



Fondazione IRCCS
Istituto Nazionale dei Tumori

Sistema Socio Sanitario



Regione
Lombardia



UNIVERSITÀ
DEGLI STUDI
DI MILANO

5th Milan NET Conference

A live and web multimodal meeting
among active Italian NET Centers

Wednesday June 12th, 2019
Milan

Circulating tumor cells, DNA and MicroRNAs
as prognostic markers for NETs - **M. C. Zatelli**

Section of Endocrinology & Internal Medicine
Dept of Medical Sciences
University of Ferrara



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NEN PROGNOSIS

Depends on

- disease extent
- histological grade
- site of the primary tumor



5-year survival rates

60-90% in patients with localized NENs following surgery
50-75% in patients with regional lymph node involvement
25-40% of patients with distant metastases

Modlin et al. Cancer 2003;97: 934



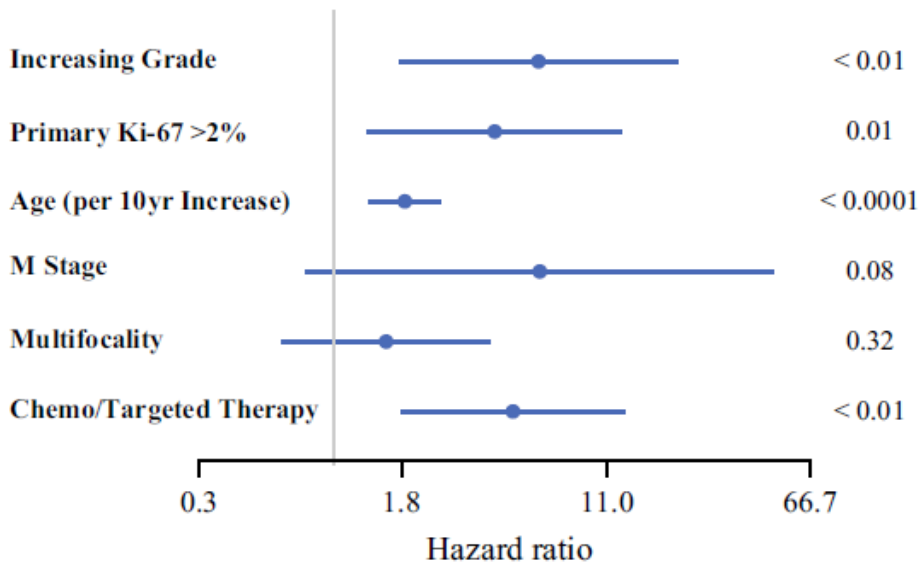
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PROGNOSTIC MARKERS



Multivariate analysis of factors affecting overall survival

AGE

Ki-67

grading

Keck et al. Ann Surg Oncol (2017) 24:2206-2212



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PROGNOSTIC MARKERS

Ki-67



Ki-67 index and mitotic count

markers of cell proliferation

strong indicator of aggressive phenotype

TECHNICAL ISSUES

HETEROGENEITY



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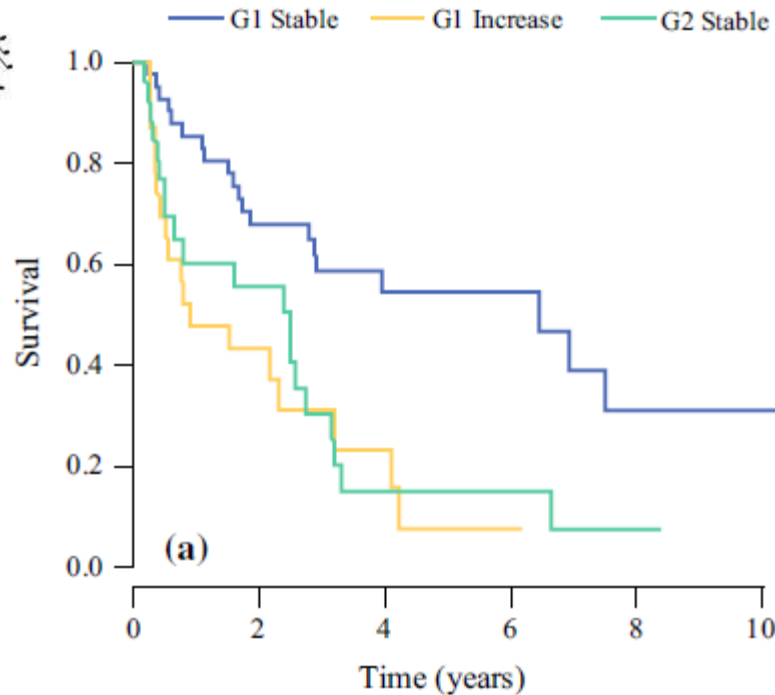
PROGNOSTIC MARKERS

grading

30% of GEP-NEN patients had M with a different grade than their primary

When grade increased, PFS and OS significantly decreased.

Determining the grade in both the primary tumor and a metastasis is important for estimating prognosis and to help inform decisions regarding additional therapies



Keck et al. Ann Surg Oncol (2017) 24:2206-2212



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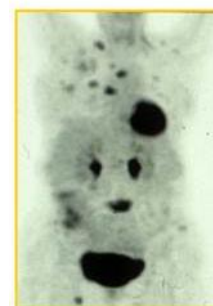
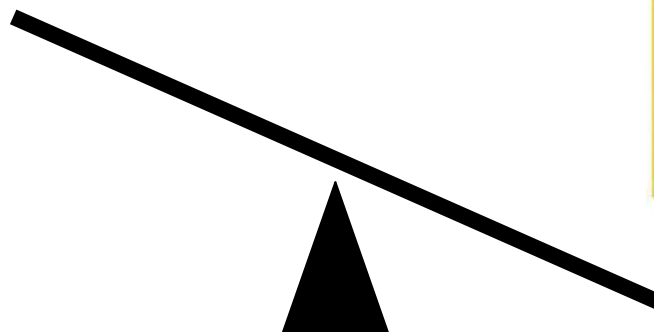
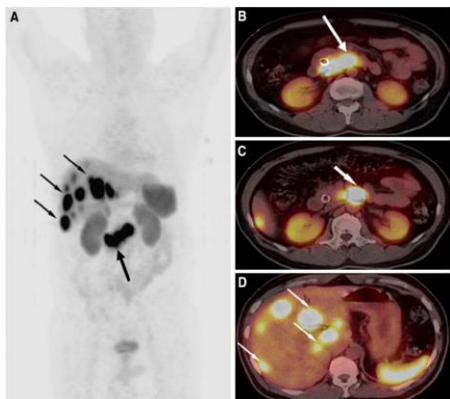
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PROGNOSTIC MARKERS

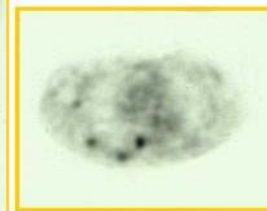
Nuclear imaging



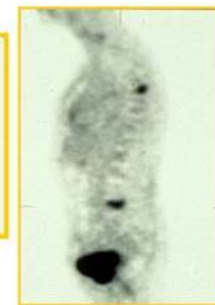
⁶⁸Ga-DOTATOC PET



Frontal projection



Transaxial



Sagittal

¹⁸F-FDG PET



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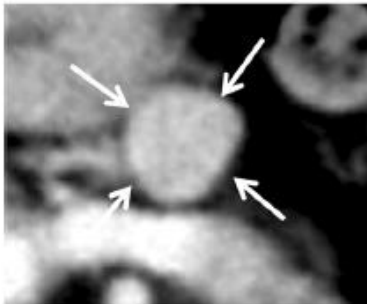
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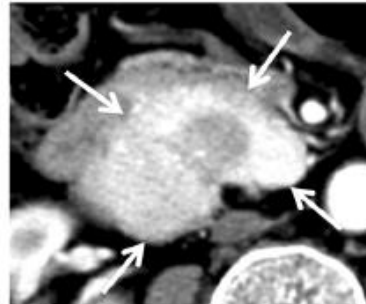
PROGNOSTIC MARKERS

...SHAPE?

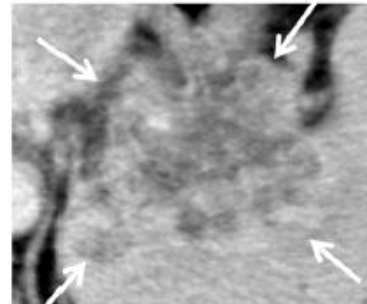
Type I



Type II



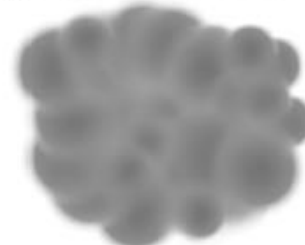
Type III



Single nodular



Single nodular with extranodular growth



Confluent multinodular



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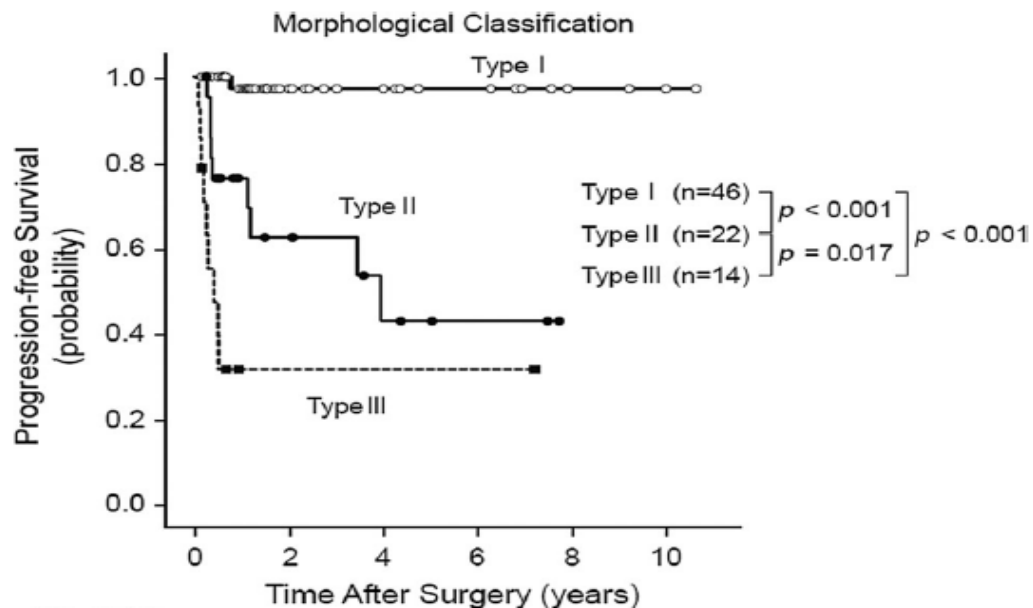
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PROGNOSTIC MARKERS

SHAPE



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PROGNOSTIC MARKERS

GENETICS

Gene mutations

Protein expression

DAXX
ATRX

DAXX
ATRX

mainly G2 tumors
advanced stage

Jiao et al. 2011 Science 331:1199–1203
Gross et al. 2006 Endocr Relat Cancer 13:535–540.
Marinoni et al. 2014 Gastroenterology 146: 453-460e5.
deWilde et al. 2012 Mod Pathol 25:1033–1039.
Singhi et al. 2017 Clin Cancer Res 23:600–609.



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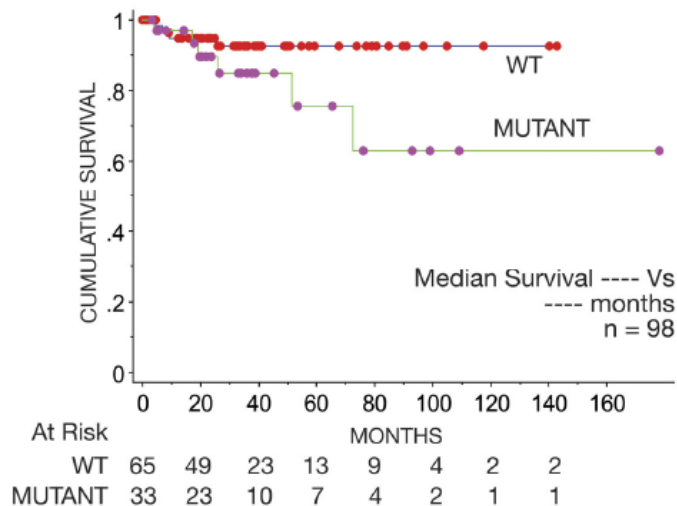
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PROGNOSTIC MARKERS

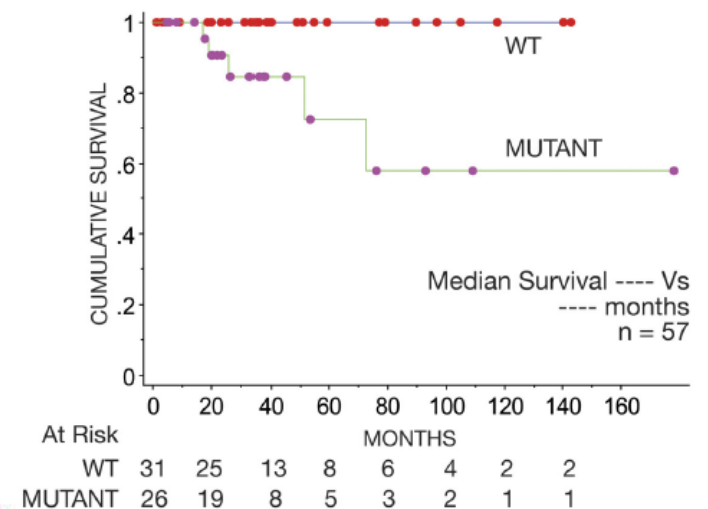
GENETICS



A. DAXX / ATRX (Whole Cohort)



B. DAXX / ATRX (WHO G2 Cohort)



Scarpa et al. 2017 Nature 543: 65



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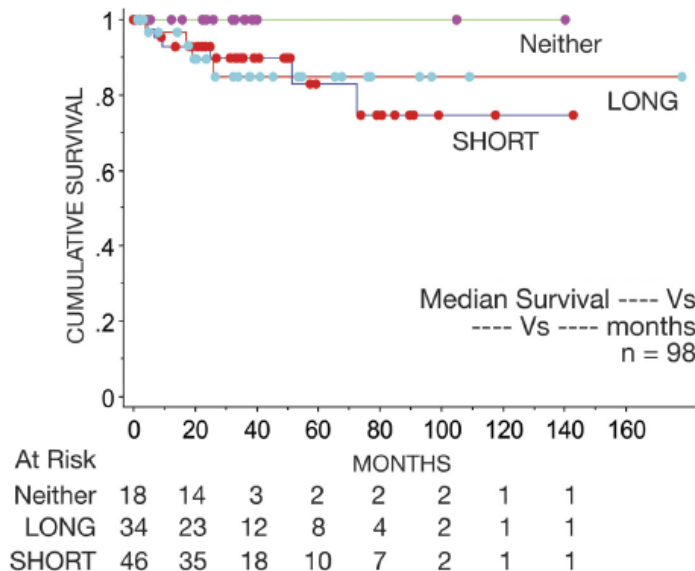
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PROGNOSTIC MARKERS

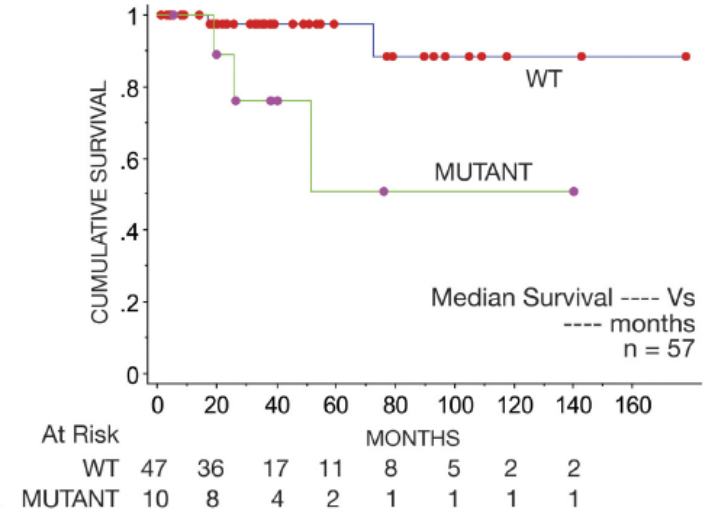
GENETICS



C. Telomere Length (Whole Cohort)



D. mTOR Pathway (WHO G2 Cohort)



Scarpa et al. 2017 Nature 543: 65



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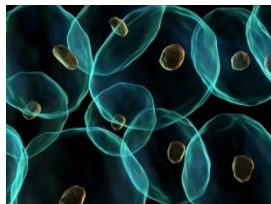
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PROGNOSTIC MARKERS

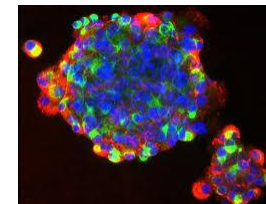
CELL-FREE TUMOR DNA



normal cells



DNA shedding



neoplastic cells



potential biomarker

Tsang et al. 2007 Pathology 39:197
Valenti et al. 2009 Cancer Lett 273:122
Dalle Carbonare et al. 2011 Urol Oncol



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PROGNOSTIC MARKERS

CELL-FREE TUMOR DNA

plasma DNA vs. metastasis biopsies

(34 patients covering 18 different tumor types)

46 genes and >6800 COSMIC mutations

97% mutations identified in metastasis biopsies were detected in matched ctDNA



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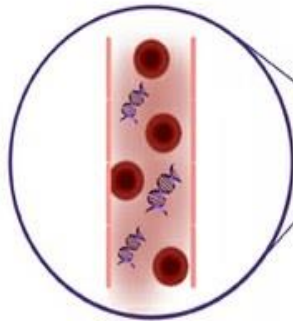
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PROGNOSTIC MARKERS

CELL-FREE TUMOR DNA



Tumour DNA can be found circulating in the bloodstream of patients



- potential alternative and/or replacement to tissue biopsies
- irrespective of cancer type and metastatic site
- multiplexed mutation detection
- useful in selecting personalized therapies



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PROGNOSTIC MARKERS

CELL-FREE TUMOR DNA

challenge

Relative lack of recurrent mutations in NENs as compared to other tumors



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PROGNOSTIC MARKERS

NET TEST

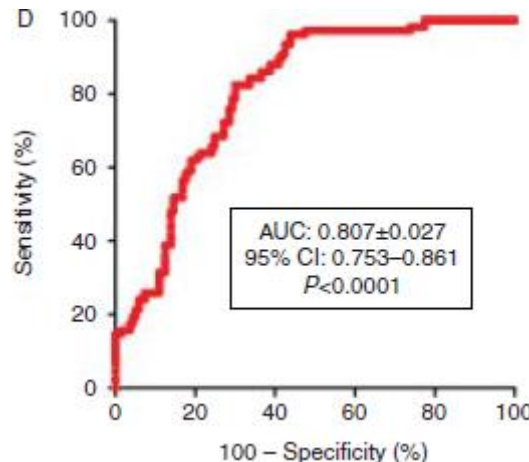
Blood and tissue neuroendocrine tumor gene cluster analysis correlate, define hallmarks and predict disease status

Proliferome
Growth factor signalome
Metabolome
Secretome I (general)
Secretome II (progressive)
Epigenome

Apoptome
Plurome
SSTRome

*Ki67, NAP1L1, NOL3, TECPR2
ARAF1, BRAF, KRAS, RAF1
ATP6V1H, OAZ2, PANK2, PLD3
PNMA2, VMAT2
PQB1, TPH1
MORF4L2, NAP1L1, PQB1, RNF41,
RSF1, SMARCD3, ZFHX3
BNIP3L, WDFY3
COMMD9
SSTR1, SSTR3, SSTR4, SSTR5*

Capacity of differentiating progressive disease from stable disease



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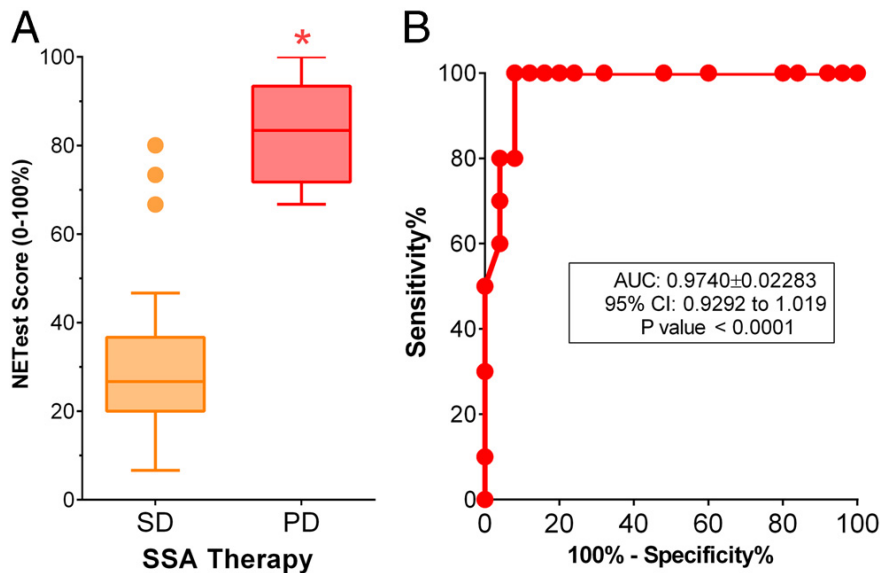
Circulating tumor cells, DNA and microRNAs as prognostic markers for NETs

PROGNOSTIC MARKERS

NET TEST



test set = 35 SSA-treated GEP-NEN



NETest significantly increased in the PD (n 10) vs SD (n 25)

Associates with response to medical therapy



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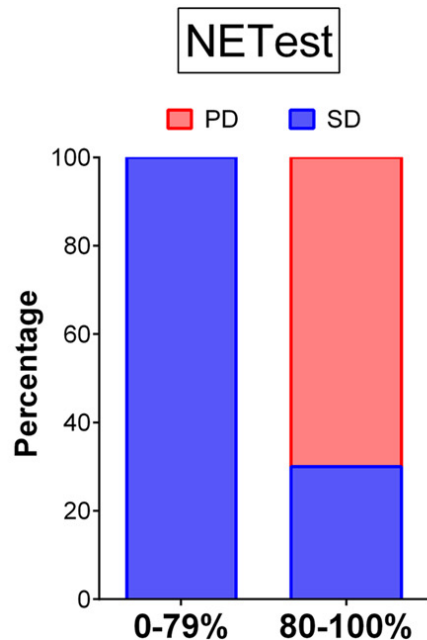
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PROGNOSTIC MARKERS

NET TEST

prospective set = 28 SSA-treated G1–G2 GEP-NENs



elevated NETest (80–100% activity; P .002, measured anytime during therapy) predicts therapeutic responsiveness

Predicts response to medical therapy



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PROGNOSTIC MARKERS

NET TEST



35 GEP-NET

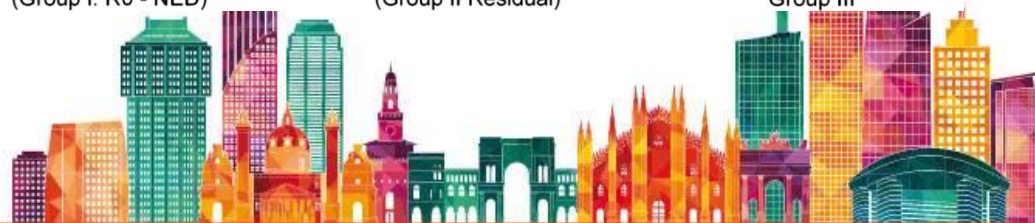
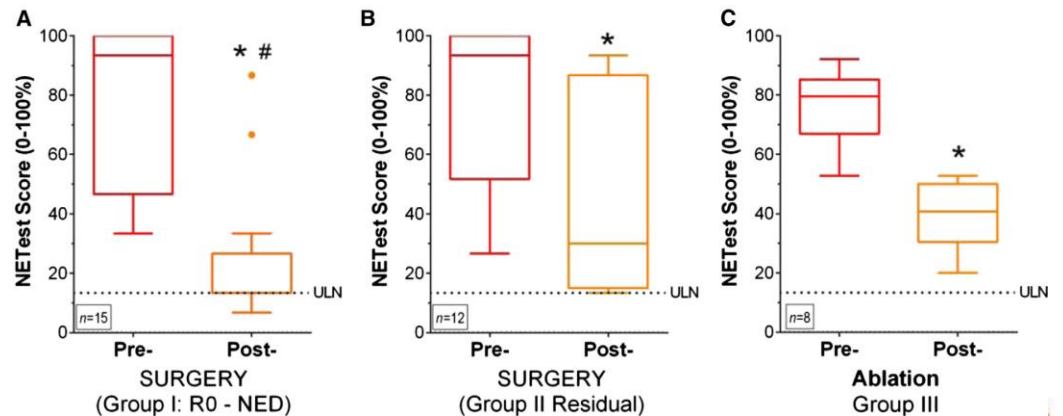
27 surgery

15 R0

12 residual

8 ablation

Predicts response to surgery



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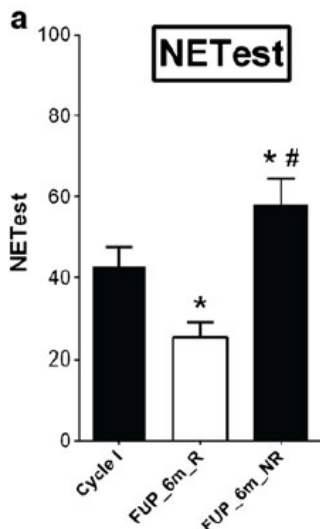
Circulating tumor cells, DNA and microRNAs as prognostic markers for NETs

PROGNOSTIC MARKERS

NET TEST

54 NET patients (M: F 37:17)
13 bronchial
35 GEP-NET
6 CUP

177Lu-based-PRRT (6.5-27.8 GBq)



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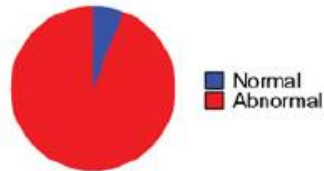
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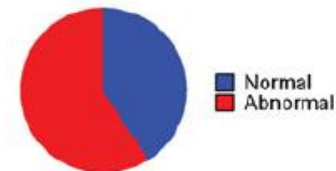
PROGNOSTIC MARKERS

NET TEST

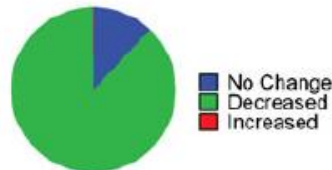
Pre-PRRT
(Cycle I) $n=54$



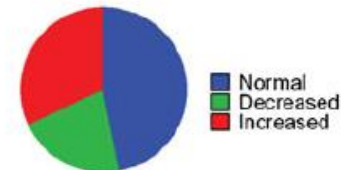
$p=0.0004$



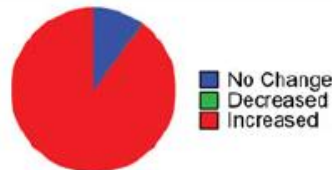
Responders
 $n=39$



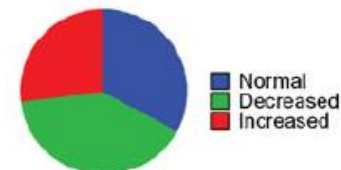
$p=0.0002$



Non-Responders
 $n=15$



$p=0.0068$



Predicts response to PRRT

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PROGNOSTIC MARKERS

NET TEST



NET gene transcript signature may be useful
in patients clinical management



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PROGNOSTIC MARKERS

Review

M C Zatelli et al.

CTCs and miRNA as prognostic markers in NENs

24:6

R223-R237

Circulating tumor cells and miRNAs as prognostic markers in neuroendocrine neoplasms

Marla Chiara Zatelli¹, Erika Maria Grossrubatscher², Ella Guadagno³, Concetta Sciammarella⁴, Antongiulio Faggiano⁵ and Annamaria Colao⁴



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PROGNOSTIC MARKERS

miRNA	De-regulation	NEN histology	Number of cases	Prognostic role	References
miR-92a2*	Up-regulated	SCLC	31	Correlation with chemoresistance and reduced OS	Ranade et al. (2010)
miR-150 and miR-886-3p	Down-regulated	SCLC	82	Correlation with reduced OS and PFS	Bi et al. (2014)
miR-886-3p	Down-regulated	SCLC	82	Correlation with reduced OS and PFS	Cao et al. (2013)
miR-7	Up-regulated	SCLC	44	Correlation with chemoresistance and reduced OS	Liu et al. (2015)
miR-192, miR-200c, miR-205	Down-regulated	SCLC	50	Correlation with increased OS	Mancuso et al. (2016)
miR-21	Up-regulated	Lung NENs	63 (19 TC, 6 AC, 19 LCNEC, 19 SCLC)	Correlation with presence of lymph node metastases in TC and AC	Lee et al. (2012)
let-7d, miR-19, miR576-5p, miR-340*, miR-1286	Up-regulated	Lung NENs	12 (3 TC, 3 AC, 3 SCLC, 3 LCNEC)	Correlation with OS	Mairinger et al. (2014)
miR-409-3p, miR-409-5p, miR431-5p	Down-regulated	Lung NENs	37 (22 TC, 15 AC)	Correlation with presence of lymph node metastases	Rapa et al. (2015)
miR-21	Up-regulated	Pancreatic NEN	40	Correlation with Ki-67 index and liver metastases	Roldo et al. (2006)
miR-642, miR-210	Up-regulated	Pancreatic NEN	37	Correlation with Ki-67 index (miR-642) and with metastatic spread (miR-210)	Thorns et al. (2014)



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PROGNOSTIC MARKERS

miRNA	De-regulation	NEN histology	Number of cases	Prognostic role	References
miR 196a	Up-regulated	Pancreatic NEN	37	Correlation with advanced stage, lymph node metastases, higher mitotic count, higher Ki67 index, reduced OS and DFS	Lee et al. (2015)
miR-183, miR-375	Up-regulated	MTC	45	Correlation with lymph node, residual disease after surgery, distant metastases and survival	Abraham et al. (2011)
miR-224	Up-regulated	MTC	40	Correlation with the absence of node metastases, lower stage at diagnosis and biochemical cure during follow up	Mian et al. (2012)
miR-21	Up-regulated	MTC	64	Correlation with basal calcitonin levels, lymph node metastases and advanced disease at the end of follow up	Pennelli et al. (2015)
miR-1225-3p	Up-regulated	PC	34	Correlation with recurrence in sporadic PC	Tombol et al. (2010)
miR483-5p	Up-regulated	PC	24	Correlation with metastatic spread and shorter DFS	Meyer-Rochow et al. (2010)



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PROGNOSTIC MARKERS



Conclusions

The available literature data clearly show that tissue miRNA profiling may potentially represent a prognostic biomarker in NENs. However, the role of circulating miRNAs in these settings is far to be consolidated.



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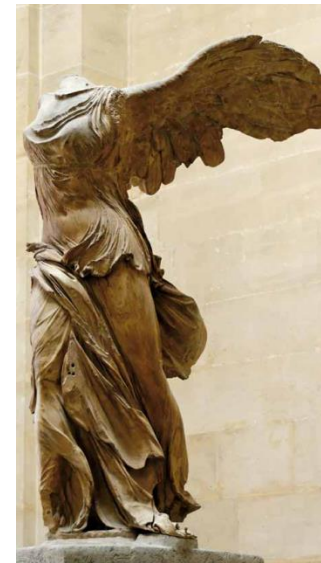
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PROGNOSTIC MARKERS

Studies prospectively evaluating circulating miRNA in different NEN types (and stages) and their levels after the different available therapeutic approaches are still lacking. On the contrary, studies employing CTC count as a marker of NEN prognosis report very promising results that need to be validated in further clinical trials. Studies on selected validation cohorts with long-term clinical follow-up are necessary to further qualify CTC as biomarkers in NENs.



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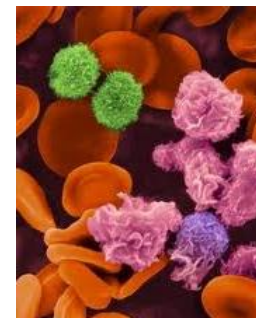
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PROGNOSTIC MARKERS

CIRCULATING TUMOR CELLS

circulating tumor cells
can be used as sentinels



blood can be proposed as a surrogate of tissues for
diagnostic analyses



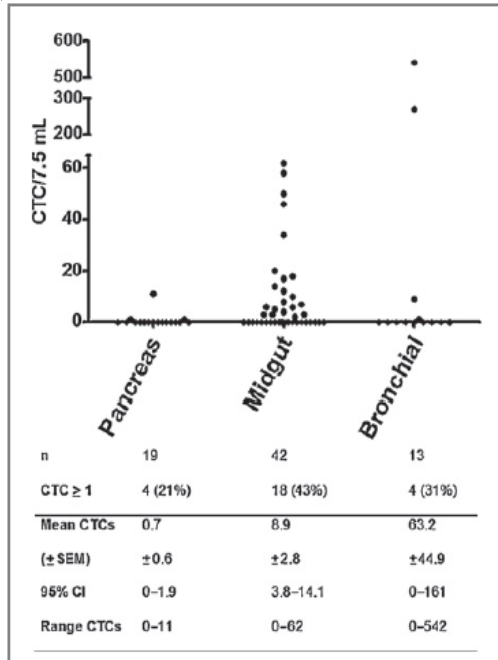
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PROGNOSTIC MARKERS



CIRCULATING TUMOR CELLS

No CTCs



stable disease

CTC levels correlate with

- urinary 5-HIAA levels
- burden of liver metastases

but not with

- Ki-67
- serum CgA

Khan et al. Clin Cancer Res 2011, 17: 337



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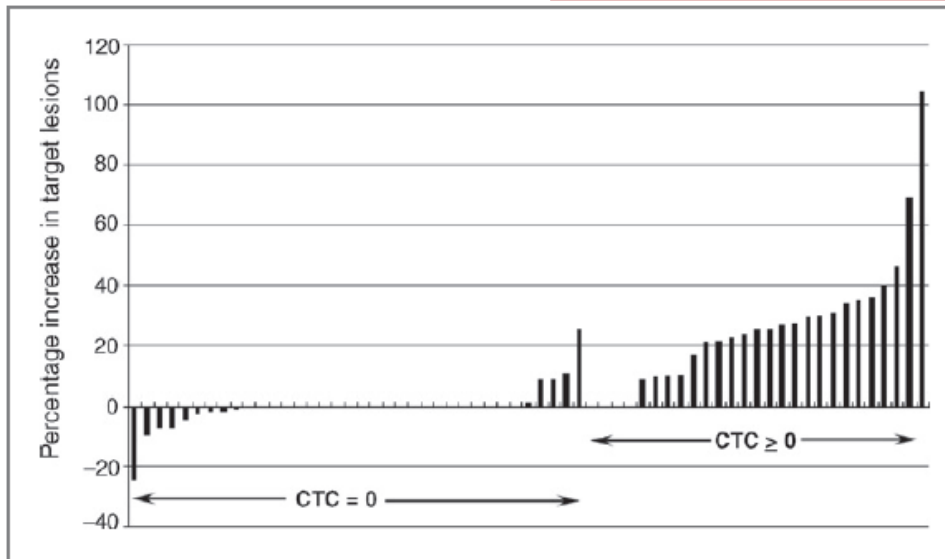
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PROGNOSTIC MARKERS

CIRCULATING TUMOR CELLS



CTCs seem to be associated with progressive disease and may provide useful prognostic information given the variable survival rates

Khan et al. Clin Cancer Res 2011, 17: 337



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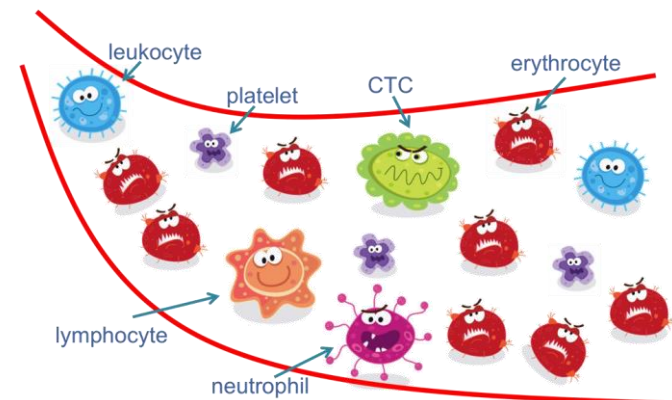
PROGNOSTIC MARKERS

CIRCULATING TUMOR CELLS

single-center prospective study, 176 patients with metastatic NETs

Presence of CTCs was associated with

- increased burden
- increased tumor grade
- elevated serum CgA



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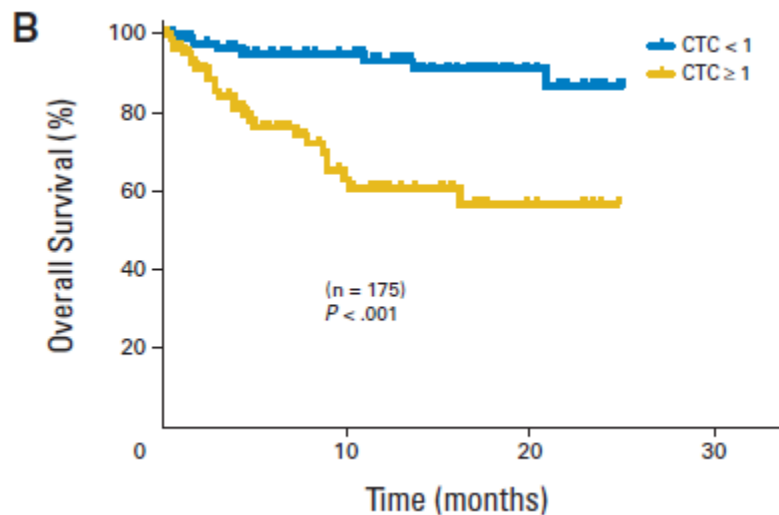
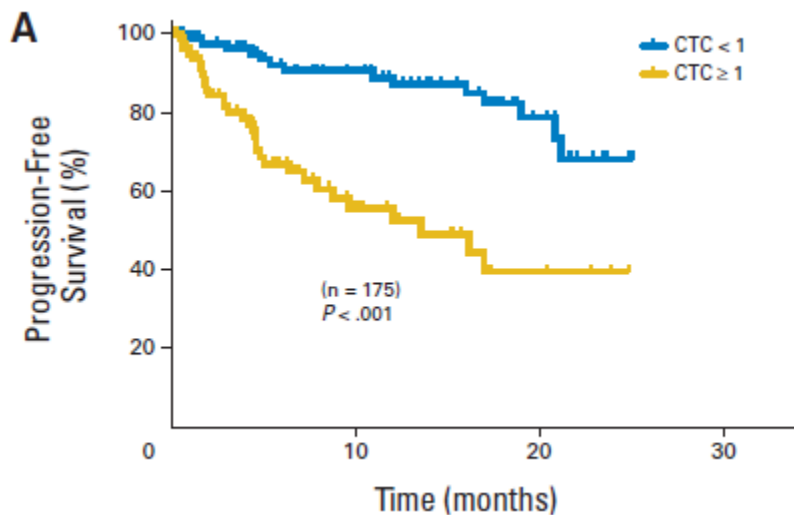
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PROGNOSTIC MARKERS

CIRCULATING TUMOR CELLS



CTCs correlate with progression-free survival independently of grade, tumor burden, and CgA



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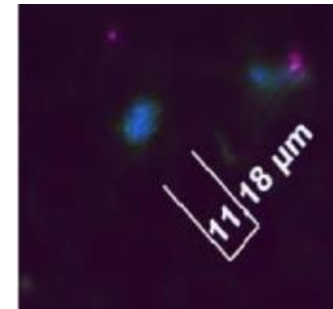
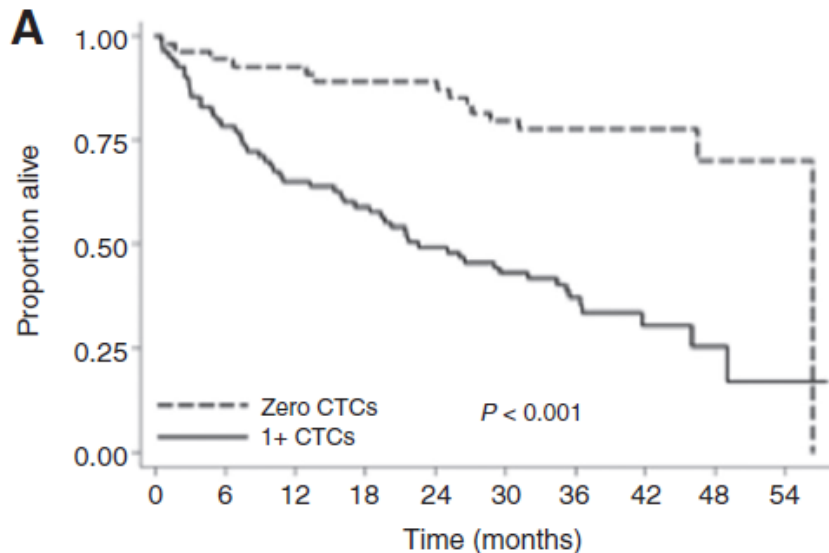
Circulating tumor cells, DNA and microRNAs as prognostic markers for NETs

PROGNOSTIC MARKERS

CIRCULATING TUMOR CELLS



138 patients with metastatic NENs



Number at risk

Zero CTCs	55	52	51	49	47	42	30	16	5	1
1+ CTCs	83	65	54	48	40	35	23	10	3	1



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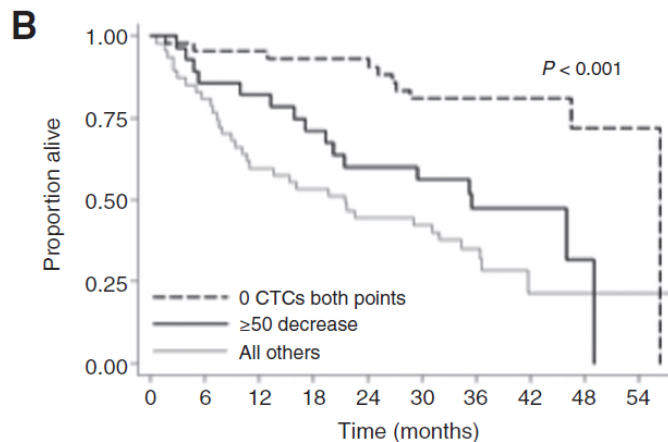
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PROGNOSTIC MARKERS

CIRCULATING TUMOR CELLS

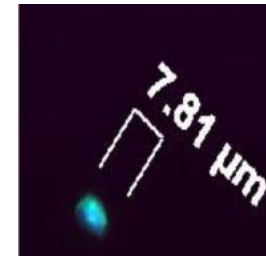


138 patients with metastatic NENs



	Number at risk									
	0	6	12	18	24	30	36	42	48	54
0 CTCs both points	43	41	41	40	39	34	26	15	4	1
≥50 decrease	28	24	23	19	16	15	11	6	1	0
All others	47	38	28	25	20	19	13	3	1	1

Changes in CTCs at first posttreatment time (3 – 5 weeks)



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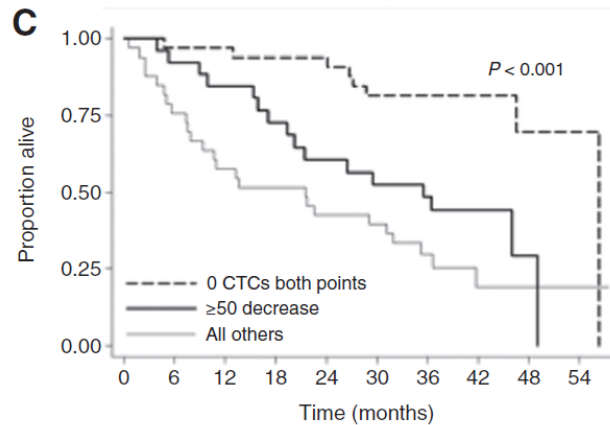
Circulating tumor cells, DNA and microRNAs as prognostic markers for NETs

PROGNOSTIC MARKERS

CIRCULATING TUMOR CELLS



138 patients with metastatic NENs



Changes in CTCs at second posttreatment time point (10–15 weeks)

	Number at risk									
0 CTCs both points	33	32	32	31	30	26	24	13	4	1
≥50 decrease	26	24	22	18	15	13	12	5	1	0
All others	33	25	19	17	14	13	8	3	1	1



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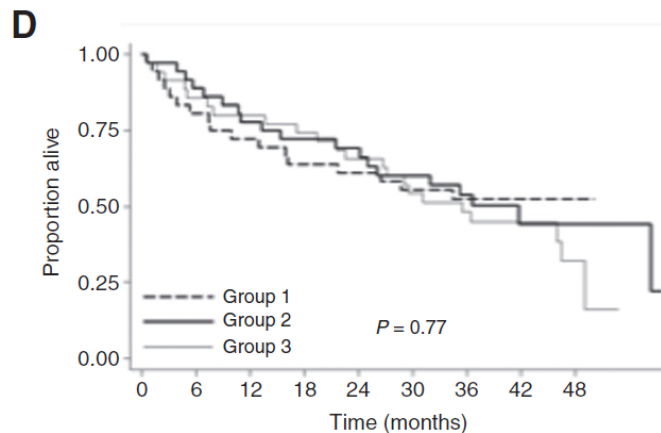
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PROGNOSTIC MARKERS

CIRCULATING TUMOR CELLS



138 patients with metastatic NENS



OS dependent on changes in CgA at first posttreatment time point

Number at risk

Group 1	36	29	26	23	22	20	17	7	1
Group 2	36	32	28	25	23	20	16	7	3
Group 3	35	30	28	26	23	19	15	10	2



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Translational Relevance

There is an increasing range of therapeutic options available for patients with neuroendocrine neoplasms (NEN) but no validated predictive biomarkers to direct treatment selection or sequence. Having previously demonstrated the prognostic relevance of circulating tumor cells (CTC) in NENs, we have evaluated their role as predictive biomarkers in response to therapy. We show that a poor outcome group can be defined by the presence of >8 CTCs at 3 to 5 weeks after therapy, or by a <50% fall or a rise in CTC number at the same time point compared with baseline. The association of change in CTC number is an independent prognostic variable and allows serial monitoring of response to therapy. These findings will require further external validation but may present the opportunity for adaptive trials in NENs, in which evidence-based sequencing strategies can be defined.

Changes in CTCs are associated with response to treatment and OS in metastatic NENs, suggesting CTCs may be useful as surrogate markers to direct clinical decision making



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skeletal involvement

SSTR expression

tumor heterogeneity

tracking expression over time and during therapy



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Series	Findings	Reference
79 metastatic NENs: – 19 pancreatic – 42 midgut – 13 bronchopulmonary – 5 unknown primary	<ul style="list-style-type: none">Moderate correlation ($r=0.5$, $P=0.007$) between CTCs count and urinary 5-HIAA in midgut and unknown primary NENsSignificant association between CTCs count and tumor burden of liver metastase ($B=8.91$, 95% CI=4.3–13.5, $P<0.001$)No correlation between CTCs count and Ki67 ($r=0.08$, $P=0.59$) and low correlation between CTCs count and serum CgA ($r=0.246$, $P=0.03$)0 CTCs associated with stable disease ($P<0.001$)	Khan et al. (2011)
175 metastatic NENs: – 42 pancreatic – 101 midgut – 17 bronchopulmonary – 12 unknown primary – 3 hindgut	<ul style="list-style-type: none">Significant association between CTCs count (≥ 1) and grade ($P=0.036$), tumor burden $>25\%$ ($P<0.001$) and serum chromogranin A >120pmol/L ($P<0.001$), respectivelyCTCs count ≥ 1 related with worse PFS (HRs: 6.6, $P<0.001$) and OS (HRs: 8.0, $P<0.001$)Within grade 1, two CTCs-based subgroups: HRs=5.0 for PFS ($P=0.017$) and HRs=7.2 for OS ($P=0.023$)Within grade 2, two CTCs-based subgroups: HRs=3.5 for PFS ($P=0.018$) and HRs=5.2 for OS ($P=0.036$)	Khan et al. (2013)
138 metastatic NENs: – 31 pancreatic – 81 midgut – 12 bronchopulmonary – 11 unknown primary – 3 hindgut	<ul style="list-style-type: none">Significant association ($P<0.001$) between the first post-treatment (after 3–5 weeks) CTCs count and progressive disease (PD): PD in 8% of patients with 'favorable count' (0 CTCs at baseline and after treatment, or $\geq 50\%$ CTCs reduction after treatment) vs 60% in unfavorable group ($<50\%$ CTCs reduction or increase)Changes in CTCs count at the first post-treatment time (after 3–5 weeks) strongly associated with OS ($P<0.001$): the best outcome in group with 0 CTCs count at baseline, followed by the group with $\geq 50\%$ CTCs reduction after treatment (HRs=3.31; 95% CI=1.50–7.32) and then the group with $<50\%$ CTCs reduction or increase (HRs=5.07; 95% CI=2.48–10.38)In multivariate analysis changes from baseline CTCs count ($P=0.0002$) and grade ($P=0.0046$) resulted independent prognostic factors	Khan et al. (2016)



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Series	Findings	Reference
34 Merkel cell carcinomas	<ul style="list-style-type: none">• Correlation between CTCs positivity (≥ 1 CTCs) and extent of disease ($P=0.004$)• Statistically significant difference in median OS between CTCs positive and CTCs negative samples ($P=0.0003$), also in case of regional node metastases ($P=0.015$)	Blom et al. (2014)
30 Merkel cell carcinomas	<ul style="list-style-type: none">• Significantly higher CTCs count in patients with active disease• Increasing CTCs count associated with development of new metastases	Gaiser et al. (2015)
59 Small cell lung cancers	<ul style="list-style-type: none">• Association between CTCs count < 2 and prolonged OS and PFS ($P \leq 0.001$)• CTCs count decrease after the first cycle of therapy correlated with longer OS and PFS ($P \leq 0.001$)• CTCs count decrease after four cycles of therapy correlated with longer OS ($P=0.05$) and PFS ($P=0.007$)• CTCs count < 2 after the first cycle of therapy is an independent prognostic factor for OS in multivariate analysis ($HRs=3.5$, $P=0.09$)	Hiltermann et al. (2012)
31 Small cell lung cancers	<ul style="list-style-type: none">• Identification of chemosensitive and chemorefractory patients by CTCs copy-number aberrations profile and observation of significant difference ($P=0.0166$) in PFS between these two groups• Difference in CTCs copy-number aberrations profile between initial and acquired chemoresistance	Carter et al. (2017)



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“CTCs are a promising prognostic markers for patients with NETs and should be assessed in the context of clinical trials with defined tumor subtypes and therapy”



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PROGNOSTIC MARKERS



Despite the identification of CTCs, ctDNA and miRNAs as circulating biomarkers capable of providing prognostic and predictive information in patients with NET, they have not been incorporated into routine clinical practice. This is due in part to technological limitations hampering routine analysis, as well as limited data regarding the implications of clinical decision making based on these biomarkers.

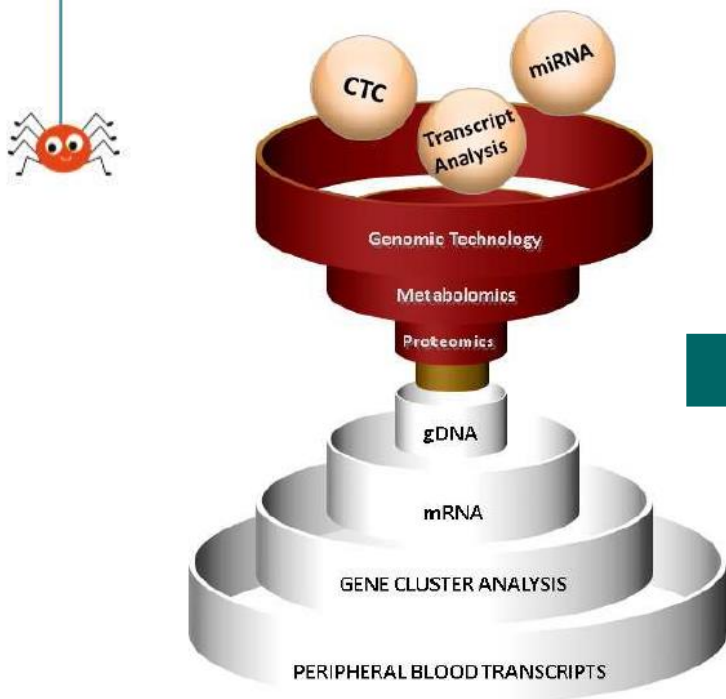


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PERSONALIZED
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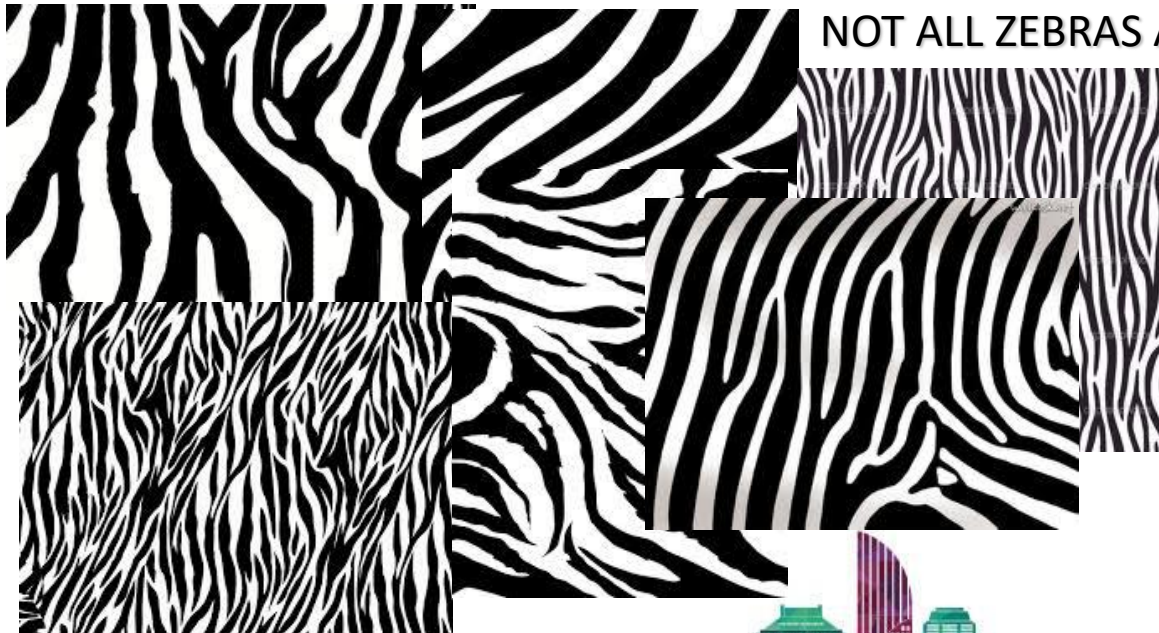
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PROGNOSTIC MARKERS

THERE ARE A LOT OF ZEBRAS

NOT ALL ZEBRAS ARE THE SAME



ENEAA

6th workshop ParaSellar Lesions



organized by

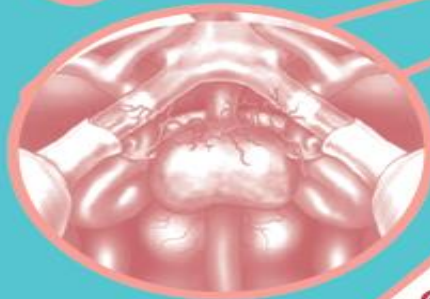


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Grazie per l'attenzione