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Less frequently mutated genes in colorectal cancer: evidences from next-generation sequencing of 653 routine cases

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▶ Additional material is published online only. To view please visit the journal online (http://dx.doi.org/10.1136/jclinpath-2015-203403).

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Received 15 September 2015
Revised 28 December 2015
Accepted 29 December 2015
Published Online First 21 January 2016

To cite: Malapelle U, Pisapia P, Sgariglia R, *et al*. *J Clin Pathol* 2016;**69**:767–771.

ABSTRACT

Aims The incidence of *RAS/RAF/PI3KA* and *TP53* gene mutations in colorectal cancer (CRC) is well established. Less information, however, is available on other components of the CRC genomic landscape, which are potential CRC prognostic/predictive markers.

Methods Following a previous validation study, ion-semiconductor next-generation sequencing (NGS) was employed to process 653 routine CRC samples by a multiplex PCR targeting 91 hotspot regions in 22 CRC significant genes.

Results A total of 796 somatic mutations in 499 (76.4%) tumours were detected. Besides *RAS/RAF/PI3KA* and *TP53*, other 12 genes showed at least one mutation including *FBXW7* (6%), *PTEN* (2.8%), *SMAD4* (2.1%), *EGFR* (1.2%), *CTNNB1* (1.1%), *AKT1* (0.9%), *STK11* (0.8%), *ERBB2* (0.6%), *ERBB4* (0.6%), *ALK* (0.2%), *MAP2K1* (0.2%) and *NOTCH1* (0.2%).

Conclusions In a routine diagnostic setting, NGS had the potential to generate robust and comprehensive genetic information also including less frequently mutated genes potentially relevant for prognostic assessments or for actionable treatments.

INTRODUCTION

Antiepidermal growth factor receptor (*EGFR*) therapy is not effective in patients with metastatic colorectal cancer (CRC) harbouring mutations at codons 12 and 13 in *KRAS* exon 2.[1] More recent evidences showed that the so-called expanded *RAS* mutations (exon 3 and exon 4 of *KRAS* and exons 2, 3 and 4 of *NRAS*) also have negative predictive value.[2] The extension of community *KRAS* testing to all *RAS* mutations favoured the implementation of multitarget testing methodologies. Next-generation sequencing (NGS), matched with multiplex capture of targeted gene regions and analysed by bioinformatics tools, enables the simultaneous detection of multiple mutations in multiple genes. The development of affordable benchtop sequencers, such as the Ion Torrent Personal Genome Machine (PGM; Life Technologies, Carlsbad), and of relatively small, focused gene panels, such as the Ion AmpliSeq Colon and Lung Cancer Panel,[3] enabled our laboratory to adopt NGS as a stand-alone diagnostic test to genotype *KRAS NRAS* and *BRAF*.[4] In a previous validation study, all point mutations detected in these genes by Sanger sequencing were also correctly identified by NGS.[4] The latter, however, proved to be more sensitive, and, remarkably, less costly.[4]

NGS may also identify rarer patient-specific somatic mutations. The latter are of unclear significance, as their incidence rates have not been established with certainty. In fact, while there is a wealth of data regarding *RAS/RAF/PI3KA* and *TP53* gene mutations, the information on less frequently mutated genes is mostly derived by the genomic scale analysis of a limited number of CRC samples.[5] Conversely, in its daily diagnostic practice, our laboratory, an Italian accredited reference centre for *RAS* testing, has generated a large database of CRC samples sequenced with the PGM/Colon Lung Cancer Panel, whose interrogation can be useful to better define the incidence rate of rare mutations. Thus, besides *KRAS*, *NRAS*, *BRAF*, *PIK3CA* and *TP53* alterations, this paper focuses on mutations occurring in other receptor tyrosine kinase (RTK) genes (*ALK*, *EGFR*, *ERBB2*, *ERBB4*, *FGFR1*, *FGFR2*, *FGFR3*, *MET*, *DDR2*), in RTK signalling genes (*AKT1*, *PTEN*, *MAP2K1*, *STK11*) and in other well-known cancer-related genes (*NOTCH1*, *CTNNB1*, *SMAD4*, *FBXW7*).

METHODS

Patients and samples

This study includes a series of 653 CRC tissue samples (398 men and 255 women) referred from 18 institutions located all over South Italy between January 2014 and March 2015. Mean patient age was 66.8 years (range, 29–96 years). Following current international guidelines, one single tumour sample was tested for each patient.[6]

NGS analysis

Tumour cell enrichment, DNA extraction and NGS analysis on the Ion Torrent PGM by using the AmpliSeq Colon and Lung Cancer panel were performed, as previously described,[4] and detailed in online supplementary information (file 1). The Torrent Suite V.4.0 analysis pipeline was used to assess the sequencing data and to perform adapter trimming, alignment QC and base calling. Single-nucleotide polymorphisms, insertions and deletions (del) were identified using a Torrent Variant Caller plug-in (V.4.0-r76860), optimised for low-frequency variants assessment. The criteria for evaluation of any variant as reportable were the following: minimum coverage depth of 100×, minimum variant frequency of 5% and confirmation by the Integrative Genomics Viewer visual inspection. Sequence variants, deemed real and reportable

Table 1 Twenty-two multiple gene mutation analysis by the Ion Torrent AmpliSeq Colon and Lung Cancer Panel in routine samples of colorectal cancer

Total cases analysed	n=653
Wild type in all 22 gene analysed	n=154 (23.6%)
Mutated at ≥1 of 22 genes analysed	n=499 (76.4%)
Total mutations	n=796
Mutated genes	17/22

by criteria listed above, were further assessed by the ClinVar Database (http://www.ncbi.nlm.nih.gov/clinvar/, last accessed 30 November 2015) for classifying a genetic alteration as germline or somatic.

RESULTS

One or more gene mutations were detected in 499/653 (76.4%) tumours in 17 of the 22 genes included in the panel (table 1), for a total of 796 mutations that are listed in online supplementary information (file 2). A representative case is reported in figure 1. Only three genes (*DDR2*, *FGFR1* and *FGFR2)* did not harbour any alteration, while two genes *(FGFR3* and *MET*) only harboured germline variants as reported in online supplementary information (file 3). Single mutations were found in 274 patients (41.9%), double mutations in 177 patients (27.1%) and 3 or more mutations were found in 48 patients (7.4%). Coexisting mutations in different genes are reported in online supplementary table S1.

Mutations occurred in *TP53* (n=240; 38.8%), *KRAS* (n=247; 37.8%), *NRAS* (n=30; 4.6%) and *BRAF* (n=63; 9.6%). *KRAS* and *NRAS* mutations were mutually exclusive. *KRAS* and *NRAS* coexisted with *BRAF* mutations in four and in one instances, respectively. In most of these cases (4/5), *BRAF* mutations occurred outside of codon 600. *PIK3CA* gene mutations occurred in 98 (15%) cases. More frequently, *PIK3CA* mutations were detected together with other gene mutations; *PIK3CA* was the only mutated gene in 15/98 (15.3%) samples.

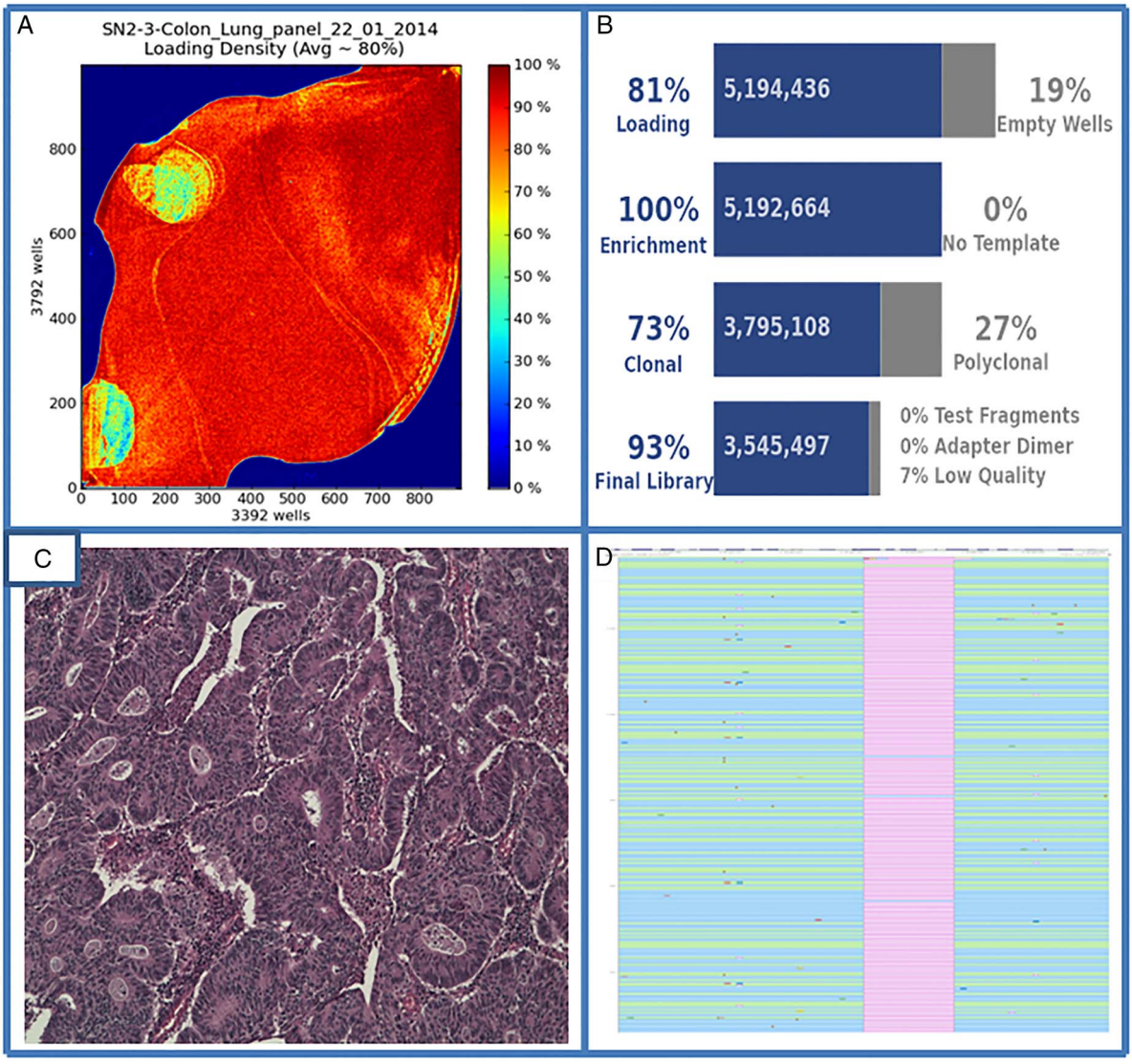

Figure 1 Loading density (A) and performance parameters (B) of an Ion Torrent sequencing run, carried out using a 316 chip, are shown. DNA extracted from the colorectal cancer (CRC) shown in (C) harboured an epidermal growth factor receptor p.E746_A750delELREA mutation. (D) was observed with a Genome Brower web app.

Table 2 Number and percentage of cases of each gene sequenced by the Ion Torrent AmpliSeq Colon and Lung Cancer Panel

Gene	Number of mutated cases (%)
KRAS	247* (37.8%)
TP53	240† (36.8%)
PIK3CA	98‡ (15%)
BRAF	63 (9.6%)
FBXW7	39 (6%)
NRAS	30 (4.6%)
PTEN	18 (2.8%)
SMAD4	14 (2.1%)
EGFR	8 (1.2%)
CTNNB1	7 (1.1%)
AKT1	6 (0.9%)
STK11	5 (0.8%)
ERBB4	4 (0.6%)
ERBB2	4 (0.6%)
NOTCH1	1 (0.2%)
ALK	1 (0.2%)
MAP2K1	1 (0.2%)

Note: *DDR2*, *FGFR1*, *FGFR2*, *FGFR3* and *MET* genes did not harbour any alteration.
*4/247 cases harboured 2 *KRAS* mutations.
†5/240 cases harboured 2 *TP53* mutations.
‡1/98 cases harboured 2 *PIK3CA* mutations.

Number and percentage of mutated cases of each gene are reported in table 2 and exons and codons involved are detailed in online supplementary information (file 4).

Besides *RAS/RAF/PI3KA* and *TP53* gene mutations, the Ion AmpliSeq Colon and Lung Cancer Panel provided information on additional targets, such as RTK genes, RTK signalling genes and other well-known cancer-related genes, as it follows.

RTK gene mutations

ALK: in one case (0.2%) the p.L1196M mutation was detected in association with two mutations of the *TP53* gene. ***EGFR***: mutations occurred in eight (1.2%) cases, with exon 19 deletion evident in four instances (n=3 p.E746_E749delELRE; n=1 p.E746_A750delELREA, as shown in figure 1). Most cases (7/8) were associated with other gene alterations; in particular, five cases harboured a KRAS mutation. ***ERBB2***: mutations occurred in four (0.6%) cases, with the V842I being detected in three instances. ***ERBB4***: mutations occurred in four cases (0.6%).

RTK signalling genes mutations

AKT1: the E17K mutation occurred in six cases (0.9%). ***PTEN***: mutations occurred in 18 (2.8%) cases. ***MAP2K1***: in one case (0.2%) the K57N mutation was associated with *PIK3CA* mutation. ***STK11***: mutations occurred in five cases (0.8%).

Other cancer-related genes

NOTCH1: mutation occurred in one case (0.2%) and remarkably this case had five additional gene mutations occurring in *TP53*, *KRAS*, *PTEN*, *ERBB4* and *PIK3CA*. ***CTNNB1***: mutations were detected in seven cases (1.1%), being always associated with at least one other concurrent mutation. In particular, *CTNNB1* mutations were consistently associated with the constitutive activation of the *RAF/MEK/ERK* pathway by either *KRAS* (n=4) or *BRAF* (n=3) concurrent mutations. ***SMAD4***: mutations were found in 14/653 (2.1%) samples, and in combination with other mutations (9/14). ***FBXW7***: mutations were identified in 39/653 patients (6%), singly (n=7) and associated with KRAS (n=20).

DISCUSSION

This study evaluated in CRC routine samples a broad set of genes for mutational events. Previous evidences regarding the *RAS/RAF/PI3KA* gene were confirmed. *KRAS* and *NRAS* mutations were always mutually exclusive,[5] whereas occasionally *BRAF* (mostly no V600E) mutations coexisted with an *RAS* gene alteration.[7] The frequent association of *PIK3CA* mutations with the *RAS/RAF* alterations was also confirmed.[5] Our data straighten the view that the simple distinction of tumours in *RAS*, *BRAF* or *PIK3CA* does not apply to CRC with combined *RAS/RAF* genetic changes.[7] We also confirmed that one of the most frequently mutated genes in CRC is *TP53*, whose mutation rate in our study was 38.8%.

Additional information was generated on other potentially actionable components of the CRC genomic landscape, such as RTK genes. Remarkably, the *ALK* p.L1196M gatekeeper mutation, which confers high-level resistance to crizotinib in lung cancer, was for the first time detected in CRC. *EGFR* mutations were also detected, as shown in figure 1, and their mutation rate (1.2%) was lower than that (4.5%) reported in the Tumor Cancer Genome Atlas (TCGA).[5] While *KRAS* and *EGFR* mutations are normally exclusive, concomitant *KRAS* and *EGFR* mutations were also detected (see online supplementary table S1), confirming previous NGS findings.[8] Other mutations include those involving *ERBB2*; in particular, the V842I *ERBB2* mutation associated with breast cancer[9] was detected in three instances. Remarkably, in CRC preclinical models *HER2* mutations were resistant to cetuximab and panitumumab and responsive to second-generation *HER2/EGFR* irreversible tyrosine, afatinib and neratinib.[10] Clinical trials targeting *HER2* activating mutations in metastatic CRC are ongoing.[11] *ERBB4* mutations occurring in 0.6% of the cases have an uncertain prognostic significance. In fact, the TCGA data set indicated a survival disadvantage in colorectal carcinoma with *ERBB4*,[5 12] whereas another study showed that the *ERBB4* mutant clones are not selected in metastatic spread.[13]

A number of rare mutations occurring in the *PI3K/AKT/mTOR* pathway are potentially actionable. As an example, *AKT1* mutations were associated with primary resistance to anti-*EGFR* therapy.[14] In our study, *AKT1* was mutated in 0.9% of cases, being mutually exclusive with *PIK3CA* alterations, as previously shown.[14] The recent association between E17K *AKT1* and tumours with mucinous morphology was observed only in one of our six cases.[14] Previous studies showed a wide range of *PTEN* mutation rates (0.7%[15] to 6%[16]). In our study, the mutation rate of *PTEN* was 2.8%. Interestingly, a total of 11 different mutations were found, according to the notion that mutations in tumour suppressor genes do not strongly cluster in single mutational hot spot.[17] Another RTK signalling gene included in our panel is the *STK11* gene. We confirm that somatic *STK11* mutations rarely occur in somatic CRC (0.8%).[18] Earlier studies reported that *STK11* mutant neoplasms had alterations in nucleotide metabolism that confer hypersensitivity to deoxythymidylate kinase inhibition, proposing that deoxythymidylate kinase is a possible therapeutic target.[19]

Interestingly, *CTNNB1* mutations detected in 1.1% of the cases were always associated with at least one other concurrent mutation (see online supplementary table S1). In particular, *CTNNB1* mutations were consistently associated with the constitutive activation of the *RAF/MEK/ERK* pathway by

either *KRAS* (n=4) or *BRAF* (n=3) concurrent mutations, in keeping with the notion that *CTNNB1* mutations are early events in CRC carcinogenesis.[20] Conversely, our data confirm that the occurrence of *SMAD4* mutations (2.1%) is a late event.[21] In fact, in our study 64.3% of *SMAD4* mutations occurred in combination with other alterations. *SMAD4* loss of function was associated with a worse prognosis and decreased disease-free survival and with resistance to 5-fluorouracil chemotherapy.[22 23] In this present study, *FBXW7*, a major tumour suppressor gene crucial in promoting exit from the cell cycle, was mutated in 6% of cases, which is in line with the estimated 9% of CRCs containing *FBXW7* mutations.[24 25] Preclinical data have suggested that inactivating mutations of *FBXW7* could predict sensitivity either to the *mTOR* inhibitor rapamycin,[26] or to the histone deacetylase inhibitor MS-275.[27] Noteworthy, as it was shown in previous reports *FBXW7* were often (51.2%) associated with *KRAS* mutations.[28 29] Interestingly, concurrent molecular aberrations can contribute to limited therapeutic efficacy of *mTOR* inhibitors in the presence of *FBXW7* mutations.

Certain genes included in our panel, such as *MAP2K1*, may have a future role in sensitivity, resistance or both, to a variety of preclinical drugs. Targeting of *NOTCH* signalling may be of therapeutic value in colon cancers, as activating mutations in *NOTCH-1* have been previously reported in colon cancer.[30] In our study *NOTCH* mutation occurred in one case (0.2%) and remarkably this case had five additional gene mutations occurring in *TP53, KRAS*, *PTEN*, *ERBB4* and *PIK3CA*.

In conclusion, our data confirm that CRCs consist of a group of heterogeneous disorders with a large number of diverse sets of genetic changes in oncogenes and tumour suppressor genes. In a routine diagnostic setting, the Ion PGM and AmpliSeq colon and Lung Cancer Panel had the potential to exploit even a low-input DNA to uncover multiple common mutations simultaneously and to generate robust and comprehensive genetic information. Several updates of the Ion Torrent system may soon enable to detect also gene copy number alterations and translocations to more comprehensively cover the whole spectrum of genomic alterations refining the identification of reliable and reproducible biomarkers of response/resistance to the targeted treatment of CRC.

Take home messages

- Ion Torrent Personal Genome Machine (PGM), and the Ion AmpliSeq Colon and Lung Cancer Panel, enabled our laboratory to adopt next-generation sequencing.
- Less information is available on the uncommon mutated genes of the CRC genomic landscape.
- In a routine diagnostic setting, the AmpliSeq Colon and Lung Cancer Panel had the potential to generate robust and comprehensive genetic information.

Handling editor Runjan Chetty

Contributors UM, PP and GT conceived the study and wrote the paper. RS performed the experimental part. EV, GG and CB contributed as pathologists. CC and MB contributed as oncologists.

Competing interests None declared.

Patient consent Obtained.

Provenance and peer review Not commissioned; externally peer reviewed.

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