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**UNIVERSIDADE ESTADUAL PAULISTA
“JÚLIO DE MESQUITA FILHO”
FACULDADE DE MEDICINA**

Carolina Mendonça Gorgulho

**Efeito de Células Tumorais Estressadas e Seus Exosomos
Sobre a Ativação de Células Dendríticas *in vitro***

Tese apresentada à Faculdade de Medicina,
Universidade Estadual Paulista “Júlio de
Mesquita Filho”, Câmpus de Botucatu, para
obtenção do título de Doutora em Patologia.

Orientador: Prof. Dr. Ramon Kaneno
Coorientadora: Profa. Dra. Graziela Gorete Romagnoli

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Palavras-chave: autofagia; câncer colorretal; imunoterapia; quimioresistência; quimioterapia metronômica.

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as a graduate student:**

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Chapter 1 – Review of the Literature

Developing immunotherapies for patients with colorectal cancer

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Abstract

Risk factors for colorectal cancer (CRC) include poor dietary habits, sedentarism and obesity, in addition to genetic syndromes that predispose individuals to this disease. Current treatment mainly relies on surgical excision and cytotoxic chemotherapies; immunotherapy with checkpoint inhibitors only plays a role in 4-6% of patients with MSI^{high} tumors. Tumor cells have means to limit apoptosis and utilize autophagy to survive chemotherapy leading to drug resistance and enhanced survival. Pharmacological or molecular inhibition of autophagy has been proposed to improve the efficacy of cytotoxic chemotherapy. In addition, immunotherapy with checkpoint inhibition has raised substantial interest, but most patients with CRC do not respond to this modality of treatment, despite the fact that colorectal tumors are frequently infiltrated with adaptive immune cells. Thus, the search for new therapies that can be combined with current approaches to increase their efficacy, and new knowledge of the biology of CRC are pivotal to improve the care of patients suffering from this disease. Here, we review the basic immunobiology of CRC, current 'state of the art' therapies and new therapeutic promises for the future.

Keywords: colorectal cancer, immunotherapy, autophagy, chemoresistance, metronomic chemotherapy, DAMPs, HMGB1, dendritic cells, T cells.

1.1 - Etiology and Epidemiology of Colorectal Cancer

Colorectal cancer (CRC) ranks among the third most frequent cancer in both sexes worldwide, excluding non-melanoma skin cancer, accounting for almost 10% of all diagnosed cancers (1). Although one of the most preventable and treatable types of cancers (2), recent years have seen a rising incidence of CRC, particularly in western countries, due to the ageing population, dietary habits, sedentarism and other largely modifiable lifestyle risk factors (1). The mortality rate has been decreasing since the 1980's, prior to the advent of modern screening studies (3). Calculation models to predict risk of colorectal cancer that include both genetic and environmental factors are better risk predictors than the models currently employed based solely on age and familial history (4).

About 75% of CRC patients develop sporadic disease while 15 to 20% have a positive familial history of CRC syndromes, including: 1) Lynch syndrome (also known as hereditary nonpolyposis colorectal cancer (5)), characterized by mutations in mismatch repair (MMR) genes such as *MLH1*, *MSH2*, *MSH6* and *PMS2*, leading to microsatellite instability (MSI), and 2) familial adenomatous polyposis, which arises from acquired or heritable (6) mutations in the APC gene, promoting development of colon cancer at a young age (1). An important molecular distinction between sporadic MSI and Lynch syndrome-associated CRC is that the latter does not present with *BRAF* mutations (5). Chronic colitis associated with inflammatory bowel disease is thought to be responsible for approximately 1% of CRC cases, but this number is decreasing, likely due to the success of anti-inflammatory therapies (7). Similar to other cancers, chronic inflammation is still a common anlage in patients with CRC (8).

CRC arises from accumulation of a succession of mutations that lead to genetic and epigenetic instability of normal epithelial cells, culminating in the formation of benign lesions known as aberrant crypts, which progress to adenomas and eventually to invasive cancer (1), in concert with local immune cells responding to the need for both barrier function and selective transport (9).

The identification of various polyp morphologies that can give rise to malignant tumors as well as the molecular pathways that lead to their formation and progression enables more

accurate stratification (10), hopefully leading to better treatment selection. To date, four individual common genomic/epigenomic profiles have been described in CRC: 1) chromosomal instability (the most common, characterized by the occurrence of aneuploidy) and responsive to checkpoint inhibitors; 2) MSI^{hi}, which displays a normal karyotype but unique mutations in DNA damage repair genes; 3) CpG island methylator phenotype, and 4) global DNA hypomethylation (6). These mutations converge on key signaling pathways that dictate the biological behavior of tumor cells. For example, one of the most well studied pathways that is altered in CRC is the Wnt – β -catenin pathway. Mutations in the *APC* gene prevent proteasomal degradation of the transcription factor β -catenin, leading to upregulated transcription and secretion of products of the *WNT* gene (6) and deregulated cell proliferation. Mutations in the transforming growth factor- β (TGF- β) gene (or of its receptors and other genes such as *SMAD4*) are associated with the formation and malignant transformation of benign lesions (11). Furthermore, *SMAD4* expression can be indicative of responsiveness to 5-fluorouracil (5-FU) (12). Activating mutations in the oncogene *KRAS* lead to constitutive activation of the mitogen activated kinase (MAPK) pathway via *BRAF* signaling, promoting cell proliferation and survival (6). The PI3K/AKT signaling pathway is also affected during colonic carcinogenesis, through mutations in *PIK3CA*. This promotes malignant transformation of adenomas and loss of expression of the tumor suppressor *PTEN*, found in up to 30% of CRC cases (6, 13).

CRC can be further divided into two subgroups, according to mutational burden: 1) heavily mutated tumors (>12 coding mutations per 10^6 DNA bases), which are MMR-deficient and present high MSI or 2) MMR-proficient tumors, with low MSI and therefore lower mutational burden (<8.24 mutations per 10^6 DNA bases) (10). This classification is especially important for the immunobiology of the disease and eligibility for immunotherapy, as discussed in detail below.

1.2 - Immunobiology of CRC

It is well accepted that the immune system, through both innate and adaptive mechanisms, is capable of recognizing and eliminating transformed cells, in a process termed immunosurveillance. Both T and B cells are essential for the establishment of an adaptive immune response. Maturation of these cells depend on the function of proteins rag 1 and 2,

involved in the recombination of *VDJ* genes of both T and B cell receptors (14, 15). *RAG*^{-/-} immune deficient mice are more susceptible to the occurrence of both spontaneous and chemically induced tumors, providing experimental evidence for the immunosurveillance concept (16). Thus, we are naturally equipped with effector cells and molecules capable of mediating the elimination of tumors, measurable in both experimental models and human clinical settings, in the form of tumor-specific antibodies or appearance of infiltrating $\alpha\beta$ and $\gamma\delta$ T cells.

Killing of susceptible tumor cells mediates their 'culling' or selection, enabling emergence of cells resistant to immune effectors and retaining genes associated with survival, immune evasion, and ability to escape to so-called pre-metastatic niches (17, 18). Such niches have limited or absent tissue-resident memory cells (TRMs) responsible for immunosurveillance (19), thus facilitating immune evasion and migration to distant sites. These steps as amended are known as the three E's: elimination, equilibrium and escape (20), and now the two C's: culling (selection for more potent tumor cells) and 'calling' (emigration to distant sites).

Thus, almost all CRC patients present with immune infiltration of tumors, associated with the estimated 7-10 years of host-tumor interaction before clinical diagnosis is even ascertained. The presence of tumor infiltrating lymphocytes (TILs) is, in general, considered a marker of good prognosis and is associated with an improved overall survival (OS) (21-23). Infiltration of CD8⁺ T cells within the tumor and at its margins is a better predictive factor of disease-free survival than the current applied TNM staging method (24), which uses size of the primary tumor (T), lymph node involvement (N) and presence of metastatic disease (M) as parameters. Additionally, patients who present with a Th1 gene signature have improved survival (25). CRC patients with large numbers of infiltrating NK cells also have longer survival rates (26). Similarly, the presence of NK cells in liver metastasis positively correlates with overall survival (OS) (27). The opposite seems to be the case for neutrophils, with infiltration being correlated with worse prognosis and more advanced stage of disease (28-30) although there is compelling evidence pointing to an anti-tumor supporting role for this population as well (31). Infiltration of myeloid-derived suppressor cells (MDSCs), associated with neutrophilic infiltration, in colorectal tumors is indicative of an unfavorable prognosis, being associated with nodal and distant metastasis and advanced stage of disease (32, 33). A meta-analysis of studies evaluating the association

between infiltration of tumor associated macrophages (TAMs) in several solid cancers and individual clinical parameters concluded that for CRC, TAMs are positively linked to improved OS, (although no distinction was made between M1 and M2 phenotypes) (34) and higher infiltration of CD8⁺ T cells (35). The presence of TAMs in the invasive front of colon tumors correlates with a lower incidence of metastatic disease and improved OS (36). However, immature monocytes (which can give rise to TAMs and dendritic cells [DCs]) impair the activity of cytotoxic T lymphocyte (CTL) within tumors (37).

Although the main focus of conventional vaccination-based immunotherapies thus far has been on promoting antigen presentation in the lymph nodes, interaction between antigen presenting cells (APCs) and T cells also occurs within the tumor. A minor subset of DCs has been characterized within tumors as BATF3⁺ CD8α⁺ CD103⁺ DCs in mice and CD141⁺ in humans, which are highly activated, possess alkaline endocytic compartments and are major producers of IL-12, therefore being very efficient at antigen cross-presentation as well as capable of promoting a TH1 response (38). They are transcriptionally driven by IRF8 and BATF3 and differentiate in the presence of the cytokines FLT3L and GM-CSF. These DCs are highly efficient, activating both naïve and previously activated tumor-specific CTLs *ex vivo*, albeit at higher numbers than normally found within tumors. Indeed, they are indispensable for *in vivo* tumor regression following adoptive cellular transfer, in models that exclude T cell priming in the lymph node. The transcriptional signature for this DCs subset in individual human cancers (including CRC) correlates with a favorable prognosis (38). CD103⁺ DCs also appear to be important mediators of chemotherapy-induced tumor regression in mice, since depletion of myeloid cells (but not of CD11b⁺ and CD103⁺ DCs) ameliorates the anti-tumor effect of paclitaxel in an IL-12 dependent manner (39). Additionally, a transcriptional signature enriched for IL12A and IRF8 mRNA expression is predictive of complete responses to paclitaxel in human breast cancer (39). In the normal gut, DCs also generate T regulatory cells, in accordance with the highly tolerogenic environment of this tissue which is constantly exposed to food antigens, dead and dying cells, and the microbiota (40). CD103⁺ DCs, however, apparently fail to do so in the colon of patients suffering from ulcerative colitis and induce production of pro-inflammatory cytokines by T cells co-cultured *ex vivo* with these DCs (41).

Even though the infiltration and persistence of certain immune populations can be a positive prognostic marker, it can also be detrimental in the context of chronic inflammation, which continuously generates oxidative stress, tissue and DNA damage, leading to transformation of normal epithelial cells and progression of existing tumors (42). Not only chronic inflammation but also the gut microbiome has been investigated regarding its role in carcinogenesis and tumor progression (42). Colonic tumors exhibit increased tissue permeability, facilitating penetration of commensal bacteria, activating myeloid immune cells within the tumor via MyD88 engagement, and thus perpetuating tumor-promoting inflammation (43). Commensal bacteria can also elicit inflammatory responses in an opportunistic manner via expression of virulence-associated genes. For example, CRC patients who are seropositive for *H. pylori* present with much higher levels of activated Th1 T cells than their seronegative counterparts when compared to healthy controls (44). *H. pylori* seropositive patients also display higher activity of the immunosuppressive enzyme IDO, suggesting that not only does *H. pylori* induce chronic inflammation in the CRC setting, but it can also mediate suppression of tumor-specific effector cells. *H. hepaticus* is another example of a microbe associated with the induction of colitis and CRC, in a variety of mouse models (45-47). *B. fragilis* infection promotes CRC in mice, with the participation of immuno-modulatory Th17 and $\gamma\delta$ T cells (48, 49). Additionally, *B. fragilis* infection in CRC patients is correlated with a worse prognosis (42, 50-52). *In vitro* studies demonstrate that *E. faecalis* induces oxidative stress in immune cells, and DNA damage and genomic instability in colonic epithelial cells (53, 54).

Chronic inflammation also enhances gut susceptibility to tumor-promoting bacteria. Colibactin, a genotoxin produced by a strain of *E. coli*, induces hepatocyte growth factor (HGF) production, the major ligand for the Met membrane tyrosine kinase signaling receptor, thereby promoting tumor cell proliferation in a CRC xenograft model (55). Within the colon of patients with inflammatory bowel disease (IBD), colibactin-producing *E. coli* are enriched and associated with a worse prognosis (42, 56-58). In contrast, the balanced interplay between immunity and microbiota can either delay the onset of CRC or of its progression, suggesting that some components of our microbiome and their metabolites can serve a protective role, including the presence of *Bifidobacterium lactis* (59), *Lactobacillus acidophilus* (60) and others.

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