

Genomics and Epidemiology for Gastric Adenocarcinomas (GE4GAC)

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WHY GASTRIC CANCER?

- 4th most common malignancy in the world
- 2nd most common cause of cancer-related death
- Important geographic variation:

High-risk areas: Japan, Korea, Latin America (Brazil, Peru), Russia

Low-risk areas: USA, Israel, Kuwait, Canada, UK



Estadiamento indeterminado

In Brazil (INCa, 2016)

- 3rd more incident tumor in men
- 5th more incident tumor in women
- 20.5k new cases/year
- 14.2k deaths/year

Overall 5-year survival rates (all stages) (Jemal et al., 2010; Theuer et al., 2000)

- 40-60% in Japan
- 15-30% in the USA

-Ethnicity and treatment response (Kim et al., 2010):

Group	Chemotherapy + Bevacizumab	Chemotherapy + placebo
Asians	13.9	12.1
Non-asians	11.5	6.5*
		*p<0.01

Message: the disease is different according to the ethnical background!



Module 1 - Epidemiology

To collect epidemiologic information from ~2,000 individuals:
Control 1 – Cancer prevention program: no cancer and no gastric complains.

Control 2 – Endoscopic controls (some gastric issues, no cancer)Cases – diagnosis of gastric adenocarcinoma

- Detailed socio-demographic information
- Data regarding diet, ethanol & tobacco consumption
- Use of drugs such as aspirin, anti-inflammatory agents, antibiotics, proton-pump inhibitors, sweeteners
- Brazil: Southeast, North, Northeast
- Peru?

Dynamic alterations in gastric cancer...

Intestinal type: ~54%

Presents as "glandular structures" in histology Higher prevalence of *H. pylori* infections *Declining globally* Male:Female ratio = 2:1

Older patients

Better prognosis

Diffuse type: ~32%

Infiltrative lesions Loss of CDH1 (20%)

Male:Female ratio = 1:1

Incidence is is not declining so fast (growing?)

Younger age Worse prognosis

Mixed type: ~14%

Idade ao diagnóstico	%
<20 anos	0.1
20-34	1.7
35-44	4.5
45-54	12.2
55-64	20.4
65-74	24.7
75-84	24.3
>84 anos	12.2



Module 2 – Molecular Biology

Full support from the epidemiology module

- 2.1 Microbiome analysis
- 2.2 Early Onset/Familial Gastric Cancer
- 2.3 Markers of neoadjuvant chemotherapy response
- 2.4 Markers of prognosis



Module 2.1 – Microbiome Analysis

- Gastric juice collected from >150 patients
- Biopsies available for ~90%

A Trial and Error Approach



Microbiome

Human Genome

Nayak & Turnbaugh, 2016

Microbiome and chemotherapy response?



Trends in Immunology

Klevorn & Teague, 2016

Oral Cancer - Species Richness



Thomas et al., in preparation

Best predictive genera PCoA plot – public dataset





Rectal Cancer



Thomas et al., *in preparation*

Non-Cancer A Rectal-Cancer





Non-cancer Rectal-cancer

Non-cancer Rectal-cancer

Non-cancer Rectal-cancer

Thomas et al., in preparation

Non-cancer Rectal-cancer

Non-cancer Rectal-cancer



Gastric cancer - bacterial diversity



Abundance of distinct genera









Shotgun metagenomics?

Microbiome manipulation?

www.metasub.org

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METHODS

MetaSUB Metagenomics & Metadesign of Subways & Urban Biomes

letaSUB



* Negative for CDH1



Why should we study the double-stranded transcriptome?





PCA3 is located in the intronic antisense strand of PRUNE2



Salameh et al., 2015

PCA3 regulates mRNA and protein levels of PRUNE2



















Mature PCA3 forms a dsRNA complex with immature PRUNE2

dsRNA – trigger anti-viral response?

ADAR1 – Double-stranded RNA-specific deaminase

PCA3, PRUNE2 & ADAR1 co-localize in the cell nucleus and are resistant to RNAseA treatment



Sensitive to RNAse-H treatment (dsRNA)

If the PCA3/PRUNE2/ADAR complex is functional, we should detect RNA editing



RNA editing was also observed in prostate cancer samples





If PCA3 and ADAR1 act blocking PRUNE2, we shall be able to reduce tumor growth if we control these transcripts





The study of the ds-transcriptome (dsRNA-Seq) in gastric cancer may reveal novel actionable targets for this malignancy



- Gene panel (~160 transcripts) based in the 4 most recent comprehensive studies of gastric cancer genomics (200 cases)
- Evaluate the effect of cumulative mutations and prognosis
- WES for polar cases (disease free-survival)
- Gene panel v2.0
- Molecular Ancestry studies

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shRNA ADAR1: increases PCA3 & PRUNE2 levels (protein and mRNA)



RNA-ChIP: ADAR1 and paraspeckle proteins are in the same complex as PCA3 & PRUNE2



Paraspeckle-proteins: nuclear retention/degradation

