31P Liquid biopsies in clinical practice

NHS South East Genomic Medicine Service Alliance

NHS South East Genomic Laboratory Hub

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Background

Liquid biopsies have emerged as a non-invasive and cost-effective alternative to tissue biopsies and are increasingly used for tumour profiling in clinical practice. However, there is still uncertainty on how results should be interpreted by treating oncologists.

Here, we used liquid biopsies to characterise patients with advanced cancer and provide clinical interpretation and recommendations via the Genomic Tumour Advisory Board (GTAB) of the NHS South East Genomic Laboratory Hub.

Methods

Twenty-seven (27) patients with metastatic or unresectable disease were offered circulating tumour DNA (ctDNA) assay testing between November 2021 to January 2022 at St George's University Hospital in London, UK. Written consent was obtained for all patients.

ctDNA was isolated from peripheral blood using the FoundationOne® Liquid CDx assay that reports genomic alterations in 324 genes, microsatellite instability and blood tumour mutational burden. Assays were provided by Roche through a Familiarisation Programme. Results were reviewed by the GTAB to identify patients potentially eligible for NHS-approved clinical trials based on a genomic biomarker as well as those requiring referral to Cancer Genetics.

Patient Characteristics

Median age of patients was 54 years (29-85) and males were prevalent (63%). 85% of patients were previously treated and 33% had received more than two lines of treatment. The patient characteristics are shown in Table 1 and the primary sites of cancer are shown in Figure 1.

	Number of Patients (%)
Age (range)	52 (29-85)
Sex	
Male	17 (63%)
Female	10 (37%)
Tumour site	
Colorectum	11 (41%)
Lung	5 (19%)
Breast	4 (15%)
Renal	4 (15%)
Penis	2 (7%)
Ovarian	1 (4%)
Metastatic	27 (100%)
Lines of Treatment	
Naïve	4 (15%)
1	3 (11%)
2	11 (41%)
3	6 (22%)
4	1 (4%)
5	2 (7%)

Table 1. Patient characteristics including age, sex, extent of disease and previous lines of treatment.

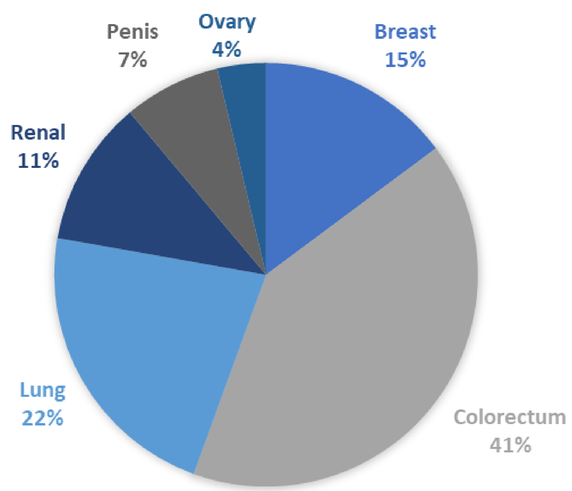

Figure 1. Primary site of cancer.

Results

ctDNA was not isolated in two patients (7%) due to low tumour burden. We identified a variant of clinical significance in 16 patients (59%). Known targets that were also identified with standard tissue testing were identified in five patients (19%) and there was 100% concordance between tissue and blood testing. Thirteen patients (48%) were eligible for at least one NHS-approved clinical trial based on a genomic biomarker and two patients were eligible for two trials. Germline mutations were identified in two patients (7%) and they were referred to Cancer Genetics for further management. Results were available within two weeks from testing. A summary of the results is shown in Table 2 and Figure 2.

Result	Number of Patients (%)
Failed	2 (7%)
No variants of clinical significance	11 (41%)
Variants of clinical significance	16 (59%)
Known target	5 (19%)
Clinical trial	13 (48%)
Germline	2 (7%)

Table 2. Results of ctDNA testing. Variants of clinical significance included genomic biomarkers for NHS-approved cancer treatments and NHS-approved clinical trials.

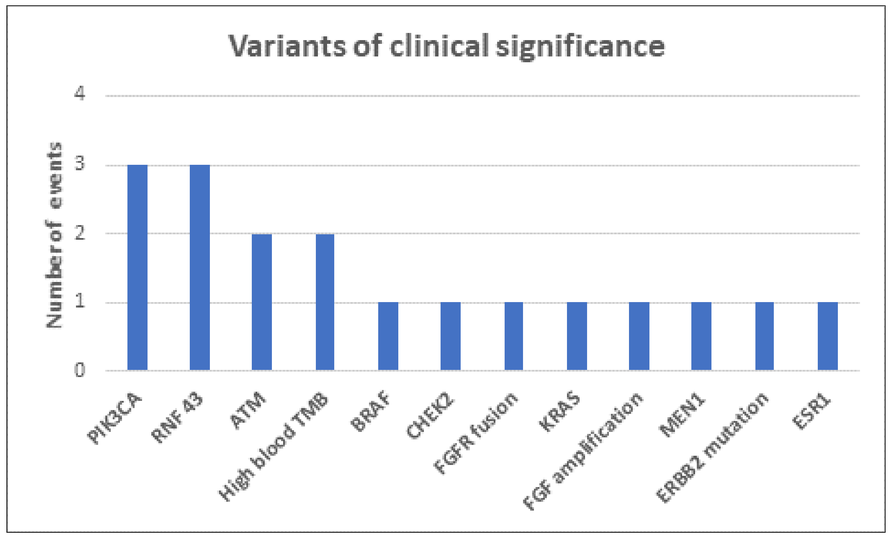

Figure 2: Variants of clinical significance identified in the cohort. Some patients had more than one variant.

Conclusion

We found that 48% of heavily pre-treated cancer patients were eligible for a clinical trial based on a genomic biomarker identified in ctDNA. Our results further support the benefits of molecular profiling for allocating patients to clinical trials. Importantly, the results highlight the need to support oncologists with clinical interpretation and recommendations of findings through a GTAB for subsequent patient management.

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