Review Article

Boule and the Evolutionary Origin of Metazoan Gametogenesis:
A Grandpa’s Tale

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The evolution of sex remains a hotly debated topic in evolutionary biology. In particular, studying the origins of the molecular mechanisms underlying sexual reproduction and gametogenesis (its fundamental component) in multicellular eukaryotes has been difficult due to the rapid divergence of many reproductive proteins, pleiotropy, and by the fact that only a very small number of reproductive proteins specifically involved in reproduction are conserved across lineages. Consequently, during the last decade, many efforts have been put into answering the following question: did gametogenesis evolve independently in different animal lineages or does it share a common evolutionary origin in a single ancestral prototype? Among the various approaches carried out in order to solve this question, the characterization of the evolution of the DAZ gene family holds much promise because these genes encode reproductive proteins that are conserved across a wide range of animal phyla. Within this family, BOULE is of special interest because it represents the most ancestral member of this gene family (the “grandfather” of DAZ). Furthermore, BOULE has attracted most of the attention since it represents an ancient male gametogenic factor with an essential reproductive-exclusive requirement in urbilaterians, constituting a core component of the reproductive prototype. Within this context, the aim of the present work is to provide an up-to-date insight into the studies that lead to the characterization of the DAZ family members and the implications in helping decipher the evolutionary origin of gametogenesis in metazoan animals.

1. Preliminary Considerations on the Evolution of Sexual Reproduction

The appearance of sexual reproduction constituted an important breakthrough with critical genetic, cellular, physiological, and evolutionary implications. This is mainly due to three reasons [1, 2]. Firstly, it provided a mechanism for DNA crossing-over and recombination during meiosis [3] leading to the generation of genetically diverse gametes [4, 5]. Second, it permitted the differentiation of a germinal cell lineage in multi-cellular eukaryotes, responsible for the generation of haploid gametes through a sequential process known as gametogenesis [6]. Third, sexual reproduction involved the differentiation of two sexes in which male- and female-specific gametes are generated by means of a sequential process involving sex determination, mitotic proliferation, meiosis, and gamete differentiation [7, 8].

The evolution of sexual reproduction has represented an important milestone in evolutionary biology due to its relevance to the genetic diversification of individuals within a species and its consequences for speciation. Many aspects of the unique cell division process of meiosis associated with sexual reproduction are well known to have been highly conserved across eukaryotes (i.e., the key components of the meiotic machinery for chromosomal synapses and recombination), sharing a common evolutionary origin [9–12]. However, the complexity of sexual reproduction goes beyond meiosis ultimately leading to the differentiation of sexually dimorphic male sperm and female eggs through a process known as gametogenesis. In metazoan animals, sex-specific gametes are produced, displaying distinct differentiation patterns that result in different size, motility and gamete morphologies. These are sex-specific or sex-biased, with no conserved male- or female-specific gametogenic
2. Gametogenesis Involves Tough Decisions

During the early stages of gametogenesis (premeiotic gametogenesis), animal germ cells proliferate through mitotic divisions while kept on an undifferentiated state mediated by RNA-binding proteins [13]. During the process, the first critical decision that germ cells must take involves the arrest of mitotic divisions in order to enter into the meiosis stage that will lead to the subsequent formation of the haploid sex-specific gametes. To this end, germ cells must be informed (via somatic cell signaling) of whether they are in a male or in a female body in order to subsequently differentiate into male-specific spermatozoa or female-specific eggs, with this constituting a second critical decision. The timing of the first of these decisions (mitosis/meiosis) is often sex-specific and closely related with the second decision (sperm/egg).

The molecular mechanisms underlying such critical choices during early (premeiotic) gametogenesis have been a subject of debate during the last ten years, leading to the proposal of two main models that differ in the steps involved in how the two basic decisions are made (Figure 1). The first model (model 1) involves a single sex-specific regulator responsible for both the entrance in meiosis and the determination of sperm or egg cell differentiation. A second model calls for the presence of a gender-neutral regulator responsible for the switch from mitosis to meiosis, as well as a second sex-specific regulator involved in the sperm/egg decision [22].

Recent reports have provided evidence favoring model 1 over model 2, arguing that RNA-binding proteins are responsible for keeping germ cells on an undifferentiated...
state during mitotic proliferation [23–25], while maintaining the reversibility of such process that would allow for a transient regulation in a yet unknown fashion. Indeed, RNA-interference experiments on key regulators carried out in nematodes have revealed that sexual identity is labile, with adult females generating eggs that are amenable to switch and follow a spermatogenic development [26] and vice-versa [27]. Notably, the decision about the sexual fate of germ cells appears to be adopted at around the same time they exit mitosis to enter meiosis, underscoring the connection between the two processes [28]. On the other hand, while certain sex-specific decisions occur around the time when germline cells undergo meiosis, other decisions happen far earlier [29]. Although it is still premature to determine the universality of such mechanism, the model in which a conserved factor directs the main decisions within the core mechanism of germ cell development, may provide a very interesting insight into the evolution of the gametogenesis and sex reproduction processes.

Once the choices for mitosis/meiosis and male/female have been taken, germ cells undergo a postmeiotic cell differentiation leading to the formation of sex-specific gametes. Many of the structures and proteins appearing during these late stages seem to be related to the establishment of reproductive barriers that have critical implications for the process of speciation [30]. Therefore, it is not surprising that in many instances they evolve rapidly. However, it is important to note that although the alteration of any of these genes often leads to intraspecific infertility, none of the trends associated with them appear to be critical for proper zygote formation nor pose a roadblock for the differentiation process. This suggests that while genes involved in gamete specialization are very important for different aspects of intra-and interspecific fertilization [31] they are not the core determinants of gametogenesis.

3. The DAZ Gene Family Encodes Widely Conserved Gametogenic Factors

Although the major steps of dimorphic (male/female) gametogenesis in animals are very similar, the identification of male- and female-specific gametogenic factors common to all lineages of animals has shown to be anything but obvious [13, 14]. Reproductive proteins are often involved in other general cellular processes (besides reproduction itself), and, thus, the relevant question pertains as to whether such conservation is due to their crucial role in gametogenesis or whether it is the result of the pleiotropic functions they perform in their reproductive and somatic functions [32–34]. The key to solve this paradox probably lies in the identification of remnants of an ancient gametogenic core, lending support to a common origin of sexually dimorphic traits among animals, or in other words, the identification of conserved male- or female-specific gametogenic proteins across large evolutionary ranges. According to Xu and collaborators [7, 8], the components of such gametogenic core in the reproductive prototype should fulfill four requirements, including: (a) presence in most of major lineages of multicellular animals with sexual reproduction, (b) evolutionary origin at the same time as sexual reproduction, (c) conservation of sequence expression and function in different phyla; and most importantly (d) being selectively involved in gametogenesis in one of the two sexes and being excluded from any other pleiotropic process outside reproduction that could condition their evolutionary conservation.

Among all reproductive-associated genes known to date, the Deleted in AZoospermia (DAZ) gene family has probably been the group of reproductive factors fulfilling the above criteria that have attracted more interest from researchers during the last ten years. In humans, the DAZ gene family encompasses three genes referred to as BOULE, DAZ-like (DAZL), and DAZ encoding translational regulators with common features, including the presence of a RNA-binding domain with signature (ribonucleoprotein, RNP) RNP-1/RNP-2 motifs, as well as DAZ repeats rich in N, Y, and Q residues ([7, 8, 35], Figure 2(a)). The BOULE gene maps to chromosome 2 in humans and to chromosome 3 in mouse, at a region where a male sterile mutation is located which is syntenic to human chromosome 2 [8]. Human BOULE shares identical RNP-1 and RNP-2 motifs with fly and nematode boule [36, 37]), acting as a meiotic regulator expressed during late stages of male-specific meiosis (Figure 2(b)). Although defects in BOULE cause meiotic arrest predominantly in males, interference with meiosis in females has been also indicated in the nematode boule homolog known as daz-1 [37]. In contrast, mutations on the DAZL gene (located at chromosome 3 in humans) interfere with both male and female germ cell development [8], with an expression pattern that begins early in development and continues through the meiotic divisions of gametogenesis (Figure 2(b)). Finally, the DAZ gene emerged on the Y chromosome in humans showing structural (protein 95% similar) and functional similarity to DAZL (Figure 2(b)). However, in contraposition to DAZL, DAZ expression is restricted to males [8, 35], albeit is not essential for the completion of spermatogenesis [38, 39], and its deletion is linked to infertility [7, 8].

The evolutionary conservation observed in the DAZ family members across different animal lineages, together with the lack of evidence of positive Darwinian selection acting on their members, have sparked the interest in this family as potential remnants of an ancient gametogenic core providing support to a common origin for gametogenesis in metazoans. However, and most importantly, the relevance of the study of the DAZ gene family within this context is further supported by the fact that all DAZ members are restricted to germ cells, eliminating the potential masking effects of pleiotropy in the study of the evolution of reproductive mechanisms.

4. The Conservation of Boule Supports a Common Evolutionary Origin of Gametogenesis from an Ancestral Prototype in Metazoans

Molecular evolutionary and phylogenetic analyses indicate that the DAZ gene family consists of two subfamilies
(DAZL and BOULE) involved in different stages of germ cell development ([8], Figure 3). BOULE represents the ancestral single copy gene founder of the DAZ family, (the “grandfather” of DAZ) giving rise to DAZL (the “father” of DAZ) through gene duplication events most likely in the ancestral lineage of bony fishes before the emergence of tetrapods [7, 8]. A gene duplication process seems to be also responsible for the emergence of DAZ from DAZL, appearing in the Y chromosome of primates after the divergence between New World monkeys and Old World monkeys (Figure 3), approximately 30–40 MYA [8]. Y-linked DAZ went through two more gene duplication events as recently as 55,000 years ago, giving rise to a cluster of four DAZ genes [40–42]. While it seems clear that both BOULE and DAZL are subject to purifying selection, the selective process guiding DAZ evolution has been controversial as purifying selection both at the RNA-recognition motif (RRM) as well as in their genomic structure (intron-exon boundaries). These data suggest that BOULE was already present 600 MYA in urbilaterians as well as in eumetazoans, evolving under a strong purifying selection process, whose intensity is not even relieved by the presence of a partially redundant Dazl function [7, 45].

In order to completely fulfill the requirements defined in the previous section for a general gametogenic factor, it remained to be demonstrated that the functional constraints acting on Boole were restricted to one sex. In the case of protostomes, the analysis of Boule expression revealed a different requirement for male (Drosophila) and female (nematode) reproduction [36, 37]. In deuterostomes, the expression of a Boule homolog was also reported both in testes and ovaries of the fish medaka [46]. The answer to this apparent contradiction came from recent studies carried out in mouse, unveiling the presence of 2 different Boule transcripts as a result of alternative splicing that result in a major male-specific type and a secondary type expressed in males but also in early embryonic male and female gonads [7]. Thus, while urbilaterian Boule was important for gametogenesis ancestrally, experimental data seems to suggest that the predominant expression of Boule in animals was restricted to testes. Indeed, and although exceptions to the male-specific function of Boule also happened during evolution in a lineage-specific manner such as in nematodes, the functional relevance of Boule in male gametogenesis has been further assessed using mice mutants producing...
a truncated Boule protein. The resulting male homozygous phenotype matches exactly the mutant boule phenotype in *Drosophila*, supporting the role of Boule as a reproductive factor widely conserved (structurally and functionally) across eumetazoan animals [7].

5. Concluding Remarks and Future Perspectives

The evolution of sex has constituted a very important subject in evolutionary biology since the very beginning of this discipline, and the study of the evolution of the molecular mechanisms underlying sexual reproduction has proven to be quite challenging due to the rapid divergence of an important part of the reproductive proteins and to the masking effect of pleiotropy (somatic functions in addition to reproductive functions). Within this complex scenario, the characterization of conserved gametogenic factors encompassing reproductive-exclusive roles within the DAZ family has been critical in order to help decipher the evolutionary origin of gametogenesis in metazoan animals. *BOULE* represents the most ancestral DAZ member, encompassing an essential reproductive-exclusive requirement in urbilaterians and a high degree of conservation across metazoan animals resulting from purifying selection. This provides support to its role as an ancient male gametogenic factor whose function has been conserved over 600 MY of evolution. Interestingly, the members of the DAZ family share a common molecular nature (RNA-binding proteins) with the molecular signals mediating the entrance of germ cells into meiosis and the differentiation of sperm/eggs. The functional prevalence of *BOULE* throughout metazoan evolution, together with the increasing support favoring a single decision model (responsible for both the entrance to meiosis and the determination of sperm or egg cell differentiation), seem to suggest that male- and female-specific gametogenesis evolved from a common somatic ancestral prototype. This likely took place early in metazoan evolution, instead of arising independently in different lineages.

Although the key role of Boule constituting a core component of the metazoan reproductive prototype seems to be well established, further studies will be necessary in order to clarify certain aspects pertaining its evolutionary origin, including detailed analyses of Boule expression in additional protostomes and deuterostomes, its characterization in outgroup of bilaterians, as well as the characterization of its subcellular expression. Furthermore, and as previously suggested by Xu and collaborators, the search for a female-specific core component of the reproductive prototype that performs a role as a gametogenic factor (similar to Boule in males) will be of an utmost importance [7, 8]. From a more general perspective, the studies reviewed in the present work raise several new questions regarding the specific mechanisms involved in gametogenesis and their evolution. For instance, how do novel regulators of gametogenesis such as the (inhibitor of growth) ING2 protein, a potential tumor suppressor involved in the regulation
of human spermatogenesis through p53- and chromatin-mediated mechanisms [47], fit into the picture? are these regulators evolutionarily conserved or are they circumscribed to certain mammalian lineages? if so, when and how were they recruited into spermatogenesis? the answers to such questions will help to increase our knowledge on the origin and the functional evolution of sexual reproduction, probably one of the most important processes in Biology.

**Nonstandard Abbreviations**

DAZ: Deleted in azoosperma

DAZL: DAZ-like

MY: Million years

RRM: RNA-recognition motif.

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**References**


