastasis (SoM) and its impact on clinical outcomes in 8 cancer cohorts[3]

GEORGE ET. AL. | ABSTRACT #6590 | POSTER #82

BACKGROUND

The prognosis of metastatic cancer is in general poor. This can be affected by several factors including age, histology, treatment choices & SoM etc.

CONCLUSIONS

The patterns of cancer metastasis and the absolute and relative prognosis for a particular SoM is dependent on the primary cancer type. Such insights from a large real-world data study can impact clinical decisions regarding the aggressiveness of treatment based on the primary cancer type as well as the metastatic site.

RESULTS

140K patients were included in this study of which 60K patients had a SoM. The distribution of SoM is dependent on the primary cancer type. For example, in breast & prostate cancer, bone metastasis accounts for 50-80 % of the metastatic cohort whereas it is only 8-21% in lung & melanoma. As expected, the overall values of OS/PFS were primarily governed by the primary cancer type (Table), but this analysis provides further interesting insights: 1. Within a cohort, there were significant differences in the prognosis of patients based on the SoM . Brain & liver had a poorer prognosis compared to the other SoM across most cohorts. 2. The relative prognosis for some SoM were dependant on the primary cancer type. For example, there was a very significant difference between the OS/PFS values in the breast cancer cohort when comparing brain vs bone as SoM. However, in the lung cancer cohort, this difference was less pronounced, and the trend was flipped. 3. For some cohorts the SSM for certain sites had a worse prognosis than the MSM. In breast cancer the OS of the brain & liver SoM was worse than the MSM. 4. The TTM is also dependent on the primary cancer and there is a correlation between the average TTM and the OS of the cohort.

Metastatic patient counts and outcomes (OS/PFS in years) for 4/8 cancer cohorts

	SSM	*Bone*	*Lung*	*Liver*	*Brain*	*MSM*
Primary Cancer Type (Mets/overall counts)	Count / OS (in yrs) / PFS (in yrs)					
Breast (12346 / 49361)	7110 / 5.17 / 1.5	3695 / 5.33 / 1.65	1372 / 5.84 / 1.6	613 / 3.05 / 0.91	361 / 2.35 / 0.71	5236 / 3.23 / 0.83
NSCLC (26667 / 52814)	15666 / 1.6 / 0.68	3285 / 1.19 / 0.54	5412 / 1.93 / 0.77	938 / 0.99 / 0.49	3797 / 1.54 / 0.68	11001 / 1.1 / 0.46
Melanoma (3220 / 10479)	1702/ 4.61 / 0.76	130 / 2.45 / 0.42	453 / 7.39 / 1.26	120 / 1.67 / 0.38	301 / 1.3 / 0.41	1518 / 2.01 / 0.38
Prostate (7087 / 10679)	5555 / 4.38 / 1.48	4470 / 4.25 / 1.44	137 / 6.13 / 2.46	48 / 3.35 / 1.19	14 / 0.22 / 0.19	1532 / 3.46 / 1.11

meetings.asco.org/abstracts-presentations/226782

Assessment of electronic health record (EHR) –based machine learning (ML) in predicting risk of brain metastasis among patients with early-stage non–small-cell lung cancer (eNSCLC)[4]

HONARVAR ET. AL. | ABSTRACT #2036 | POSTER #393

BACKGROUND

Among patients (pts) with eNSCLC, development of brain metastasis (BM) is a poor prognostic sign, but routine surveillance for BM is not recommended post-therapy. EHR-based ML algorithms may identify pts who would benefit from active brain MRI surveillance and/or treatment intensification in the early-stage setting.

CONCLUSIONS

An EHR-based ML model identified risk factors for developing BM among pts with eNSCLC and may identify pts who would benefit from active brain MRI surveillance and treatment intensification.

RESULTS

Among 7473 pts in 18 mos model, median age was 68.4 years (IQR 13.2), 50.5% were female, and 10.9% were black. Demographics were similar for 6863 pts in 24 mos model. 6.4% and 8.3% developed BM at 18 and 24 mos. Ability of GB, RF, and LR models to predict BM was similar with validation AUPRC of 0.109 at 18 mos and 0.137 at 24 mos. In the GB model, BM prevalence in high-risk vs. low-risk group was 10.3% vs. 3.1% at 18 mos and 13.4% vs. 4.4% at 24 mos. In both landmark models, N0 stage and surgery within 90 days after index diagnosis were protective against BM, while presence of EGFR targetable mutations, adenocarcinoma (AD) histology, higher platelets (PLT), and history of pneumonia were risk factors. A glucose-by-histology interaction was found: For pts with normal blood glucose (GLU), risk of BM was independent of histology, for pts with high GLU, AD conferred greater risk of BM.

Feature	*18-mos BM risk**	*24-mos BM risk**
Surgery	0.86 (0.61, 0.97)	0.86 (0.60, 0.99)
N0 stage	0.89 (0.69, 0.98)	0.87 (0.61, 1)
AD histology	1.14 (1, 1.45)	1.18 (1, 1.82)
EGFR exon 19 deletion or L858R	1.13 (1, 1.50)	1.15 (1, 1.53)
History of pneumonia	1.07 (1, 1.24)	1.10 (1, 1.43)
PLT > 330 vs < 205 10^3/mL	1.06 (1, 1.31)	1.07 (1, 1.32)
Interactions % BM	1.09 (1.05, 1.15)	
GLU: histology	GLU ≥ 107: (AD = 11.4, non-AD = 6.0); GLU < 107: (8.2, 8.8)	(14.4, 6.7); (10.9, 10.8)

** (mean OR, 95% CI)*

meetings.asco.org/abstracts-presentations/222667

Electronic health record (EHR)-based machine learning (ML) to predict disease recurrence after surgical resection of early-stage non-small cell lung cancer (eNSCLC)[14]

PISANO ET. AL. | ABSTRACT #6626 | POSTER #118

BACKGROUND

Surgical resection (SR) is a guideline-recommended definitive therapy for patients (pts) with eNSCLC. However, 30–50% pts develop disease recurrence (DR) within the first 5 years (yrs) after surgery. ML applied to routinely collected EHR data could facilitate timely identification of pts at risk of DR who would benefit from enhanced surveillance or initial treatment (Tx) intensification.

CONCLUSIONS

ML applied to structured and unstructured EHRs identified predictors of risk of DR at 2 yrs after surgery in eNSCLC and may identify high-risk pts who would benefit from enhanced surveillance plans and Tx intensification in the eNSCLC setting. The model indicated favorable outcome from adjuvant targeted therapies in EGFR mutated pts.

RESULTS

Among 3597 pts, median age was 68.3 yrs (IQR 12.5), 51.8% were female, and 8.6% were Black. 24.4% developed DR within 2 yrs. GB, RF, and LR models had similar ability to predict DR at 2 yrs with mean hold-out set AUPRC of 0.33. In GB model, DR prevalence at 2 yrs was 34% in the high-risk vs. 18% in the low-risk group in hold-out set. N0 stage, T stage < 3, receipt of adjuvant immune checkpoint inhibitor (ICI), and presence of EGFR mutations were protective against DR at 2 yrs, while history of anemia and congestive heart failure (CHF) were risk factors (Table). SHAP revealed a N stage-by-adjuvant therapy and a N stage-by-CHF interaction: benefit from adjuvant chemotherapy (CT) was limited to higher N stages, while adjuvant ICI was beneficial for all N stages. CHF was a risk factor for lower N stages but not for higher N stages.

Feature importance	*(Mean OR, 95% CI)*
Adjuvant ICI	0.78 (0.66, 0.92)
N-stage (0 vs >0)	0.80 (0.74, 0.92)
T-stage (< 3 vs ≥ 3)	0.84 (0.79, 0.88)
History of anemia	1.30 (1.18, 1.56)
History of CHF	1.16 (1.06, 1.28)
EGFR exon 19 deletions or L858R	0.94 (0.89, 0.97)

Interactions	*% DR at 2 yrs*
N-stage-by-CHF	N=0: (CHF = 33.7, no CHF = 20.4); N>0: (32.6, 31.1)
N-stage-by-adjuvant CT	N=0: (CT = 20.1, no CT = 21.4); N>0: (27.8, 33.9)

Enhancement in line of therapy (LoT) derivation from real-world data (RWD) from electronic health records (EHR) via integration of medical claims data[6]

AGRAWAL ET. AL. | ABSTRACT #6514 | POSTER #6

BACKGROUND

Clinical RWD derived from EHRs require identification of lines of therapy (LoT) which are typically not captured in EHR and must be abstracted from other clinical and medication data. EHR data has significant missingness which can be complemented with other data sources such as medical claims data. In this study, we demonstrate how our proprietary line of therapy algorithms for solid cancers show significant improvements when built using integrated EHR and claims data when compared to EHR data alone.

CONCLUSIONS

Deriving LoTs by integrating data from multiple data sources such as EHR and claims can significantly improve its accuracy.

RESULTS

The inclusion of medication data from claims significantly increased (7-22%) the number of patients for which LoTs could be extracted from the EHR data. Furthermore, we observed increases in number of lines per patient, length of lines and medications per line across cohorts. The distance between index date and 1st line start date was shortened in a subset (2-12%) of patients as a result. In a small fraction of cases, we even observed removal of false lines as some of the lines moved to adjuvant/neoadjuvant setting by filling in missing medication from claims. Overall, 7-39% patients in the LoT cohorts were impacted by addition of claims. Results for a few cancer types are presented in Table 1. We also compared the top LoTs derived from the integrated dataset against the standard of care for that cancer and observed very good concordance.

Impact analysis of claims integration on LoTs for 5/14 solid cancer cohorts

Cancer Indication	*Breast*	*Lung*	*Prostate*	*Pancreas*	*Renal*
# Pts with LoTs before claims integration	49826	53961	24309	12584	6639
# Pts with LoTs post claims integration	54557	57806	27191	13631	7478
# Pts added due to addition of claims	5034	3960	3019	1066	866
# False positive pts removed due to claims integration	303	115	137	19	27
# Pts with enhanced LoTs	18104	5421	9417	1461	1733
# Pts with decrease in days between index date and LoT start date	3680	1318	3018	308	442
# Total pts impacted	23441 (47.1%)	9381 (17.6%)	12436 (51.7%)	2527 (20.2%)	2626 (39.5%)

Development of natural language processing (NLP) models for extracting key features from unstructured notes to create real-world data (RWD) assets for clinical research at scale[7]

AGRAWAL ET. AL. | ABSTRACT #6607 | POSTER #99

BACKGROUND

RWD derived from Electronic Health Records (EHR) has detailed clinical information about patient journeys that can assist in clinical research, trial design, safety assessments etc. However, much of the vital information is locked away in unstructured clinical texts and needs to be converted to structured format to be useful for downstream applications. We demonstrate how this can be achieved at scale with a high degree of accuracy through NLP.

CONCLUSIONS

NLP models can be developed and used to enrich structured RWD data by extracting information from unstructured documents thus significantly improving the utility of this data for downstream applications. Given the high accuracy of these models and the scale at which they can be run, this can be a good alternative to human curation or can augment human curation enabling the creation of very large-scale datasets for clinical research.

RESULTS

The NLP models significantly improved the fill rate of key clinical variables and were able to extract the information from clinical notes with high accuracy (Table). For some variables, all or most of the data was extracted via NLP. Metastatic status via NLP included distant metastasis, locally advanced disease and no metastasis whereas in the structured data, only data for distant metastasis was present. In the case of Performance Status (PS), NLP significantly increased longitudinal capture, thus increasing the density of this variable per patient.

Performance of NLP models and their contribution to enriching structured RWD

NLP Field (# of patients = 98676)	*Stage at Dx*	*T Stage at Dx*	*N Stage at Dx*	*M Stage at Dx*	*NSCLC / SCLC*	*Tumor Histology*	*Tumor Grade*	*Meta-static Status*	*Metastatic Site*	*Lung Cancer Surgery*	*PS*
# of unique patients in RWD	57065	50139	51897	55035	0	10534	2771	34067	31510	0	70773
# of unique patients in RWD-NLP	83864	66138	66724	66593	88795	94677	56662	92627	47004	22844	82679
% contribution from NLP	32	20.9	22.2	17.4	100	88.9	95	63.2	33	100	58*
Precision/ Recall	0.92/0.87	0.92/0.83	0.89/0.85	0.9/0.81	0.98/0.91	0.87/0.88	0.91/0.90	0.88/0.87	0.94/0.97	0.87/0.67	0.97**

** Calculated based on patients where at least 1 PS value was added by NLP. ** Accuracy.*

meetings.asco.org/abstracts-presentations/221843

Real-world response endpoints in patients with mNSCLC treated with chemotherapy across real-world datasets[8]

MCKELVEY ET. AL. | ABSTRACT # 6595 | POSTER #87

BACKGROUND

Response Evaluation Criteria in Solid Tumors (RECIST) based response rate (RR) is used for efficacy evaluation in clinical trials and relies on imaging data collected at specified timepoints for uniform assessment. In routine clinical practice, the method and timing of response assessment can vary, and imaging data from electronic health records (EHR) and other real world (rw) sources may not be available. Friends of Cancer Research formed a multi-stakeholder partnership to assess available data attributes to measure response across RWD sources to inform development of a consistent method for measurement.

CONCLUSIONS

The rwRR among pts with mNSCLC calculated using the clinician assessment was relatively consistent across all RWD sources, with consistent trends in time to event endpoints. While variability in the availability of data components to assess response was observed, the demonstrated feasibility of response endpoints based on clinician assessment suggests further exploration may inform drug effectiveness evaluation with RWD.

RESULTS

The availability of data components varied across RWD sources (Table). Images were not widely accessible, thus response was analyzed using clinician response assessments (median proportion of pts evaluable, 77.5%). Of these assessments, the majority relied on imaging interpretation. The median rwRR was 46% with a median rwDOR of 119 days. The table provides median rwTTD, rwTTNT, and rwOS across data sources.

Group	*Pts Evaluable for rwR (Pts Ev) by Images*	*Pts Ev by Radiology Reports*	*Pts Ev by Clinician Response Assessment*	*rwRR*	*Median rwDOR, days (95% CI)*	*Median rwTTD, days: Responders /Non-Responders (R/NR)*	*Median rwTTNT, days: R/NR*	*Median rwOS, days: R/NR*
A	3.5%	73%	79.5%	42%	115 (86, 199)	142/69	200/100	375/245
B	0.5%	55%	80.5%	53%	133 (108, 182)	128/84	209/98	464/314
C	40.5%	77%	77.5%	46%	146 (102, 210)	147/63	234/93	832/213
D	0%	0%	74%	40%	100 (74,-)	105/70	140/115	614/414
E	79.5%	79.5%	76%	38%	119 (98, 231)	132/48	235/93	474/184
F	0%	66.5%	69%	52%	182 (147, 287)	99/43	219/109	436/353
F	0%	85.5%	88.3%	49%	105 (7, 672)	112/21	198/61	392/86

** n=200 pts except G: n=180.*

meetings.asco.org/abstracts-presentations/221825

Pitfalls with analyses of real-world data: A look at ASCO's CancerLinQ Discovery Multiple Myeloma dataset[9]

SHOU ET. AL. | ABSTRACT #e20033

BACKGROUND

Real world data (RWD) are increasingly used in oncology research. Yet, a big limitation of RWD is missing data, potentially generating misleading conclusions. Methods for handling missing data include excluding patients with missing variables, using machine-based or statistically-imputed values, or using proxies (surrogates). Another limitation deals with excluding deaths at time zero, which may lead to misleading conclusions when analyzing survival of patients with aggressive cancers. This work highlights the impacts data exclusion, variable surrogacy, and death at time zero have on survival analysis results.

RESULTS

Despite the strong, positive correlation between recorded MM diagnosis date and date of first anti-myeloma therapy, there was a statistically significant difference in survival of MM patients with a known vs. presumed date of diagnosis (median OS 115 vs. 45 months, HR 2.54, 95% CI 2.41-2.69, p< 0.001). Dropping vs. including deaths within one month of diagnosis resulted in a marked difference (i.e., nearly 1 year) in median OS from the date of diagnosis of any SPM (113 vs. 103.5 months) as well as sAML (41 vs. 30.5 months).

CONCLUSIONS

Although RWD hold promise, oncologists must be aware of common pitfalls in survival analyses: missing data, variable surrogates, and deaths at time zero being dropped. Patients with a recorded date of MM diagnosis appear to be fundamentally different from those who don't have a date of diagnosis but do have a date of anti-myeloma therapy recorded. For aggressive malignancies, excluding patients who died at time zero can lead to over-estimation of survival. Adding a small constant (0.5) to the time variable can enable the inclusion of patients who die quickly after their cancer diagnosis. In conclusion, when utilizing RWD to guide clinical decision making, it is important to be aware of common threats to data validity, which can produce misleading results.

meetings.asco.org/abstracts-presentations/222477

Identification of biomarkers for early progression in muscle invasive bladder cancer (MIBC) using real-world data[10]

SINGH ET. AL. | ABSTRACT #e16568

BACKGROUND

MIBC accounts for ~25% of all newly diagnosed bladder cancers and is associated with a high rate of recurrence despite radical treatment. The time to progression (TTP) can vary significantly between patients and can affect their prognosis. We leveraged a real world clinico-genomics database to classify patients as early vs late progressors, understand its impact on their outcomes and identify genetic drivers of early progression.

CONCLUSIONS

Using our Genome360 bladder dataset, we have identified prognostic biomarkers for early progression in MIBC. This may provide clinicians with a tool to identify and modify treatment for a subset of MIBC patients who are at risk of early progression on standard of care therapies.

RESULTS

The TTP exhibited a bimodal distribution with a break at around 500 days, so we chose this as the cut-off to define early (N = 203) vs late progressors (N = 51). As expected, there was a significant difference in the median PFS of early vs late progressors (0.62 vs 2.41 years ($p < 1e-6$)). The OS was also significantly different (1.98 vs 4.36 years ($p = 6e-6$)). We further identified mutations in 6 biomarkers which were enriched in early vs late progressors. These were CDK12 ($p = 0.05$), EGFR ($p = 0.034$), LRP1B ($p = 0.05$), MET ($p = 0.045$), PTEN ($p = 0.026$) and SMAD4 ($p = 0.047$). These patients were primarily treated with platinum-based therapies +/- gemcitabine/PD-L1 therapies in-line with MIBC treatment guidelines. The identified driver genes activate PI3K-AKT-MTOR, JAK-STAT3, b-catenin and ERK pathways which are known to interfere with the mechanism of action of platinum-based therapies, thus potentially forming the basis of early progression.

Evaluating clinical trial inclusion/exclusion criteria from claims using generative artificial intelligence[11]

MUELLER ET. AL. | ABSTRACT #e13566

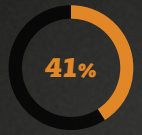
BACKGROUND

Increasing enrollment in oncology clinical trials (CTs) requires identification of trial-eligible patients from routine health data. However, identification of CT-eligible patients is limited by inadequate access to EHR and its relevant clinical features to evaluate inclusion/exclusion (I/E) criteria in large populations. Artificial Intelligence (AI) applied to large-scale administrative claims may accelerate pre-screening of large patient cohorts against common I/E criteria related to stage and performance status (PS).

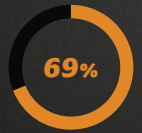
CONCLUSIONS

Generative AI can leverage claims-only data to evaluate common pre-screening I/E criteria in large cohorts and outperforms models based on limited diagnosis codes. Rather than building one model per criterion per indication, Generative AI enables a systematic and reliable solution that can be readily scaled in future large-scale CT screening.

RESULTS



Were confirmed stage IV at baseline



Had good PS

Among 92,895 patients, 48,331 (52%) were women, 63,620 (68%) were ≥65 years old, 54,495 (59%) were White, and 6,603 (7%) were Black. 38,229 (41%) were confirmed stage IV at baseline and 64,177 (69%) had good PS. In the test set predicting good PS, area under the receiver operating characteristic curve (AUROC) was 0.8 and under the precision-recall curve (AUPRC) was 0.89 for the Generative AI model. This corresponded to an Equal Error Rate (EER) operating point with good precision and recall (both 0.82). Performance metrics for the stage IV endpoint were also acceptable (AUROC 0.84, AUPRC 0.87, EER operating point 0.77). Comparator stage IV precision was 0.73 and recall was 0.47.

meetings.asco.org/abstracts-presentations/224889

Real-world outcomes in patients (pts) with metastatic triple-negative breast cancer (mTNBC) treated with sacituzumab govitecan (SG) in 2L+ in the United States (US)[12]

KALINSKY ET. AL. | ABSTRACT #e18879

BACKGROUND

Pts with mTNBC have poor prognosis and limited treatment options. SG is an anti—Trop-2 antibody-drug conjugate approved in multiple countries for pts with mTNBC who received at least 1 prior systemic therapy and in the US for pts with pretreated HR+/HER2- mBC. In the pivotal phase 3 ASCENT study (NCT02574455), SG demonstrated superior efficacy over single-agent chemotherapy and a manageable safety profile in pts with safety profile in pts with mTNBC (Bardia A, et al. *NEJM*. 2021). This study is, to our knowledge, the first to describe real-world treatment patterns and dosing with SG and its impact on clinical outcomes in pts with mTNBC in the US.

CONCLUSIONS

Pts who were treated with SG in routine clinical practice were older, more ethnically diverse, and presented with worse performance status than pts enrolled in the ASCENT trial but demonstrated a similar survival benefit. The proportion of pts treated with 2L SG increased from 2020 to 2022, reflecting an expected dynamic of post approval drug uptake in routine practice.

RESULTS

In total, 230 pts met the eligibility criteria and were included for analysis. All pts were female; 64% were White and 26% Black; median age was 60 years (IQR, 49-69); 71% of pts presented with ECOG performance status ≤1; 71% had visceral metastases and 7% had brain metastases at baseline. The median time from mBC diagnosis to SG treatment initiation was 11.8 months (IQR, 7.6-19.2). Most pts (66%) were treated in a community setting; 34%, 28%, 19%, and 20% of pts were treated with SG in the 2L, 3L, 4L, and 5L+ setting, respectively. Between 2020-2022, there was a trend in the distribution of SG use shifting to earlier line settings, see Table. Median starting dose was 10 mg/kg (IQR, 9.8-10.1). Median follow-up duration was 7.2 months (IQR, 3.9-11.1). Median rwOS (95% CI) from index date was 10 months (8.3-11.1) among all pts. Median rwOS (95% CI) was 13.9 months (9.79-not estimable) and 8.4 months (7.7-10.3) among pts treated with SG in 2L and in 3L+ setting, respectively. Analyses on real-world patterns of SG use are ongoing and additional results will be provided.

SG use by line of therapy by index year

n (%)	*2020*	*2021*	*2022*
Second-line	21 (21)	44 (45)	12 (36)
Third-line	27 (27)	26 (27)	11 (33)
Fourth-line	24 (24)	13 (13)	6 (18)
Fifth-line+	28 (28)	14 (14)	4 (12)

meetings.asco.org/abstracts-presentations/224165

Treatment patterns and outcomes among locally advanced cervical cancer patients receiving concurrent chemoradiotherapy[15]

COUTINHO ET. AL. | ABSTRACT #e17511

BACKGROUND

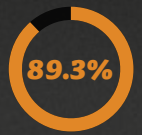
Concurrent chemoradiotherapy (CCRT) is standard treatment for patients with locally advanced cervical cancer (LACC). However, little is known on the real-world treatment patterns and outcomes among LACC patients. This study evaluated patient characteristics and treatment patterns of LACC patients, and real-world outcomes among patients receiving CCRT as the first treatment after diagnosis (CCRT-first) in US academic and community settings.

CONCLUSIONS

In US clinical practice during 2010-2018, most LACC patients received CCRT as the first treatment after diagnosis. The high proportion of patients who develop persistent disease after CCRT indicates a need for improved first treatment options.

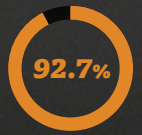
RESULTS

1.6 Months
Median rwTOT of the 229 CCRT-first patients



Had squamous cell histology

Had stage III disease



Had no evidence of performance status impairment,

Overall, 300 patients with LACC were included. At LACC diagnosis, median age of patients was 51 years, 53.7% were White, 30.0% were Black, 48.0% were peri/postmenopausal, 50.3% were treated in community settings, and 21.7% had only public insurance (11.0% Medicaid, 10.7% Medicare; 56.3% had no documentation of insurance). Distributions were similar among CCRT-first patients. First treatment after diagnosis included CCRT (N=229), surgery (N=28), systemic therapy (N=11), and radiation therapy alone (N=5). 27 were untreated, and 29 patients received CCRT after another therapy. Of the 229 CCRT-first patients, median (95% CI) rwTOT was 1.6 (1.4-1.7) months; 78.2% received cisplatin within CCRT, and median duration of cisplatin treatment was 35 days; 28.4% received a systemic therapy after CCRT, and 11.8% further initiated a second systemic therapy. 27 patients had recurrent disease after complete response (median rwRFS not reached). 179 patients had persistent disease after CCRT, among whom median (95% CI) rwPFS was 29.7 (16.9-59.3) months from CCRT start.

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Electronic health record (EHR) and genomics-based machine learning (ML) to predict therapeutic effectiveness among patients with hormone-receptor positive (HR)+/HER2- advanced breast cancer (aBC)[5]

HATHI ET. AL. | ABSTRACT #e13574

BACKGROUND

Patients (pts) with HR+/HER2- aBC may eventually become resistant to endocrine therapies and CDK4/6 inhibitors (CDK4/6i). ML algorithms on EHR linked with NGS data may enable more accurate predictions of therapeutic resistance and identify clinicogenomic (CG) risk factors.

CONCLUSIONS

ML on EHR linked with NGS data enables identification of high-risk pts and multimodal predictors of CDK4/6i resistance among women with HR+/HER2- aBC, identifying both known and undescribed interactions between clinical and genomic risk factors as well as co-alteration risk factors.

RESULTS

Among 624 pts (CDK4/6i treated = 519) with median age = 62.5 years and 10.5% black, 46.8% developed TP. The test cumulative dynamic ROC-AUC in the best-performing XGB model was 0.68. The precision at 180 days (%TP = 27) was 40%. The 180-day cumulative incidence of TP in low- and high-risk groups was 11.6% vs 37.7%. Higher line number, lower hemoglobin (HGB), higher alkaline phosphatase (ALP), presence of liver metastasis, and history of thoracic radiation were clinical risk factors. Genomic risk factors were FGF aberrations, alterations in TP53 and in genes within the MAPK, cell cycle, and ESR pathways, and co-alterations in the PIK3CA+TP53, and MAPK+ESR pathways. ALP-by-TP53 interaction was found. ALP level was a risk factor in TP53-wildtype (wt) but not in TP53-mutant (mut) pts.

TP Risk Predictors	*Mean HR (95% CI)*
Line number (≥ 2 vs 1)	1.39 (1.12, 1.85)
HGB (≥ 13.5 vs 11.5)	0.75 (0.55, 0.96)
ALP (u/L) (≥ 121 vs <69)	1.18 (1.04, 1.39)
History of thoracic radiation	1.11 (1.0, 1.31)
TP53 (wt vs mut)	1.47 (1.35, 1.63)
MAPK pathway	1.33 (1.22, 1.50)
FGF aberrations	1.10 (1.0, 1.19)
ESR signaling	1.09 (1.05, 1.15)
Cell cycle pathway	1.09 (1.02, 1.24)
PIK3CA + TP53	1.08 (1.0, 1.35)
MAPK + ESR signaling	1.08 (1.0, 1.16)

meetings.asco.org/abstracts-presentations/219631

A real-world study of US patients with metastatic ovarian, fallopian tube, and peritoneal cancer (mOFPC) using integrated electronic health records (EHR) and claims datasets[15]

AVINASH ET. AL. | ABSTRACT #e17548

BACKGROUND

Ovarian cancer is the most lethal gynecologic cancer. Detailed epidemiologic descriptions from a real-world database of a large population of ovarian and related cancer patients can provide insights into the characteristics, treatment patterns, and outcomes of these patients, and could serve as a useful benchmark while developing new therapies.

CONCLUSIONS

This study describes the characteristics of a large US real-world cohort of mOFPC patients. Here we have presented data on the overall cohort, but further analysis of outcomes stratified by treatment arms, biomarkers and histology can be performed to better inform best treatments for specific sub-cohorts.

RESULTS

The top 5 histologies and biomarkers tested in this mOFPC cohort are presented in Table. The median OS from start of 1st LoT for this cohort was 2.45 years. The median TTD and TTNT across all 1st line therapies were 2.5 months and 5.5 months respectively. Top 2 treatments given as 1st LoT after metastatic diagnosis are also presented in Table. Chemotherapy (cis/carboplatin + pacli/docetaxel) and chemotherapy + bevacizumab were the most common 1st LoTs and there was no difference in the OS of patients treated with these two LoTs.

meetings.asco.org/abstracts-presentations/223435

mOFPC cohort characteristics

Histology	*Counts (%)*
Serous / Clear Cell / Endometrioid / Mucinous / Other	2971 (47.76) / 212 (3.41) / 181 (2.91) / 137 (2.20) / 2720 (43.72)
Biomarkers	***Tested / Tested Positive***
BRCA1	1501 / 272
BRCA2	1414 / 170
ESR1	903 / 627
TP53	661 / 354
PGR	589 / 238
Top 2 treatments - 1st LoT (8308 patients with systemic anti-cancer therapies after metastasis)	***Counts***
Cis/Carboplatin + Pacli/Docetaxel	3297
Cis/Carboplatin + Pacli/Docetaxel + Bevacizumab	457

Biomarker testing and treatment patterns in US patients (pts) with advanced/ metastatic non-small cell lung cancer (NSCLC) harboring MET amplification[16]

RYDER ET. AL. | ABSTRACT #e21057

BACKGROUND

Limited published evidence exists on pts with advanced stage NSCLC harboring MET amplification (METamp), a rare oncogenic driver. We report here real-world biomarker testing and treatment patterns for these patients.

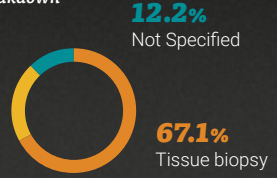
CONCLUSIONS

In this cohort of pts identified in a US community oncology setting, biomarker screening even for rarer genetic alterations occurred. Concomitant genetic alterations to METamp were infrequent except for alterations of EGFR and KRAS. The frequency of pts with high level of METamp in the cohort may explain the lower frequency of other biomarkers, as high level of amplification indicates a cleaner MET profile. Overall MET inhibitor treatment was not common. Screening for novel and rare biomarkers such as METamp as a primary or secondary oncogenic driver is becoming increasingly important to enable efficacious targeted treatment.

RESULTS

Of 8,454 pts with lung cancer with minimum 1 molecular test including *MET*, 164 had *MET*amp.

Pts testing breakdown



Of 127 pts tested for PD-L1 were positive

At least 64.5% of pts were highly MET amplified (either gene copy number ≥8 or by liquid biopsy ++, +++). Other mutations screened for were ALK, ROS1 and EGFR (99.4%, 98.2% and 97.6%), with oncogenic ALK, ROS1 fusions and activating EGFR mutations in 0.6% and 13.1%, respectively. BRAF and KRAS were less frequently screened for (90.2% and 87.2%), with potential oncogenic alterations in 2.0% and 12.6%. Of 127 pts tested for PD-L1 (by immunohistochemistry), 63.0% were positive, and 72.5% had tumor proportion score ≥50. Eighteen pts had METamp detected after receiving an EGFR tyrosine kinase inhibitor (TKI), indicating METamp as a secondary oncogenic driver. RB1 loss and MYC amplification, as potential mechanisms of MET inhibition resistance, were not frequently screened for (30.5% and 46.3%). RB1 loss was identified in 2.0% and MYC amplification in 15.8%. Next generation sequencing was the most frequent diagnostic used overall. A total of 144 pts (87.8% of 164 pts) received first-line (1L) anticancer therapy; platinum-based chemotherapy 57/144 (39.6%), immune-checkpoint inhibitors 50/144 (34.7%) or EGFR TKI monotherapy 24/144 (16.7%), other 2/144 (1.4%) and MET TKIs (mainly crizotinib) were used in 11/144 pts (7.6%) in 1L, 14/78 (17.9) in second line and 7/42 (16.7%) in third line.

meetings.asco.org/abstracts-presentations/218979

Treatment outcomes in patients (pts) with advanced/metastatic non-small cell lung cancer (NSCLC) harboring MET amplification as a secondary oncogenic driver[17]

RYDER ET. AL. | ABSTRACT #e21056

BACKGROUND

There is limited published evidence on the treatment outcomes of pts with oncogene driven NSCLC who have developed resistance to targeted therapies or novel therapies such as immune checkpoint inhibitors (ICIs) and have MET amplification (METamp). METamp has been identified as a secondary driver of EGFR TKI resistance. We report here on real-world (rw) outcomes for these pts.

CONCLUSIONS

METamp as a secondary driver of resistance is a new target for systemic therapy in pts with EGFR-mutant NSCLC who have developed resistance to EGFR TKIs. Overcoming this resistance using combinations with MET inhibitors is currently under investigation in several clinical trials. The analyses reported here suggests that the treatments available and current standard of care result in poor outcome for pts with METamp, highlighting the high medical unmet need in this population.

RESULTS

Subgroup 1

2.2 Months
Median rw progression-free survival

Rw overall response rate

In subgroup 1, 35 pts had METamp detected (21.3%) after disease progression on a targeted therapy or ICIs (EGFR TKI n = 17, ICIs n = 11, other n = 7). Of those pts, 27 received a subsequent systemic therapy after disease progression. The rw overall response rate (ORR) was 18.5% (95% CI: 6.3, 38.1), the median rw progression-free survival (PFS) was 2.2 months (95% CI: 1.6, 4.2) and the median overall survival (OS) from start of the subsequent therapy was 11.3 months (95% CI: 3.4, 21.3). In subgroup 2, 17 pts had METamp detected after disease progression on an EGFR TKI (erlotinib or afatinib n = 13, osimertinib n = 4). Of those pts, 15 received a subsequent systemic therapy after disease progression. The rw-ORR was 13.3% (95% CI: 1.7, 40.5), median rw-PFS was 2.1 months (95% CI: 1.1, 4.6), and median OS from start of the subsequent therapy was 8.5 months (95% CI: 1.7, 15.2).

AUTHORS

01 Abstract #6604. Jarushka Naidoo, Douglas Buckner Johnson, Charlotte Doran, Yuexi Wang, Yan Zhang, Trong Kim Le, Sari Hopson, Brian Dreyfus, Lincy S. Lal, Charmy Vyas, Shay Goldstein, Zara Izadi; Beaumont RCSI Cancer Center, Dublin, Ireland, Vanderbilt University Medical Center, Nashville, TN, ConcertAI, Cambridge, MA, Bristol Myers Squibb, Princeton, NJ, Bristol-Myers Squibb, Princeton, NJ

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03 Abstract #6590. Rohini George, Neeraj Singh, Laura Vidal, Ewa Hajek, Dorota Skalska, Kamal S. Saini, Smita Agrawal; ConcertAI, Bengaluru, Karnataka, India, Labcorp Drug Development, Burlington, NC, Labcorp, Warsaw, Poland, Labcorp Oncology, Durham, NC

04 Abstract #2036. Hossein Honarvar, Deep K Hathi, Ravi Bharat Parikh, Rahul K Das; ConcertAI, Cambridge, MA, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA

05 Abstract #6626. Steven Pisano, Hossein Honarvar, Ravi Parikh, Rahul Das; ConcertAI, Cambridge, MA, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA

06 Abstract #6514. Smita Agrawal, Avinash P B, Rohini George, Neeraj Singh, Megha Soni, Sangavai Chakkrapani, Vandana Priya, Vivek Prabhakar Vaidya; ConcertAI, Bengaluru, Karnataka, India

07 Abstract #6607. Smita Agrawal, Rohini George, Vivek Prabhakar Vaidya, Sangavai Chakkrapani, Rambaksh Prajapati, Srikanth Tankala, Dhaval Parmar, Vinay Phani Santosh Lakkimsetty, Tapasya Bhardwaj, Ashwani Ashwani, Emma Mendonca, Babu Narayanan, Krishna Kumar Swaminathan, Pranay Mukherjee; ConcertAI, Bengaluru, Karnataka, India, ConcertAI, Bengaluru, India, Syneos Health, Bengaluru, India, Merck & Co., Inc., Pune, India, Self, Bengaluru, India

08 Abstract #6595. Brittany Avin McKelvey, Elizabeth Garrett-Mayer, Andrew J. Belli, Thomas D. Brown, Jessica Dow, Janet L. Espirito, Paul Kluetz, Xinran Ma, Andrea McCracken, Pallavi Shruti Mishra-Kalyani, Yanina Natanzon, Danielle Potter, Donna Rivera, Hillary Stires, Mark Stewart, Jeff Allen; Friends of Cancer Research, Washington, DC, American Society of Clinical Oncology, Alexandria, VA, COTA Inc, Boston, MA, Syapse, San Francisco, CA, Tempus Labs, Inc., Chicago, IL, Ontada, Irving, TX, Oncology Center of Excellence, U.S. Food and Drug Administration, Silver Spring, MD, Flatiron Health, New York, NY, Guardian Research Network, Spartanburg, SC, US Food and Drug Administration, Ellicott City, MD, ConcertAI, Cambridge, MA, IQVIA, Horsham, PA, Oncology Center of Excellence, Office of the Commissioner, U.S. Food and Drug Administration, Silver Spring, MD

09 Abstract #e20033. Karen J Shou, Jennifer A Thornton, Kevin Sunderland, Christin DeStefano; Walter Reed National Military Medical Center, Bethesda, MD, David Grant USAF Medical Center, Fairfield, CA

10 Abstract #e16568. Neeraj Singh, Rohini George, Smita Agrawal; ConcertAI, Bengaluru, Karnataka, India

11 Abstract #e13566. Judith Mueller, Ravi Bharat Parikh, Andrew Noble; ConcertAI, Cambridge, MA, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA

12 Abstract #e18879. Kevin Kalinsky, Laura Spring, Clinton Yam, Aliki Taylor, Nikoleta Sjekloca, Alpana Kaushiva, Catherine Lai, Ioanna Ntalla, Rita Nanda; Winship Cancer Center of Emory University, Atlanta, GA, Massachusetts General Hospital Cancer Center and Harvard Medical School, Boston, MA, MD Anderson Cancer Center, Houston, TX, Gilead Sciences Europe Ltd., Stockley Park, United Kingdom, ConcertAI, Cambridge, MA, Gilead Sciences Inc., Foster City, CA, University of Chicago Medical Center, Chicago, IL

13 Abstract #e17511. Francesca Coutinho, Mugdha Gokhale, Charlotte Doran, Matthew Monberg, Karin Sayuri Yamada, Lei Chen; ConcertAI, Cambridge, MA, Merck & Co., Inc., Rahway, NJ

14 Abstract #e13574. Deep K. Hathi, Steven Pisano, Hossein Honarvar, Ravi Bharat Parikh, Rahul K. Das; ConcertAI, Cambridge, MA, Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA

15 Abstract #e17548. Avinash P B, Gabriel Funingana, Neeraj Singh, Rohini George, Anna Sowa, Sangavai Chakkrapani, Vandana Priya, Vivek Prabhakar Vaidya, Laura Vidal, Kamal S. Saini, Smita Agrawal; ConcertAI, Bengaluru, Karnataka, India, Cambridge University Hospitals NHS Foundation Trust, Alexandria, United Kingdom, LabCorp, Burlington, NC, Labcorp Drug Development, Burlington, NC, Labcorp Oncology, Durham, NC

16 Abstract #e21057. Alex Ryder, Dina Oksen, Emmanuelle Boutmy, Yuexi Wang, Alnecia R. Nisbett, Christopher Stroh, Andreas Johne; West Cancer Center & Research Institute, Germantown, TN, the healthcare business of Merck KGaA, Darmstadt, Germany, ConcertAI, Memphis, TN, ConcertAI, Cambridge, MA, Cambridge, MA

17 Abstract #e21056. Alex Ryder, Dina Oksen, Emmanuelle Boutmy, Barbara Ellers-Lenz, Christopher Stroh, Niki Karachaliou; West Cancer Center & Research Institute, Germantown, TN, the healthcare business of Merck KGaA, Darmstadt, Germany, Merck KGaA, Darmstadt, Germany, Global Clinical Development, the healthcare business of Merck KGaA, Darmstadt, Germany

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