Role of compensatory meiosis mechanisms in human spermatogenesis

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Abstract

Disturbances of checkpoints in distinct stages of spermatogenesis (mitosis, meiosis, and spermiogenesis) contribute to impaired spermatogenesis; however, the efficiency of meiotic entry has not been investigated in more detail. In this study, we analyzed azoospermic patients with defined spermatogenic defects by the use of octamer-binding protein 2 for type A spermatogonia, sarcoma antigen 1 for mitosis–meiosis transition and SMAD3 for pachytene spermatocytes. Especially patients with maturation arrest (MA) at the level of primary spermatocytes showed significantly reduced numbers of spermatogonia compared with patients with histologically intact spermatogenesis or patients with hypospermatogenesis (Hyp). For a detailed individual classification of the patients, we distinguished between ‘high efficiency of meiotic entry’ (high numbers of pachytene spermatocytes) and ‘low efficiency of meiotic entry’ (low numbers of pachytene spermatocytes). Only patients with histologically normal spermatogenesis (Nsp) and patients with Hyp showed normal numbers of spermatogonia and a high efficiency of meiotic entry. Of note, only patients with histologically Nsp or patients with Hyp could compensate low numbers of spermatogonia with a high efficiency of meiotic entry. In contrast, patients with MA always showed a low efficiency of meiotic entry. This is the first report on patients with impaired spermatogenesis, showing that half of the patients with Hyp but all patients with MA cannot compensate reduced numbers in spermatogonia with a highly efficient meiosis. Thus, we suggest that compensatory meiosis mechanisms in human spermatogenesis exist.

Introduction

In about half of infertile couples, male infertility plays a role and almost 30% are caused by a male factor alone (Brugh & Lipshultz 2004). Besides analysis of semen parameters, a histological evaluation is indicated especially to confirm obstructive azoospermia in men with testes of normal size and normal levels of reproductive hormones (Dohle et al. 2012).

The dynamics of spermatogenesis are crucial for elucidation of impaired spermatogenesis, which is caused by many factors such as X-ray, chemotherapy, infections, chromosomal defects, diabetes mellitus, or alcohol abuses (Cerilli et al. 2010). Although a lot of aberrations during mitosis (Steger et al. 1998, Bar-Shira Maymon et al. 2003) and meiosis (Gonsalves et al. 2004, Egozcue et al. 2005) have been described, only recently it has been shown that also reduced numbers of Sertoli cells or spermatogonia (including the stem cells) contribute to impaired spermatogenesis (Hentrich et al. 2011). However, in humans the stem cell niche is still poorly characterized, but A_dark as well as A_pale spermatogonia seem to contain subpopulations of spermatogonial stem cells (Dym et al. 2009). Of note, in primates, the A_pale spermatogonia also contain few spermatogonial stem cells (Hermann et al. 2010).

The testicular stem cells in rat and mouse are localized nearly exclusively in a stem cell niche adjacent to the interstitium (Chiarini-Garcia et al. 2001, 2003). The stem cell niche is characterized by a microenvironment which is influenced also by Leydig cells and blood vessels (Shetty & Meistrich 2007, Yoshida et al. 2007). Furthermore, also Sertoli cells and peritubular cells contribute to the self-renewal of the spermatogonial stem cells (Dadoune 2007, de Rooij 2009).

Especially in patients with maturation arrest (MA) a significant reduction in dividing spermatogonia during mitosis was observed (Steger et al. 1998, Bar-Shira Maymon et al. 2003), whereas in hypospermatogenesis (Hyp)-accelerated apoptosis rather than proliferative dysfunction was suggested to be responsible for reduced spermatogonial cell numbers (Takagi et al. 2001). In addition, in cases with MA reduced recombination rates (up to 50%) were found (Gonsalves et al. 2004, Egozcue et al. 2005).
et al., 2005) and an increased frequency of genetic abnormalities (Weedin et al., 2011).

In this study, we analyzed germ cell numbers in the early phase of spermatogenesis with an emphasis on mitosis–meiosis transition. Furthermore, we classified the deficiencies individually by distinguishing between high and low efficiency of meiosis. Our main finding in this study was that cases with histologically normal spermatogenesis (Nsp) and cases with Hyp could compensate reduced numbers of spermatogonia with a highly efficient meiosis suggesting a compensatory mechanism.

Materials and methods

Patients

Testicular biopsies were obtained from 90 patients between 1998 and 2012 and were indicated because of normogonadotropic obstructive or non-obstructive azoospermia. After written informed consent, biopsies were taken under general anesthesia. The Ethics Committee of the Medical Faculty of the Justus-Liebig-University, Giessen, Germany approved the study (75/00 and 56/05). After fixation in Bouins solution and embedding in paraffin, 5 μm sections were stained with hematoxylin and eosin and spermatogenesis was evaluated histologically according to the scoring system of Bergmann & Kliesch (1998, 2010). The patients were classified into histologically Nsp (n ≥ 30; median age 39, range 16–56; mean score 9.93, range 9–10), Hyp (n ≥ 30; median age 37, range 18–63; mean score 8.43, range 6–10), and MA at the level of spermatocytes (MA, n = 30; median age 34.5, range 17–69; mean score 0).

Antibodies

To classify especially early stages of spermatogenesis (spermatogonia and mitosis–meiosis transition), we identified several highly robust markers with a good signal-to-noise ratio and distinct expression pattern in human germ cells. For a detailed analysis of impaired spermatogenesis, three markers were chosen (Table 1), octamer-binding protein 2 (OCT2 (POU2F2)) for early spermatogonia (Lim et al., 2011), sarcoma antigen 1 (SAGE1) for dividing and differentiating spermatogonia (Lim et al., 2011), and mitosis–meiosis transition (Looijenga 2011), and SMAD3 for pachytene spermatocytes (Hentrich et al., 2011).

Immunohistochemistry

Immunohistochemistry was carried out on 5 μm sections of bouin-fixed, paraffin-embedded specimen, as published previously (Konrad et al., 2007). The Envision System from Dako (Hamburg, Germany) combined with DAB staining was used according to the manufacturer’s instructions. Counterstaining was done with hematoxylin. The antibodies used for detection are given in Table 1. Digital images were obtained with the inverse microscope FSX100 (Olympus) using the Olympus FSX-BSW Software. The images were processed with Adobe Photoshop 7.0.

Table 1 Antibodies used for quantification of distinct germ cell types.

<table>
<thead>
<tr>
<th>Protein</th>
<th>Source</th>
<th>Catalog number</th>
<th>Species</th>
<th>Clonality</th>
<th>Dilution</th>
</tr>
</thead>
<tbody>
<tr>
<td>OCT2</td>
<td>Novocastra (Wetzlar, Germany)</td>
<td>NCL-OCT-207</td>
<td>Mouse</td>
<td>Monoclonal</td>
<td>1:75</td>
</tr>
<tr>
<td>SAGE1</td>
<td>Sigma–Aldrich (St. Louis, USA)</td>
<td>HP003033</td>
<td>Rabbit</td>
<td>Polyclonal</td>
<td>1:2000</td>
</tr>
<tr>
<td>SMAD3</td>
<td>Enogene Biotech (Frankfurt, Germany)</td>
<td>E021324</td>
<td>Rabbit</td>
<td>Polyclonal</td>
<td>1:300</td>
</tr>
</tbody>
</table>

Quantification of germ cells

The numbers of germ cells were obtained from 26.63 ± 12.58 tubular cross sections per specimen representing Nsp, Hyp, and MA for each staining. As published recently (Hentrich et al., 2011) and also shown in this study, it was sufficient to use ~15–35 nearly round cross sections for quantification; we never observed outliers.

There is no consensus on how quantification of testicular biopsies with an emphasis on impaired spermatogenesis should be performed. The number of Sertoli cells is different in patients
with MA or Hyp (Hentrich et al. 2011). Thus, the Sertoli cell to germ cell ratio is not applicable for the quantification of germ cell numbers.

Statistical analysis

Values from each experiment were used for calculation of the means (per cross section) and the respective S.E.M. Differences between the groups were calculated with the test from Mann–Whitney. The P values below 0.05 were considered statistically significant.

Cut off values to distinguish between normal germ cell numbers vs reduced germ cell numbers were determined with receiver operating characteristic-curves and area under the curve. Besides sensitivity and specificity also the positive likelihood ratio was calculated. For all statistical analyses GraphPad Prism 6 (San Diego, CA, USA) was used.

Results

Identification of germ cell markers for early spermatogenesis

We identified the expression of OCT2 mainly in spermatogonia $A_{\text{dark}}$, but also in very few spermatogonia $A_{\text{pale}}$ (Fig. 1A, D and G). Often the OCT2-positive spermatogonia were localized in small groups in close proximity to interstitial arterioles or venules, which is in accordance to the characteristics of the stem cell niche in murine testis (Shetty & Meistrich 2007, Yoshida et al. 2007) and thus have been also termed as reserve stem cells (Dym et al. 2009). However, we found also OCT2-negative $A_{\text{dark}}$ and $A_{\text{pale}}$ spermatogonia.

We identified SAGE1 in very few spermatogonia $A_{\text{dark}}$, but in nearly all $A_{\text{pale}}$ and type B spermatogonia as well as in (pre)-leptotene spermatocytes and round spermatids (Fig. 1B, E and H), thus representing mitotic spermatogonia and transition of mitosis into meiosis. For characterization of pachytene spermatocytes, we used SMAD3 (Fig. 1C, F and I).

Analysis of meiosis efficiency

All three markers were used for the quantification of germ cell numbers (early spermatogenesis) per cross section and thus also for individual classification of meiosis efficiency in cases of impaired spermatogenesis. Quantification of OCT2-positive spermatogonia showed nearly identical values for Nsp and Hyp, but cases with MA demonstrated a significant reduction of $\approx 50\%$ (Table 2). Of note, quantification of SAGE1-positive germ cells (spermatogonia up to (pre)-leptotene spermatocytes) revealed strongly and significantly reduced cell numbers in Hyp and in patients with MA compared with the controls with histologically Nsp (Table 2). Similarly, SMAD3-positive pachytene spermatocytes were reduced by 47% in Hyp and by 91% in cases with MA compared with Nsp (Table 2).

Individual classification of patients with impaired spermatogenesis

For a detailed individual classification of the patients, we determined the cut off values for all three markers to distinguish between normal and lower germ cell numbers (Table 3). Furthermore, we classified spermatogenesis into ‘high efficiency of meiotic entry’ (high numbers of SMAD3-positive spermatocytes, Fig. 2A) and ‘low efficiency of meiotic entry’ (low numbers of SMAD3-positive spermatocytes, Fig. 2B). Both groups could be further divided into four subgroups according

### Table 2 Numbers of distinct germ cells per cross-section in impaired spermatogenesis

<table>
<thead>
<tr>
<th></th>
<th>OCT2: Early spermatogonia</th>
<th>SAGE1: dividing/differentiating spermatogonia</th>
<th>SMAD3: pachytene spermatocytes</th>
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<tr>
<td>$n$</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nsp</td>
<td>30</td>
<td>15.62 (0.82)</td>
<td>16.35 (0.92)</td>
</tr>
<tr>
<td>Hyp</td>
<td>30</td>
<td>11.16 (0.61)</td>
<td>8.64 (0.56)</td>
</tr>
<tr>
<td>MA</td>
<td>30</td>
<td>9.10 (0.77)</td>
<td>1.53 (0.36)</td>
</tr>
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</table>

### Table 3 Statistical analysis of the three markers used for individual classification.

<table>
<thead>
<tr>
<th></th>
<th>OCT2 (Cut off $= 1.06$)</th>
<th>SAGE1 (Cut off $= 10.84$)</th>
<th>SMAD3 (Cut off $= 8.6$)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Sensitivity</td>
<td>Specificity</td>
<td>LR+</td>
</tr>
<tr>
<td>Nsp/Hyp</td>
<td>23</td>
<td>87</td>
<td>1.8</td>
</tr>
<tr>
<td>Nsp/MA</td>
<td>57</td>
<td>87</td>
<td>4.3</td>
</tr>
<tr>
<td>Hyp/MA</td>
<td>57</td>
<td>77</td>
<td>2.4</td>
</tr>
</tbody>
</table>

Values for sensitivity and specificity are given in %; LR+, positive likelihood ratio; Nsp, normal spermatogenesis; Hyp, hypospermatogenesis; MA, maturation arrest.
to the cut offs values for early spermatogonia and dividing/differentiating spermatogonia (Fig. 2). The individual evaluation of each patient revealed that patients with histologically Nsp (n=29) or patients with Hyp (n=14) showed a high efficiency of meiotic entry and normal numbers of early spermatogonia or dividing/differentiating spermatogonia (Fig. 2A). Remarkably, only patients with histologically Nsp (seven from seven) as well as patients with Hyp (seven from 14) could compensate low numbers of spermatogonia with a high efficiency of meiotic entry (Fig. 2). In contrast, patients with MA always showed a low efficiency of meiotic entry and also revealed defects more often in the numbers of dividing/differentiating spermatogonia compared with defects in early spermatogonia (Fig. 2B). Especially subgroup 5 indicates missing compensatory mechanisms in meiosis as patients with normal numbers of spermatogonia showed low efficiency of meiosis (Fig. 2B).

**Discussion**

Besides the identification and evaluation of markers for early spermatogenesis, the primary aim of this study was the individual classification of defects in the early phase of spermatogenesis in cases of impaired spermatogenesis.

Intriguingly, the expression of OCT2 was found primarily in clusters of human A\text{dark} spermatogonia in a stem cell niche most often adjacent to the interstitial vasculature. This suggests that OCT2 is expressed very early in human spermatogenesis, most likely in stem cells as described by Lim et al. However, as also shown by Lim et al. (2011), as well as in this study, only a subgroup of A\text{dark} spermatogonia is OCT2-positive. In this study, identification of few OCT2-positive A\text{pale} spermatogonia is in accordance to results obtained in monkeys (Hermann et al. 2010), which showed that this subgroup also consists of undifferentiated spermatogonia, possibly stem cells. Thus, we believe like Dym et al. (2009) and Hermann et al. (2010) that both A\text{dark} and A\text{pale} spermatogonia contain spermatogonial stem cells. In contrast, Ehmcke et al. (2006) described that only the A\text{dark} spermatogonia comprise spermatogonial stem cells.

In line with our previous findings (Hentrich et al. 2011), we found reduced numbers of spermatogonia in cases with MA. Moreover, we observed low numbers of early spermatogonia in cases with Hyp as well as in MA, indicating deficiencies already in the early phase of spermatogenesis. Thus, without A\text{dark} spermatogonia, which contribute to stem cell renewal, spermatogenesis is severely impaired (Holstein 1999).

In addition to stem cell markers, we were also interested in identification of marker(s) for dividing and differentiating spermatogonia. We observed SAGE1 expression in very few A\text{dark} spermatogonia, but mainly in dividing spermatogonia and (pre)-leptotene spermatocytes indicating entry into meiosis. Similarly Chen et al. (2011) and Lim et al. (2011) found SAGE1 in dividing spermatogonia and meiotic entry. Interestingly, SAGE1 expression was not detectable before puberty (Lim et al. 2011), thus further corroborating the importance of SAGE1 for differentiation of spermatogonia.

We found that SAGE1-positive spermatogonia were severely reduced in patients with Hyp and MA, but only

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**Figure 2** Classification of patients into high meiosis efficiency (A) and low meiosis efficiency (B). Both groups consist of four subgroups with normal numbers of early spermatogonia (OCT2\text{+}+) and dividing/differentiating spermatogonia (SAGE1\text{+}+) or reduced numbers of early spermatogonia (OCT2\text{−}−) and dividing/differentiating spermatogonia (SAGE1\text{−}−). The cut offs values from Table 3 were used for classification. Only cases with normal spermatogenesis (Nsp) or hypospermatogenesis (Hyp) demonstrated high meiosis efficiency (A). Interestingly, only Nsp or Hyp could compensate low numbers of early spermatogonia (OCT2\text{−}−) and/or dividing/differentiating spermatogonia (SAGE1\text{−}−) with a highly efficient meiosis (A). In contrast, all cases with maturation arrest (MA) showed low meiosis efficiency besides defects in numbers of early spermatogonia or dividing/differentiating spermatogonia (B).
In this study, we found that patients with histologically Nsp showed the lowest and patients with MA the highest numbers of defects in the early phase of spermatogenesis as well as in the meiotic phase. Particularly in the subgroups 2–4 (Fig. 2A), a high meiotic efficiency but low numbers of spermatogonia, meiotic compensatory mechanisms must exist to ameliorate these defects. Obviously, all cases with MA are lacking this mechanism in addition to severely reduced numbers of spermatogonia. Interestingly, in cases with MA, the frequency of dividing/differentiating spermatogonia was completely absent in cases with MA (Luetjens et al. 2011), whereas alternatively splicing of the BOULE gene was supposed to serve as a predictive marker for meiotic efficiency (Kostova et al. 2007).

The individual classification of patients with impaired spermatogenesis by categorizing meiotic efficiency in the early phase of spermatogenesis is a promising extension of the classification system reported by Bergmann & Kliesch (1998, 2010). Although studies are lacking to assess the early phase of spermatogenesis up to pachytene, earlier studies showed up to 50% reduced recombination rates in cases with MA (Gonsalves et al. 2004, Egozcue et al. 2005). Similarly, a sixfold increased frequency of genetic abnormalities was observed in cases of MA compared with Hyp (Weedin et al. 2011).

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Received 28 May 2014
First decision 13 June 2014
Revised manuscript received 18 June 2014
Accepted 26 June 2014