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Letter to the Editor

Cancer Epidemiology, Biomarkers & Prevention

Telomere Length and Pancreatic Cancer Risk—Letter

Raffaella Mormile

In a recent publication, Antwi and colleagues (1) focused on the association between genetically predicted telomere length (TL) and pancreatic cancer risk (1). The authors used carriage of telomere-related alleles to genetically predict TL and examined its association with pancreatic ductal adenocarcinoma (PDAC; ref. 1). They conclude that common genetic determinants of short TL do not appear to influence PDAC risk (1). PDAC represents the fourth leading cause of cancer-related death in Western countries with the poorest survival rate among the common malignancies (2). Few biomarkers have been recognized to detect pancreatic cancer (3). Telomeres are complex nucleoprotein structures that are crucial for the maintenance of chromosomal integrity (3). Telomeres naturally shorten with age in all replicating somatic cells unless they are elongated by the activity of telomerase (3). It has been demonstrated that there is a statistically significant association between longer TL and increased pancreatic cancer risk (3). Moreover, telomerase activity has been described as the most reliable marker in pancreatic juice samples for diagnosis of PDAC playing a central role in diagnostic analysis (4). It has been shown that overexpression of survivin enhances telomerase activity by upregulation of human telomerase reverse transcriptase (hTERT; ref. 5). Survivin is a member of the inhibitor of apoptosis family that blocks apoptotic signaling activated by a number of cellular stresses (5). Suppression of apoptosis is assumed to contribute to carcinogenesis (5). Elevated expression of survivin observed in human cancers of varied origin has been connected with poor patient survival (2, 5). Survivin participates not only in inhibition of apoptosis, but also in prolonging cellular lifespan (5). Survivin has been found to be overexpressed in PDAC (2). High survivin concentrations and positive survivin expression have been ascertained to predict a poor prognosis for patients affected by PDAC, especially in those presenting with metastasis (2). Thus, it has been suggested that detection of serum survivin levels or tissue survivin expression could be of clinical value when identifying patients at high risk for PDAC progression (2). Taken together, I hypothesize that longer TL relates with higher risk for PDAC as a result of the increased telomerase activity triggered by survivin overexpression through transcriptional activation of hTERT. Research studies are needed to evaluate whether survivin genetic variants may contribute to pathologic development to PDAC by hTERT mutations. Understanding survivin/hTERT/TL signaling axis might represent a target to develop novel diagnostic and therapeutic strategies in the management of PDAC.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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Division of Pediatrics and Neonatology, Moscati Hospital, Aversa, Italy.

Corresponding Author: Raffaella Mormile, Division of Pediatrics and Neonatology, Moscati Hospital, Gramsci Street, Aversa 81031, Italy. Phone: 3933-9204-5468; Fax: 3908-1500-1503; E-mail: raffaellamormile@alice.it

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