Editorial

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Microbes and cancer geography: can we exploit recent lessons from the gut system to oral cancer context?

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Dear Readers,

In recent JAOS editorials, oral cancer[4] and oral microbes[3] were independently in the spotlight, and in this issue, two interesting studies[9,10] bring these topics together and lead us to an interesting discussion.

Before considering the articles published in this JAOS issue, we must consider the aspects raised by Bongers, et al.[2] (2014); Garlet and Santos[3] (2014). In summary, the authors elegantly describe the interplay of host microbiota, genetic factors and inflammation in the development of intestinal neoplasms in mice. Using interesting experimental tools such as transgenic mice, and simple but insightful strategies such as broad-spectrum antibiotics treatment, the authors demonstrate a clear relationship between bacteria and site-specific cancer development. Interestingly, the results from Lira´s group provide experimental evidence clearly in line with 'old' suggestions that bacteria 'might produce carcinogens'[1]. Evidently the cancer etiology is really complex, and translation of authors' findings to human cancer reality requires further investigation[3]. Also, while some microbes have been implicated as potential carcinogenesis trigger, probiotics microorganisms have been demonstrated to regulate intestinal inflammation and pointed as possible protective factors against the cancer development[6,8].

Back to oral cavity, one may argue that Bongers, et al.[2] (2014) data may be limited to the gut system, and that is premature to translate such finding to human oral cancer reality. However, recently an interesting parallel between the gut and oral cavity was drawn, originally focused on the host-microbe homeostasis (or the lack of) and its role in the health/disease outcome[5]. Interestingly, the gut and the oral cavity comprise a mucosal firewall in close contact with a highly diverse and abundant microbial flora. In both environments the disruption of gut host-microbe homeostasis has been associated with severe inflammatory pathologies. Please not that Bongers, et al.[2] (2014) study also demonstrates the central involvement of inflammation in intestinal cancer development, in accordance with several previous evidences. Therefore, gut and the oral cavity share features such as the mucosal nature associated with a profuse microbial flora, and the relatively common susceptibility for microbial-driven chronic inflammation.

As previously mentioned, it is obviously premature to make any strong statement regarding a possible role of oral bacteria in oral cancer only based on the gut-mouth parallel, but two studies published in this edition of the JAOS may lead us to interesting considerations.

Pan, et al.[9] (2014) from Shanghai´s Stomatological Disease Centre and Jiao Tong University, demonstrate a high prevalence of drug-resistant microbes (such as methicillin resistant *S. aureus* [MRSA]) in oral cancer patients. While such finding is properly discussed by the authors within the study limitation, and primarily interpreted as a potential side effect of the compromised immune system due cancer treatment, one may argue if such microbes really appeared after the treatment. Indeed, the cross-sectional nature of the study does not allow the determination of the time of such microbes emergence, based on the association of microbes with gut cancer it is possible to speculate that specific bacteria could be not a cause (a co-factor perhaps) and not a consequence of cancer (and its immunosuppressive treatment).

On the other hand, Zhang, et al.[10] (2014) from Jiamusi University and Qiqihaer Medical University in China demonstrate that Lactobacillus sp. A-2 metabolites have a potential role in the inhibition of growth and induction of apoptosis of human tongue squamous cell carcinoma CAL-27 cells *in vitro*. As discussed by the authors, probiotics microorganisms metabolites may have anti-tumor functions acting directly on cancer cells, but also may exert antimicrobial activities, which in theory also could interfere in cancer development, at least in the scenario described by Bongers, et al.[2] (2014).

Again, we reinforce that the translation of experimental data from the gut to oral cancer reality might be only speculative at this time. In a very astute comment focused on the bacteria-cancer link in the gut, Jobin[7] (2014) discusses the existence of layers of complexity by highlighting the interplay between host genetics, microbial location, and tumor geography. The microbial contribution to cancer development in both gut and oral cavity environments evidently requires further investigation, but the similarities between both niches may provide additional valuable clues to direct future investigations.

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