LETTER TO THE EDITOR


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I read the article Single Nucleotide Polymorphisms Of Follicle-Stimulating Hormone Receptor Are Associated With Ovarian Cancer Susceptibility (1) with much interest. First, I congratulate the authors for the wonderful presentation on SNP of FSHR in ovarian cancer. I notice some mistake and also want to add something. In the first para last but one sentence, they wrote ‘Epidemiological studies suggested that events that would increase the number of ovulation, such as pregnancy, oral contraceptive use and breastfeeding, would significantly elevate the risk of developing ovarian cancer’. This must be printing mistake because the statement is totally wrong. Contrarily, the situations those they describe actually protect women from ovarian cancer.

Not only FSH but also FSHR is already established to be able to activate oncogenic pathways in preneoplastic ovarian surface epithelial (OSE) cells (2). So, their finding has become more relevant. But the point is that, as they have agreed in their discussion, the expression of FSHR in OSE is comparatively a new finding. Why post-menopausal ovary, which is depleted of follicles entirely, will express FSHR in its surface epithelium is a central question in this context. There is some hypothesis regarding this but nothing is proved yet.

Nerve growth factor (NGF) could be responsible (3,4) for such aberrant expression of FSHR. Vascular endothelial growth factor may also be involved (5) in at least progression of such cancer working through NGF. Nonlinear dynamics and resultant chaos in endocrine feedback system could also be behind such abnormal FSHR expression. Nonlinear dynamics might also explain this abnormal expression of FSHR (6).

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References


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