Comment to the letter of Dr. Yeon-Suk Kim et al.

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Dear Editor,

The authors of “Pathobiology of myomatosis uteri: the underlying knowledge to support our clinical practice” want to thank Yeon-Suk Kim, Tae-Hee Kim, Hae-Hyeog Lee and Kisung Song for the valuable comments on their manuscript.

The performed whole-genome sequencing (WGS) seems superior in detecting mutations in non-coding regions, possibly leading to improved understanding of the pathogenesis in myoma formation. WGS, conducted in a large myoma,

supports the knowledge of the proposed selected genes, harboring single-nucleotide polymorphisms.

IL-37, a suppressor of immune response, could play a crucial role in the multi-factorial mechanism of large myoma development and growth. The documented results require further research concerning the expression of myoma-associated inflammatory interleukins and will eventually explain the failure of clinical therapies targeting monofactorial pathways.

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