

TOWARDS MOLECULAR-LEVEL UNDERSTANDING OF FERTILIZATION AND SEXUAL SELECTION



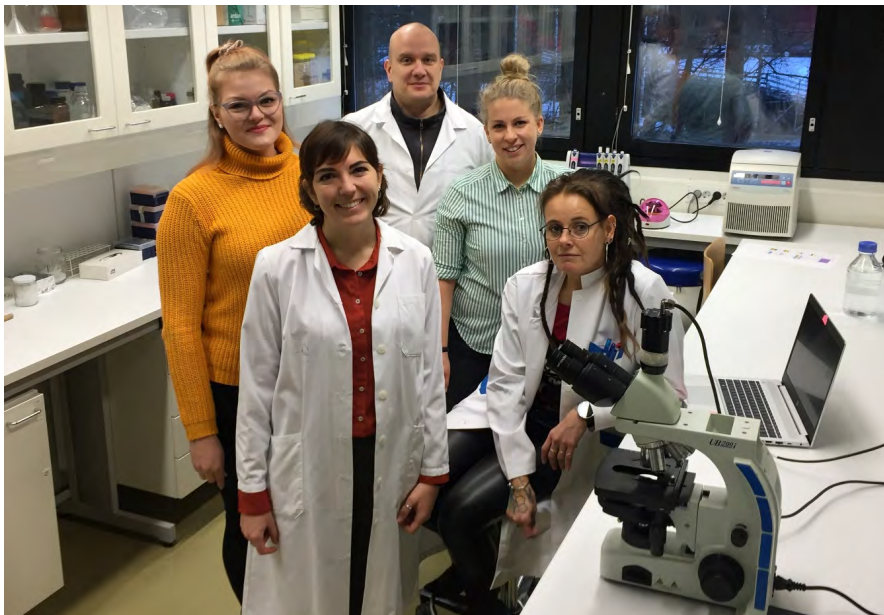
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Mechanisms of fertilization have been under intensive study for over a century. However, fertilization has remained one of the most enigmatic biological processes, which has severely restricted our understanding of reproduction and evolution. It has traditionally been assumed that fertilization is a completely unbiased process, leading to random fusion of gametes. This assumption is also a key foundation of modern genetics. On the other hand, our recent findings have indicated that gametes often combine non-randomly, which bias the fertilization towards particular (compatible) reproductive partners.

However, the molecular-level mechanisms of this emerging biological process have remained unclear. In this study, we will clarify these molecular regulatory mechanisms of life in humans by utilizing the latest advances in genomics and proteomics and interdisciplinary collaboration among experts in evolutionary biology, biochemistry, reproductive medicine, biomedicine and applied chemistry.

Mature sperm cells are believed to be incapable of expressing their genes and thus synthesizing functional gene products (RNA and proteins). Interestingly, emerging evidence indicate that genome of the

sperm may be more active than we have traditionally been assumed. If sperm turn out to be capable of expressing their genes prior to gamete fusion, it could potentially revolutionize our understanding of the molecular-level mechanisms of fertilization and the evolutionary forces behind the selective fusion of gametes. In this study, we will investigate this possibility in humans and test the novel idea that reproductive tract of the females selectively regulate sperm gene expression and thus bias sperm fertilization success towards preferred (compatible) males.



On the left to right: Tanja Turunen, Martina Magris, Jukka Kekäläinen, Annalaura Jokiniemi and Marjo Malinen. Missing: Ilkka Järvelä, Marjo Heikura and Liisa Kuusipalo.

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