Gustave Roussy Match-R study: A descriptive analysis of the molecular target population

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INTRODUCTION

MATCH-R trial is an ongoing prospective clinico-biological study, whose main objective is to understand mechanisms of acquired resistance to specific cancer therapies and guide to design new treatment strategies to overcome resistance.

Patients (pts) in case of progressive disease are required to undergo a tumor biopsy (bx) to perform extensive molecular profiling (WES and RNAseq).

OBJECTIVE

This study aims to describe the characteristics of the population, targeted treatment and molecular profile found through tumor bx for each type of solid tumor.

METHODS

We collected data from medical records and molecular profile reports from tissue bx that underwent NGS from December 2014 to December 2021 within the MATCH-R trial (NCT02517892), focusing on the molecular target group (MTG), which is the population that received target therapy prior and/or after MATCH-R bx with >1% of tumor cells (TC).

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**First author declare no conflict of interest.*

RESULTS

Characterstic	Patients (N=269)
Median age at biopsy (range) – yr	57 (23-89)
Female Sex – no. (%)	174 (65)
Patient status to the last update – no. (%)	
Alive	90 (33)
Dead	165 (61)
ND	14 (5)
Match-R pre-biopsy treatment lines	
No prior lines – no. (%)	26 (10)
1 – no. (%)	148 (55)
2 – no. (%)	60 (22)
≥3 – no. (%)	35 (13)
Match-R post-biopsy treatment lines	
No posterior lines – no. (%)	114 (42)
1 – no. (%)	104 (39)
2 – no. (%)	34 (12)
≥3 – no. (%)	17 (6)

Table 1: Patients clinical and demographic characteristics in Molecular Target Group. Within the MTG 269 pts were included; Most common cancer types were: lung [186, 69%], gastrointestinal [38, 14%], genitourinary [16, 6%], gynecological [10, 4%], endocrine [7, 3%] and breast [5, 22%]. All pts received treatment for solid tumors with a median of 4 lines (range 1-13). The median number of target therapy lines received prior and after MATCH-R bx was 1 [1-6] and 1 [1-5] respectively. Median follow-up after MATCH-R bx was 10 months [2-87].

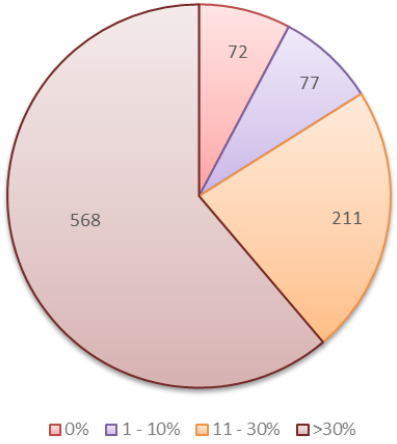

Figure 1: Tumor cells (TC) percentage per biopsy. 876 patients were enrolled of which 930 biopsies were obtained, (41 patients had more than one biopsy). 814 (87%) patients presented one biopsy with >1% viable TC. The percentage of TC was >30% among 568 bx; 11-30%: 211 bx, 1-10%: 77 bx; 0%: 72 bx.

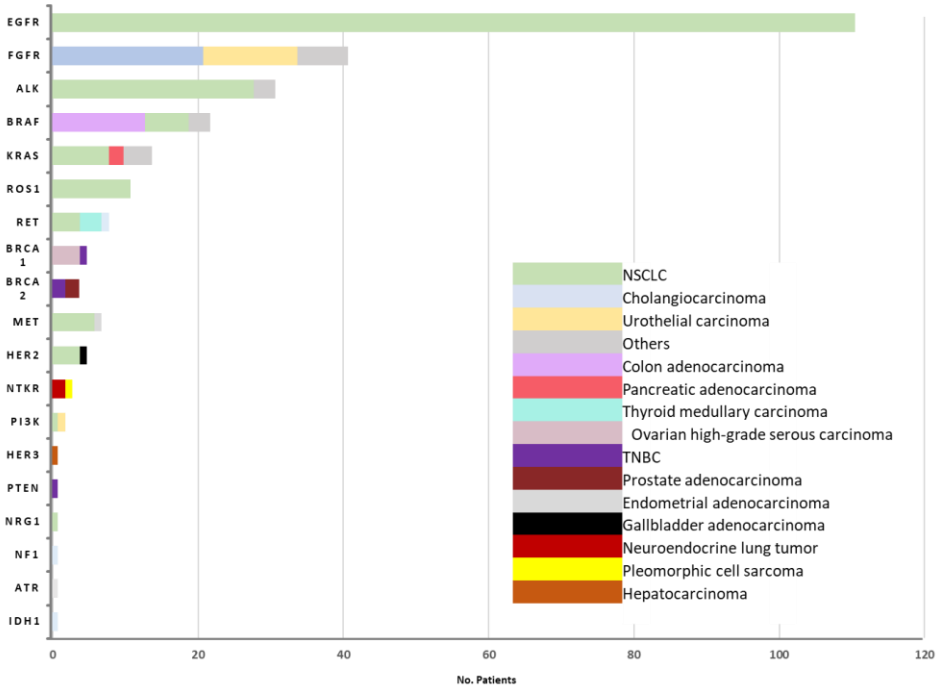

Figure 2: Molecular alterations and tumor type. The most frequently mutated/rearranged genes were EGFR (41%), FGFR 2-3 (15%), ALK (11%), BRAF (8%), KRAS (5%), ROS1 (4%), RET (3%), BRCA 1-2 (3%), MET (2.6%), HER2 (2%), NTKR (1.1%) and PIK3CA (0.7%).

CONCLUSIONS

- MATCH-R achieved an adequate tissue quality, at progressive disease, to perform extensive molecular profile.
- This study will provide valuable information that, through translational research, will allow us to understand the possible resistance mechanisms for the different treatments.
- Further updates will be provided.