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Non-coding RNA and the Reproductive System

 Springer

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Preface

Non-coding RNAs and the Reproductive System

Reproduction is a fundamental feature of all known life and can be classified into asexual and sexual reproduction. For successful sexual reproduction, both the internal and external organs have to develop and function properly to work together for procreation. Faults during development or maintenance of the reproductive system result in diseases that ultimately lead to infertility. In contrast to most other organ systems, it displays clear anatomical, morphological and molecular differences between the two sexes, male and female. These include the testes, epididymis and prostate in males and ovary, uterus and mammary glands in females, as well as the sexual dimorphism of the secondary sexual characteristics such as external genitalia. The development of these organs is tightly regulated by a network of gene expression and function in each of these organs as well as crosstalk between the organs through the production, secretion and reactivity to hormones.

Until recently, the focus of reproductive science was the identification of protein-coding genes that play important roles in the development of the different organs and are mutated in diseases affecting the reproductive system, such as disorders of sex development, endometriosis, male and female infertility, as well as testicular, ovarian, prostate and breast cancer. However, in the last decade, it became obvious that focusing on protein-coding genes will only provide one part of the picture, as the regulatory role of non-coding RNAs became more and more apparent. These RNAs, which have little to no protein-coding potential, have been shown to regulate most if not all physiological processes, including the development and function of the reproductive organs, through transcriptional, post-transcriptional and epigenetic regulation of gene expression.

Non-coding RNAs can be divided into different classes based on their size, their biogenesis and their protein partners. The main categories include microRNAs (miRNAs), small interfering RNAs (siRNAs), PIWI-interacting RNAs (piRNAs) and long non-coding RNAs (lncRNAs). While these molecular regulators have been studied extensively in the last few years, there are still many open questions with respect to their functions in driving biological processes. However, the rapid development of new technologies such as high-throughput sequencing to detect non-coding RNA expression and genome-editing tools such as the TALENs and CRISPR/CAS9 systems to analyse

their *in vivo* function has accelerated the speed of new discoveries in a way not seen before. In this book, experts in reproductive biology discuss the findings and advances we have made to elucidate the role of these new regulators of gene expression in the development of the reproductive organs and their contribution to disease. While the main focus is on the mammalian system, other model organisms that have been proven useful in the study of non-coding RNAs, such *Drosophila* and *C. elegans*, are also considered.

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