206P

WAYFIND-R: A global, real-world database of patients (pts) with a solid tumour profiled with next-generation sequencing (NGS)

Jean-Yves Blay,[1] Allan Hackshaw,[2] Christophe Le Tourneau,[3] Jan Geissler,[4] Ana Ferro,[5] Erika Schirghuber,[6] Olga Skatkova,[6] Rodrigo Dienstmann[7]

[1]Centre Léon Bérard, Lyon, France;
[2]UCL Cancer Institute, London, UK;
[3]Institut Curie, Paris, France;
[4]Patvocates, Munich, Germany;
[5]Roche Products Limited, Welwyn Garden City, UK;
[6]F. Hoffmann-La Roche Ltd, Basel, Switzerland;
[7]Oncoclínicas Precision Medicine, Oncoclínicas Grupo, São Paulo, Brazil

Introduction

- WAYFIND-R is a global, multicentre, prospective pan-cancer registry collecting long-term data from pts diagnosed with a solid tumour profiled with any NGS test used in routine care.[1] The goal is to advance precision medicine by providing high-quality real-world data to researchers internationally.[2]

Methods

- WAYFIND-R data are electronically collected into a centralised database with standardised forms and high-quality data management procedures. To ensure reliability/accuracy and a fit-for-purpose data source, data are periodically evaluated.
- Pt, tumour, biomarker and NGS data as well as molecular tumour board (MTB) decisions are collected at enrolment (baseline) and treatment and outcome data at follow-up visits, routinely performed according to current guidelines and/or local standards of care (**Figure 1A**).
- Enrolment began in September 2020. Of the 2,115 pts enrolled in WAYFIND-R (31 July 2023); 1,388 pts had complete baseline data and cancer-related details available for analysis, 1,241 carried on to the next data collection, 265 had died, 38 had ended participation and 7 are participating in a clinical trial (**Figure 1B**).

Conclusions

- WAYFIND-R is a successfully established international registry in precision oncology, across multiple countries, that will enable secondary data use by the research community worldwide.
- The collection of standardised pt and tumour data, including NGS findings, make this a high-quality cancer registry that captures the entire pt care pathway and MTB decision-making.
- WAYFIND-R has enrolled pts with >140 different cancer types from a broad range of sites and different NGS tests, indicating a comprehensive, diverse and fit-for-purpose real-world data source.
- The distribution of cancers, treatments and most commonly detected genes by NGS are broadly as expected, reflecting routine care and known genes involved in carcinogenesis.
- WAYFIND-R will enable further insights into the disease courses of pts with solid tumours, their molecular tumour profiles and clinical decision-making, treatment patterns and access to molecularly matched therapies for these pts.

ePoster

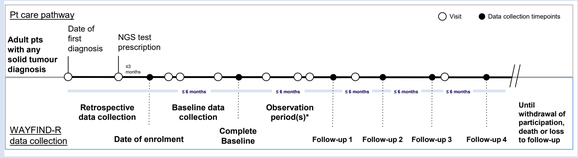
https://ter.li/e0dtur

Copies of this poster obtained through quick response and/or text key codes are for personal use only and may not be reproduced without written permission of the authors.

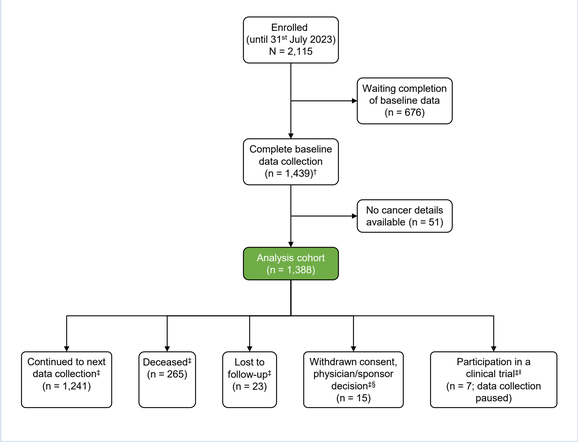
Please contact the lead author at jean-yves.blay@lyon.unicancer.fr for permission to reprint and/or distribute. Presented at the ESMO Congress 2023, Oct 20–24, 2023, Madrid, Spain.

Figure 1. WAYFIND-R data collection and analysis

A) Timeline for data collection



B) Patient attrition



*Observation periods are within 6 months of the first observation visit completion date and at least every 6 months thereafter.
†Complete baseline means that sites checked that they completed collection of baseline information on entry of the patient into the registry. It also signals if the patient will continue the participation in the registry.
‡Sum of totals might be higher than 1,388 as "Continue to next data collection" and "Death" can be selected as reason for end of study.
§Pts who ended participation still consented to have the data available in the database. Those that requested data deletion are not included in this analysis cohort.
¶For pts currently participating in a clinical trial, data collection is paused while enrolled in the clinical trial, and baseline information is available. These pts will resume follow-up once participation in the clinical trial is over.

Results

- Data were collected from 28 countries from 75 sites globally; most sites were academic institutions/university hospitals.
- The median age at diagnosis was 62 years (range: 15–91), 50% were female and 51% were White (**Table 1**); pts with breast cancer had the lowest median age at diagnosis (47 years; range: 25–81).
- Eighty percent of pts had their performance status assessed at baseline; most pts had an Eastern Cooperative Oncology Group (ECOG) performance status of 0 (42% for pancreatic cancer and 63% for ovarian cancer; **Table 1**).
- Seventy-three per cent of pts had stage assessed at diagnosis; stage IV was the most common staging at diagnosis (35% for breast cancer and 69% for colon cancer; **Table 1**).
- While the majority of pts were diagnosed the same year they enrolled in the registry, for pts with breast cancer, 52% were diagnosed more than 3 years before enrolment.
- Most pts had government insurance (61%) and 42% were retired.
- Further baseline and clinical characteristics are shown in **Table 1.**
- WAYFIND-R includes 141 cancer types and 219 morphologies (**Figure 2**). The most common morphology was adenocarcinoma (n = 584); the most common type was lung cancer (29%), followed by colon cancer (11%), pancreatic cancer (9%), breast cancer (8%) and ovarian cancer (5%).
- Half of pts had received treatment of any type (systemic or other); systemic was the most common type of treatment (81%) and chemotherapy was the most common systemic treatment (57%). At baseline, 41% of pts (n = 551) had not been reviewed by a MTB. The most frequent MTB recommendation after NGS testing (n = 298; 23%) was to start other treatment (chemotherapy: 50%; targeted therapies: 27%; immunotherapy: 19%; **Figure 3**).
- An increase in the proportion of pts receiving targeted therapies after their NGS results were available was observed (from 8% to 27%); this increase was particularly marked in ovarian cancer, breast cancer and colon cancer (**Figure 4**).
- For 82% of pts, samples for NGS testing originated from the primary tumour or from metastasis (**Figure 5**).
- The most commonly NGS-detected genes reflect known genes involved in carcinogenesis; non-NGS-assessed biomarkers detected in the most common cancer types reflect routine care (**Table 2**).

Table 1. Demographics and clinical characteristics of pts enrolled in WAYFIND-R

	Pts N = 1,388
Median age (IQR)	62 (15–91)
Sex	
Female	693 (49.9)
Male	694 (50.0)
Missing	1 (<1)
Race	
Asian	155 (11.2)
Black	4 (<1)
White	711 (51.2)
Mixed/other	101 (7.3)
Not reported*	415 (29.9)
Missing	2 (<1)
Performance status assessed at baseline	
No	254 (18.3)
Yes - ECOG PS	1,094 (78.8)
0	564 (40.6)
1	395 (28.5)
≥2	123 (8.9)
Missing	12 (<1)
Yes - Karnofsky	19 (1.4)
Missing	21 (1.5)
Cancer stage at diagnosis†	
0	6 (<1)
I	55 (5.4)
II	62 (6.1)
III	126 (12.4)
IV	598 (58.7)
Not reported	148 (14.5)
Missing	24 (2.4)
Presence of metastases at baseline	
No	231 (16.6)
Yes	1,098 (79.1)
Unknown	38 (2.7)
Missing	21 (1.5)

Data are n (%) unless stated otherwise.
*Not routinely collected at some sites. †Staging available at baseline.
ECOG PS, Eastern Cooperative Oncology Group performance status; IQR, interquartile range.

Figure 2. Distribution of pts according to cancer type and morphology

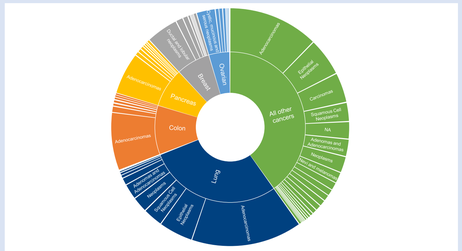


Figure 3. Distribution of pts according to cancer type and systemic treatment modalities (any line)

Figure 4. Proportion of pts who initiated immunotherapy, targeted therapy or hormone therapy before or after NGS test results were received, by most common cancer types

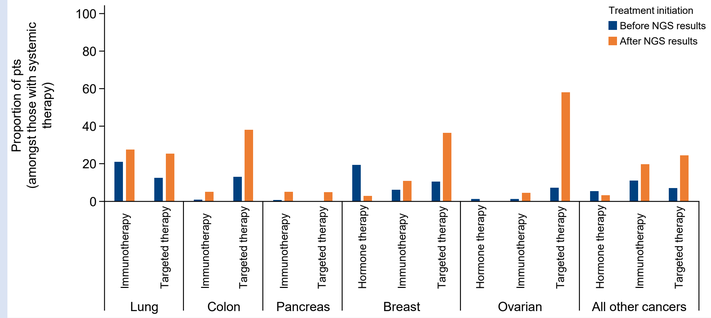


Figure 5. Distribution of pts according to biospecimen used for NGS testing

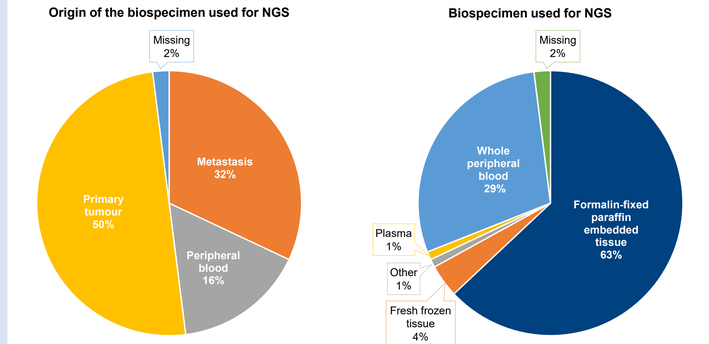


Table 2. Genes detected by NGS and non-NGS-assessed biomarkers

	Lung	Colon	Pancreas	Breast	Ovarian	All other cancers
Genes detected by NGS	n = 397	n = 145	n = 116	n = 65	n = 64	n = 530
Most commonly detected genes	*EGFR* *KRAS* *TP53* *BRAF* *MET* *ALK* *NRAS* *PIK3CA* *HER2* *ROS1*	*TP53* *APC* *KRAS* *PIK3CA* *BRAF* *NRAS* *DNMT3A* *SMAD4* *ATM*	*KRAS* *TP53* *CDKN2A* *ARID1A* *TET2* *DNMT3A* *ATM* *BRCA2* *CDKN2B*	*PIK3CA* *TP53* *ESR1* *ERBB2* *FGF19* *FGF3* *FGF4* *CCND1* *DNMT3A*	*TP53* *BRCA1* *BRCA2* *MYC* *DNMT3A* *PIK3CA* *PTEN* *MET* *RB1* *ERBB2*	*TP53* *KRAS* *PIK3CA* *APC* *CDKN2A* *BRAF* *ATM* *PTEN* *ARID1A* *EGFR*
Non-NGS-assessed biomarkers	n = 237	n = 93	n = 75	n = 65	n = 28	n = 351
Most frequently screened biomarker*	PD-L1 TTF1 ALK ROS EGFR CK7/KRT7 CK20 KRAS NTRK Fusion Napsin A	KRAS CK20 CEA CK7/KRT7 MLH1 MSH6 PMS2 CDX-2 MMR Status MSH2	CK7/KRT7 CA19-9 CK20 CEA CDX-2 PD-L1 SYP MMR Status TTF1 Ki67	HER2 Ki67 ER GATA3 PD-L1 PR CK7/KRT7 CEA RO	PAX8/PPARγ CK7/KRT7 p53 WT1 CK20 CA125 CAL/CR Ki67 ER PR	PD-L1 CK7/KRT7 CK20 TTF1 CDX-2 CEA CA19-9 HER2 MSH6 MLH1

The total number of pts does not correspond to the analytic cohort as some pts had missing data for the genes detected and only 849 pts screened for non-NGS biomarkers.
*Screening for biomarkers does not correspond to positivity or presence of the biomarker for each specific tumour type.
Biomarkers assessed by non-NGS methods, e.g., immunohistochemistry, fluorescence *in situ* hybridisation, or (quantitative/digital) polymerase chain reaction.

References

1. ClinicalTrials.gov Identifier: NCT04529122. Accessed September 2023.
2. Le Tourneau C, *et al*. *JCO Precis Oncol* 2022; **6:**e2200019

Acknowledgements

We thank the pts and their families who take part in WAYFIND-R, as well as the staff, research coordinators, and investigators at each participating institution. Research support for third-party writing/printing assistance for this poster, furnished by Eleanor Porteous, MSc, of Health Interactions, was provided by F. Hoffmann-La Roche Ltd.

JYB reports research funding (institution) from Novartis, Bayer, GSK, Pfizer, Decipher, Roche, BMS, MSD and AstraZeneca; a leadership role for Innate Pharma; honoraria from Novartis, Bayer, Pfizer, Decipher and Roche; an advisory role for Novartis, Bayer, GSK, Pfizer, Decipher, Roche, BMS, MSD and AstraZeneca. All authors received research support in the form of third-party medical writing assistance for this poster from F. Hoffmann-La Roche Ltd. Please refer to the abstract for all author conflicts of interest. This analysis was sponsored by F. Hoffmann-La Roche Ltd.