Letter from the Editor

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Recent advances in using mouse genetic models to study different diseases in humans have unexpectedly advanced studies in spermatogenesis. Using mouse models, such as conventional and conditional gene knockouts, we now have identified about 400 genes that are involved in murine spermatogenesis.¹⁻³ While the phenotypes of these mice include changes in meiosis, spermiogenesis, spermiation, spermatogonial renewal and others have been reported, the regulation of many of these gene products, in particular, the complex molecular and/or signaling networks that connect these proteins together to regulate spermatogenesis remain largely unexplored. This also illustrates that there are a lot of data in the literature that remain to be thoughtfully connected. This task of data mining is crucial to better understand spermatogenesis. Therefore, much work is needed to sort through these data to identify crucial functional studies so that better experiments can be designed and conducted. It is our hope that *Spermatogenesis*, besides publishing novel and informative findings, can serve as the media to highlight some of this important information.

This is our third year of publication since the launch of *Spermatogeneis* in January 2011. We look forward to seeing the continued growth of our journal.

C. Yan Cheng Editor-in-Chief, *Spermatogenesis*

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