Molecular pathways in post-colonoscopy versus detected colorectal cancers: results from a nested case-control study

Beatriz Carvalho, PhD

The Netherlands Cancer Institute



WEO The voice of world endoscopy











No disclosures.





Introduction

 Colonoscopy with polypectomy is not perfect in the prevention of CRC

3.7% (95% CI 2.8-4.9%) of all patients diagnosed with CRC underwent colonoscopy within 5 years¹

- Postcolonoscopy CRC (PC-CRC)²:
 - **Proximal location**
 - Flat macroscopic appearance
 - Smaller in size





1. Singh Samadder. Am J of GE. 2014 2. le Clercq ... Sanduleanu. Gut. 2014



Introduction – CRC development







Introduction

Molecular profile of PCCRCs: what do we know?

Author / Publication	Population	PC-CRC vs Detected CRC	P-value
Sawhney et al.	51 PC-CRCs,	MSI: 30.4% vs 10.3%	0.003
Gastroenterology 2006	112 prevalent CRCs		
Arain et al.	63 PC-CRCs,	CIMP: 57% vs 33%	0.004
Am J Gastro 2009	131 prevalent CRCs		
Shaukat et al.	63 PC-CRCs,	BRAF: 28% vs 19%	0.180
Dig Dis Sci 2010	131 prevalent CRCs		
Shaukat et al.	63 PC-CRCs,	KRAS: 13% vs 29%	0.030
Dig Dis Sci 2012	131 prevalent CRCs		
Nishihara et al.	62 PC-CRCs,	MSI: 25.0% vs. 13.6%	
NEJM 2013	585 prevalent CRCs	CIMP: 30.2% vs. 15.0%	
		BRAF: 21.7% vs. 13.8%	ns
Richter et al.	42 PC-CRCs,	MSI: 40.5%	
Dig Dis Sci 2014	226 controls	BRAF: 16.7% vs 10.2%	0.280
		KRAS: 28.6% vs 36.7%	0.380
		NRAS: 7.1% vs 4.0%	0.410
		PIK3CA: 16.7% vs 12.4%	0.460
Woo Lee et al.	25 PC-CRCs,	MSI: 32% vs 8.4%	0.002
Gut and Liver 2016	261 controls		



Introduction **Non-polypoid CRNs**

- Often located in the proximal colon¹
- Easily overlooked
- Challenging to resect endoscopically
- Distinct molecular features:

• More often 5q loss² • More often BRAF mutations³ • Less often 17p & 18q loss² Less often APC & KRAS mutations³





To investigate the molecular profile of PCCRCs, including both the CIN and MSI related mechanisms, in a large population-based cohort

Hypothesis: PCCRCs have a molecular profile that is different from DCRCs, presumably more similar to non-polypoid and/or sessile serrated precursor lesions









Study population



Le Clercq ... Sanduleanu. Gut. 2014





Rutter MD, Beintaris I et al. Gastroenterology. 2018 Sep;155(3)



Methods- Molecular analysis

• Whole genome DNA copy numbers

Low-coverage whole genome sequencing – Illumina

• DNA mutations \rightarrow 8 most common CRC genes

Truseq amplicon cancer panel – Illumina

• MSI status

Pentaplex Promega kit

• CIMP status

Multiplex MSP – CIMP panel - CACNA1G, IGF2, NEUROG1, RUNX3 and SOCS1 (Weisenberger et al Nat Genet 2006)







Results – Tumor selection



Bogie RMM Masclee AAM, Carvalho Bl BrJCancer 2022

*Le Clercq ... Sanduleanu. Gut. 2014 **Rutter MD, Beintaris I et al. Gastroenterology. 2018



Results – baseline characteristics

Features	PCCRCs (n=122)	DCRCs (n=98)	P value*
Mean age (SD)	71.8 (9.1)	69.4 (11.4)	0.089
Male (%)	70 (57.4)	57 (58.2)	1.000
Current/previous smoking (%)	28 (23.0)	21 (21.9)	0.980
Proximal location (%)	77 (63.6)	31 (31.6)	<0.001
Flat appearance (%)	58 (47.9)	27 (27.8)	0.004
T1 carcinoma (%)	21 (17.6)	5 (5.1)	0.009
Poor differentiation (%)	32 (29.6)	12 (12.8)	0.006
Mucinous histology (%)	17 (13.9)	13 (13.3)	1.000
Diverticulosis (%)	58 (47.5)	20 (20.8)	<0.001
Mean tumour size (SD)	3.6 (1.8)	4.6 (1.9)	< 0.001

Bogie RMM Masclee AAM, Carvalho Bl BrJCancer 2022



Results - Etiology of PCCRCs analyzed



Bogie RMM Masclee AAM, Carvalho Bl BrJCancer 2022

Etiology (WEO)

75



- Likely new PCCRC
- Possible missed lesion with prior inadequate examination
- Likely prior inadequare resection
- Previously detected lesion without resection



Results – Tumor selection and analysis



Bogie RMM ... Masclee AAM, Carvalho Bl BrJCancer 2022

*Le Clercq ... Sanduleanu. Gut. 2014



Results- PCCRCs show less copy number alterations

Molecular feature analysis

A) All PCCRCs vs DCRCs

Mutation	p-value	ł					OR [95% CI]	Mutation	p-valu	е					OR [95% CI]
APC	0.97	ŀ					1.01 [0.52, 1.98]	APC	0.899	F					0.96 [0.47, 1.92]
BRAF	0.941		;				1.04 [0.40, 2.69]	BRAF	0.487	F				—	1.41 [0.53, 3.74]
FRXW7	0 905	L			·		0 94 [0 36 2 47]	FBXW7	0.88	\vdash					1.08 [0.38, 3.10]
	0.000			1			0.04 [0.00, 2.47]	KIT	0.625	\vdash		—			0.82 [0.36, 1.86]
KIT	0.767		:				0.89 [0.41, 1.92]	KRAS	0.636	\vdash		———]			0.83 [0.37, 1.84]
KRAS	0.986	\vdash	· 	—			0.99 [0.49, 2.03]	PIK3CA	0.984				-		1.01 [0.41, 2.51]
PIK3CA	0.919	┣					0.96 [0.41, 2.24]	PTEN	0.329	F					1.67 [0.59, 4.71]
PTEN	0.566	⊢					1.34 [0.49, 3.61]	SMAD4	0.468						0.65 [0.20, 2.11]
SMAD4	0.661	 		—			0.80 [0.30, 2.15]	TP53	0.344			-			0.71 [0.35, 1.44]
TP53	0.385	 					0.75 [0.39, 1.44]	18q loss	0.005	┟	ł				0.36 [0.18, 0.73]
10	0.004		1					17p loss	0.969						1.01 [0.51, 2.01]
180 loss	0.004	╟┻╋╌┤					0.39 [0.21, 0.74]	13q gain	0.038		_				0.49 [0.25, 0.96]
MSI	0.296	F				———————————————————————————————————————	1.59 [0.66, 3.81]	MSI	0.254						1.69 [0.68, 4.16]
CIMP high	0.294	F			1		1.38 [0.75, 2.55]	CIMP high	0.267				—		1.44 [0.75, 2.75]
				1	1	I				1	1		1	I	
	()	1	2	3	4				0	1	2	3	4	
	OB: PCCBCs vs detected CBCs							OR: Biological PCCRCs vs detected CRCs							

Corrected for age and gender

Bogie RMM Masclee AAM, Carvalho Bl BrJCancer 2022

B) Biological PCCRCs vs detected CRCs







- Unsupervised hierarchial clustering
- Included molecular features:
 - Difference in univariate analysis of all PCCRC or biological PCCRC analyses
 - All mutations with observed prevalence of ≥9%
- Ward.D algorithm

Bogie RMM Masclee AAM, Carvalho Bl BrJCancer 2022

Results- PCCRCs are commonly CIMP-high





Results-Overview



Bogie RMM Masclee AAM, Carvalho Bl BrJCancer 2022



Conclusions

- MSI, hypermethylation and CIN pathways play a role in the development of PCCRCs
- Key molecular features of PCCRCs: Less often 13q gain and 18q loss More often hypermethylated and MSI
- Similar molecular features in NP-CRNs and SSA/Ps \rightarrow suggesting important contribution to PCCRCs



Discussion

• First comprehensive examination of the role of CIN- and MSIassociated mechanisms

Strengths

- case-control design
- Most likely etiologic factors identified

Limitations

- Retrospective
- Limited number of available tissue samples

Well characterized population-based collection of PCCRCs, nested



Statement

The clinical and molecular features observed in PCCRCs support the hypothesis that SSLs and non-polypoid CRNs are contributors to the development of these cancers





Acknowledgements



Department of Pathology

Gerrit Meijer Remond Fijneman Linda Bosch **Rinus Voorham** Sara de Vries

Genomics Core Facility

Christian Rausch Ron Kerkhoven Arno Velds Marja Nieuwland

Molecular Pathology

Petra Nederlof Maartje Vogel



Department of Pathology Manon van Engeland Veerle Melotte Heike Grabsch

Department of Statistics and methodology

Bjorn Winkens

Department of Gastroenterology

Ad Masclee Silvia Sanduleanu Eveline Rondagh Chantal le Clercq **Roel Bogie**

VU university medical center

Department of Pathology-**Tumor Genome Analysis Core Bauke Ylstra** Daoud Sie Martijn Cordes Paul Eijk Dirk van Essen

Department of Gastroenterology

Chris Mulder Jochim Terhaar sive Droste Frank Oort Sietze van Turenhout Ilhame Ben Larbi





Department of Gastroenterology **Evelien Dekker** Thomas de Wijkerslooth Joep ljspeert Manon van der Vlugt

zuyderland

Department of Pathology

Marius Nap Prapto Sastrowijoto



University of Leeds, Leeds, UK

Phil Quirke

Leeds General Infirmary, Leeds, UK Bjørn Rembacken

Hospital Vitkovice, Ostrava, **Czech Republic**

Martin Kliment

Tokyo Metropolitan Geriatric Hospital, Tokyo, Japan Tomio Arai







World Endoscopy Organization

