Male breast cancer: genetics, epigenetics, and ethical aspects

P. Rizzolo†, V. Silvestri†, S. Tommasi, R. Pinto, K. Danza, M. Falchetti, M. Gulino, P. Frati, & L. Ottini†

1Department of Molecular Medicine, ‘Sapienza’ University of Rome, Rome; 2National Cancer Research Centre, Istituto Tumori ‘Giovanni Paolo II’, Bari; 3Department of Anatomical, Histological, Forensic and Orthopaedic Sciences, ‘Sapienza’ University of Rome, Rome; 4IRCSS Neuromed, Pozzilli, Italy

Background and study design: Male breast cancer (MBC) is a rare disease compared with female BC and our current understanding regarding breast carcinogenesis in men has been largely extrapolated from the female counterpart. We focus on differences between the ethical issues related to male and female BC patients. A systematic literature search by using PubMed (http://www.ncbi.nlm.nih.gov/pubmed/), was carried out to provide a synopsis of the current research in the field of MBC genetics, epigenetics and ethics. Original articles and reviews published up to September 2012 were selected by using the following search key words to query the PubMed website: ‘male breast cancer’, ‘male breast cancer and genetic susceptibility’, ‘male breast cancer and epigenetics’, ‘male breast cancer and methylation’, ‘male breast cancer and miRNA’, ‘male breast cancer and ethics’.

Results and conclusions: As in women, three classes of breast cancer genetic susceptibility (high, moderate, and low penetrance) are recognized in men. However, genes involved and their impact do not exactly overlap in female and male BC. Epigenetic alterations are currently scarcely investigated in MBC, however, the different methylation and miRNA expression profiles identified to date in female and male BCs suggest a potential role for epigenetic alterations as diagnostic biomarkers. Overall, much still needs to be learned about MBC and, because of its rarity, the main effort is to develop large consortia for moving forward in understanding MBC and improving the management of MBC patients on a perspective of gender medicine.

Key words: epigenetic alterations, ethics, genetic susceptibility, male breast cancer, methylation, miRNAs

Introduction

Although rarely, breast cancer (BC) affects men. To date, in Western countries, male BC (MBC) makes up <1% of all BCs and <1% of all cancers in men [1-3]. Its incidence is estimated at <1 per 100 000 men-years [4]. Overall, recent epidemiologic studies suggest that the incidence of MBC is increasing by 1.1% yearly [1, 2]. MBC incidence is generally low when compared with female BC (FBC), but substantial variability between countries exists. The highest overall age-adjusted rates occurred in Israel (1.08 per 100 000 man-years), whereas the lowest rates were recorded in Thailand (0.14 per 100 000 man-years) [4]. Such variability in rates may be due to population-specific genetic susceptibility.

Common BC risk factors, such as genetic, hormonal, and environmental factors, are involved in the pathogenesis of BC in women as in men. The major MBC predisposition factor is a positive family history (FH) of BC. Patients with a positive first-degree FH have a 2.0-fold increased risk, which increases to more than 5.0-fold with the number of affected relatives and early onset relatives, thus suggesting a relevant role of genetic factors in MBC risk [5].

From an epidemiological point of view, MBC resembles postmenopausal FBC and generally MBC treatment follows the same indications as postmenopausal FBC. However, clinical and pathological characteristics of MBC do not exactly overlap FBC and this could explain why mortality and survival rates have improved significantly less in male than in female BC patients [6]. Thus, identification of specific MBC subgroups is essential for developing an appropriate therapeutic approach.

There is growing evidence that methylation play an important role in BC development and that identification of tumor-specific methylation profiles may allow the identification of specific biomarkers for characterizing BC subtypes [7]. In addition to methylation, the involvement of micro RNAs (miRNAs) in modulating gene expression has been recently reported in BC development [8]. Altered expression of miRNA, predicted to regulate key BC genes, is frequently observed in breast tumors [9, 10]; and significant differences in miRNA expression profiles related to hormonal status have been reported, thus allowing definition of distinct molecular subgroups of BC.

The contribution of epigenetic mechanisms in MBC is still largely unknown. In this review, we will focus on the most...
relevant genetic and epigenetic alterations in the development of MBC. Ethical issues related to MBC management will be also discussed.

**study design**

We did a systematic literature search by using PubMed (http://www.ncbi.nlm.nih.gov/pubmed/), to provide a synopsis of the current understanding and future directions of research in MBC field. We selected original articles and reviews published up to September 2012. The following search key words were used to query the PubMed website: ‘male breast cancer’, ‘male breast cancer and genetic susceptibility’, ‘male breast cancer and epigenetics’, ‘male breast cancer and methylation’, ‘male breast cancer and miRNA’, ‘male breast cancer and ethics’. The abstracts resulting from these queries were individually analyzed for relevance.

**genetics of MBC**

It is estimated that up to 10% of all MBC are hereditary forms caused by inherited germline mutations in well-identified BC susceptibility genes. By their mutation frequency and the magnitude of their impact in BC susceptibility, these genes can be divided into ‘high-penetrance’, ‘moderate-penetrance’, and ‘low-penetrance’ genes (Table 1). Mutations in the two major high-risk BC genes, BRCA1 and BRCA2, occur rarely in the population, but confer a high risk of BC to the individual [11]. A moderate risk of BC is conferred by variants in genes functionally related to BRCA1/2 in DNA repair pathways. These variants are rare, occurring in <1% of the population, and their contribution to the risk of BC is <5% [12]. Recently, a third class of low-penetrance susceptibility alleles has been identified. Due to their low penetrance, the real contribution of these common variant to MBC risk is not entirely clear.

**high-penetrance BC genes**

BRCA1 and BRCA2 are the most important BC susceptibility genes in high-risk families. In MBC cases, BRCA2 mutations are much more common than BRCA1. Mutations in BRCA2 gene are estimated to be responsible for 60%–76% of MBCs occurring in high-risk BC families, whereas BRCA1 mutations frequency ranges from 10% to 16% [13, 14]. In the frame of the first Italian multicenter study on MBC, we recently reported a frequency of BRCA1/2 mutations of about 13%, in particular, BRCA1 mutations were found in about 1% and BRCA2 mutations in 12% of MBC cases [15]. Overall, BRCA1 and BRCA2 mutations are more prevalent in men with a positive first-degree FH compared with those without FH. All known BRCA1/2 mutations are recorded in the Breast Information Core (BIC) database [16–18]. Interestingly, we observed an association between the BRCA2 N372H variant and risk of MBC in young men [19].

Specific BRCA1 and BRCA2 mutations show high frequency in specific countries or ethnic groups, particularly, in genetically isolated populations. These mutations are descented from a single founder. Founder mutations may also explain variability in BC incidence rates among countries. For example three founder mutations, two in BRCA1 (185delAG and 5382insC) and one in BRCA2 (6174delT), have been observed at higher frequency (>2% in total) in the Ashkenazi Jewish male population than in the general US population [20, 21]. Generally, BRCA1 mutations are quite rare in unselected MBC cases being more frequent in specific populations in which a founder effect is known to occur [22]. Notably, we showed a founder effect for the BRCA1 3347delAG mutation that was found in Italian MBC cases [15, 23, 24]. BRCA1/2 large-scale rearrangements, including insertions, deletions, or duplications of more than 500 kb of DNA, have been also identified in both male and female BC patients [25–28]. Interestingly, large genomic rearrangements in BRCA2 are more frequent in families with MBC [26, 29] and, on the other hand, we reported that both BRCA1 and BRCA2 rearrangements are infrequent in MBC cases unselected for FH [30].

It is now well established that, in women, BRCA-associated BCs tend to manifest specific genotype–phenotype correlations [31]. In particular, BRCA1-related BCs have distinct morphology and phenotype [32]. By contrast, BRCA2-related BCs are a heterogeneous group not fully characterized [33–35]. We recently investigated whether specific BRCA-associated phenotypes could be identified in MBC. We found that the majority of BRCA1-related MBCs are HER2 negative (HER2−),

| Table 1: Classes of male breast cancer genetic susceptibility and comparison of their different features |
|-------------------|-------------------|-------------------|
| **High penetrance** | **Moderate penetrance** | **Low penetrance** |
| **Genes** | **BRCA2, BRCA1** | **CHEK2, PALB2** | **2q35, 6q25.1 (ESR1), 10q21.2, 11q13.3, 12p11.22, 14q24 (RAD51L1) and 16q12.1 (TO3X)** |
| **Population frequency** | <0.1% | MAF 1% | MAF >10% |
| **Cancer risk (odds ratio)** | >10.0 | >2.0 | 0.76–1.57 |
| **Functional effect** | Direct effect of mutation | Direct effect of variant | Direct effect of variant; linkage disequilibrium with causal variants |
| **Strategy for identification** | Resequencing of candidate genes | Resequencing of candidate genes | Case–control studies; genome-wide association study (GWAS) |
grade 3 tumors and show high proliferative activity. Although based on a few cases, our results may suggest that BRCA1-related BCs in men represent a rare event characterized by a phenotype similar to that observed in women. On the other hand, BRCA2-associated MBCs display a characteristic phenotype not identified in women [35]. In particular, BRCA2-associated MBCs present with high tumor grade, absence of progesterone receptor (PR) expression and HER2-positive (HER2+) status [15]. Interestingly, it has been reported that the mean number of genetic aberrations in BRCA2-associated MBCs carriers is higher than in sporadic MBC [36] and specific gene copy number aberrations are associated with MBC cases [37], thus indicating that further genetic analyses on somatic alteration in MBC might provide insights into the biologic cancerous process.

**moderate-penetrance BC genes**

Direct interrogation of candidate genes involved in BRCA1/2-associated DNA damage repair pathways had led to the identification of other BC susceptibility genes, classified as moderate-penetrance genes. Variants found in this class of genes confer a smaller risk of BC than BRCA1/2. CHEK2 1100delC was the first moderate BC risk allele identified. The CHEK2 1100delC mutation has been shown to confer approximately a 10-fold increase of BC risk in men lacking BRCA1/2 mutations and it was estimated to account for 9% of familial high-risk MBC cases [38]. However, this association is not so evident in MBC series unselected for FH [30, 39–41]. The contribution of the CHEK2 1100delC mutation to MBC predisposition varies by ethnic group and from country to country. Interestingly, a decreased frequency of the 1100delC allele in North to South orientation has been observed in Europe [30, 42–44].

The involvement of BRCA2 in the Fanconi Anemia (FA) pathway promoted mutation screening of other FA genes functionally linked to BRCA2, such as PALB2, BRIP1, RAD51C, and, more recently, XRCC2 [45]. Interestingly, PALB2 mutations were found in families with both female and male BCs, suggesting that PALB2 may be involved in MBC risk [46, 47]. Moreover, PALB2 heterozygotes were 4-fold more likely to have a male relative with BC [48]. To date, five studies have reported on the frequency of PALB2 mutations in MBC [49–53]. Overall, these studies indicate that PALB2 may have a role as moderate-penetrance gene in MBC at a comparable extent as for FBC.

Recently, we investigated the role of BRIP1 in MBC susceptibility, and we found no evidence that germline variants in BRIP1 might contribute to MBC predisposition [54], thus suggesting that the contribution of BRIP1 to BC predisposition in males is less consistent compared with other moderate BC susceptibility genes such as CHEK2 and PALB2. Mutations in RAD51C were identified as BC susceptibility alleles, accounting for 1.3% of female patients from families with at least one case each of breast and ovarian cancer [55]. At present, there is no evidence that RAD51C mutations may contribute to MBC susceptibility [56]. A rare mutation in XRCC2 was newly found by whole exome sequencing in an early onset MBC patient with a strong family history of BC [57], thus suggesting that XRCC2 could be a MBC susceptibility gene.

**low-penetrance BC alleles**

A polygenic model, in which many genes that confer low risk individually act in combination to confer much larger risk in the population, has been suggested for susceptibility to BC and other common cancers [58]. BCs unaccounted for by currently known high- and moderate-penetrance BC susceptibility genes can be explained by this model. This hypothesis has recently been confirmed by multigroup collaborations working in genome-wide association studies (GWAS) carried out on very large series of BC cases and controls from different countries, in order to increase the power to detect small effects on the risk BCAC [59, 60]. GWAS have also identified associations between single-nucleotide polymorphisms (SNPs), mapping to more than 20 loci, and BC risk in women [60–66]. These SNPs act as common low-penetrance allele variants, each generally conferring a relative risk <1.40 [67, 68]. Overall, these SNPs are estimated to account for <4% of the familial risk of BC in women [60]. Many of the susceptibility alleles are in intronic portions of genes and often are noncoding regions. This might be explained by the observation that some of these loci are located in regions of linkage disequilibrium that cover different genes [67]. Furthermore, some of these SNPs could act as modulators of the risk conferred by mutations in the high-penetrance BC susceptibility genes BRCA1 and BRCA2 [69].

Also, a subtle regulatory effect of one allele in the prostate/breast cancer-associated 8q24 block, which acts as a cis enhancer of the MYC promoter, has been found [70]. Different haplotype blocks within 8q24 were specifically associated with the risk of different cancers, including prostate, colon, ovarian, kidney, thyroid, laryngeal carcinomas, and BC [71–73]. Intriguingly, many of the coding loci presently identified are in genes somatically mutated in diverse cancers, including BC. Germline variations in genes encoding for ‘driver kinases’ may also influence BC risk, thus suggesting that low-penetrance alleles might be a link between germline and somatic alterations in BC [74]. The relative risk associated with several of the loci identified to date shows BC subtype specificity in women, defined in particular by hormonal receptors status [67]. Notably, associations with most of the susceptibility loci are stronger for estrogen receptor-positive (ER+) rather than for ER-negative (ER−) BCs [75].

Common low-penetrance BC alleles associated with the risk of FBC were also investigated in MBC and SNPs at 2q35, 6q25.1 (ESR1), 10q21.2, 11q13.3, and 12p11.22 and 16q12.1 (TOX3) were confirmed to be significantly associated also with MBC risk [76, 77]. In the first GWAS on a large collaborative series of MBCs, we were able to identify a novel SNP in RAD51B at 14q24.1 that is significantly associated with MBC risk [77]. At present, whether variant alleles may be associated with specific clinical-pathologic features of MBCs is still unknown. Studies of well-defined MBC patient subgroups are needed in order to provide further insight into the role of low-penetrance alleles in MBC.

**epigenetics**

Epigenetic alterations (changes in gene activity that do not involve variations in the primary DNA sequence) play as crucial role as genetics in cancer development. Epigenetic events are responsive to environmental factors, are hereditable and
relatively stable, and regulate crucial biological processes such as X-chromosome inactivation, genomic imprinting, position effect variegation, reprogramming of the genome during differentiation and development, or RNA interference leading to post-transcriptional gene silencing. Defects in these processes have been found to be associated with many human disorders, including BC [78]. Two epigenetic mechanisms have emerged as the most critical players in transcriptional regulation: methylation of DNA and microRNA interference. These mechanisms are both involved in the initiation and progression of BC, as revealed by a large series of papers on the topic. At present, epigenetic alterations have been rarely studied in MBC.

DNA methylation

Hypermethylation of CpG islands consists of a covalent addition of a methyl group to a DNA sequence, usually a cytosine located in 5’ of guanosine. In more than 70% of genes, methylation occurs in the promoter and in the first exon regions, and it is thought to be especially relevant in reorganizing chromatin structure and in silencing important growth control pathways [79]. DNA methylation reaction is catalyzed by DNA methyl transferases (DNMTs), ubiquitously expressed in a tissue-specific way [80]. Two families of DNMTs have been identified in mammals: DNMT1, which functions in maintenance of DNA methylation during DNA replication, and DNMT3 (which include DNMT3a and DNMT3b), which is a de novo enzyme capable of methylating unmethylated or methylated DNA. DNMTs are overexpressed in various tumor types, but DNMT3b plays a predominant role in breast tumorigenesis [81]. More than 100 genes, in particular tumor suppressor genes, have been reported to be hypermethylated in female breast tumors or BC cell lines [79, 82, 83]. Many of the abnormally methylated genes are players in cell-cycle regulation (CCND2, p16INK4A, p14ARF, p15, RARBeta, RASSF1A), apoptosis (APC, HOXA5, BCL2, TWIST), angiogenesis (EFEMP1, THBS1), DNA repair (GSTP1, BRCA1, MGMT), hormone signaling (ESR1, ARH1, CYP1B1), invasion, and metastasis (CDH1, CDH3, CDH13, TIMP3). Aberrant tumor suppressor gene methylation is a key factor in BC pathogenesis. Moreover, a progressive onco-suppressor inactivation can lead gradually from a less-aggressive, hormone-dependent phenotype to a highly invasive, hormone-independent one.

Recently, Kornegoor et al. [84], investigating methylation of selected tumor suppressor genes in 108 MBC cases, demonstrated for the first time the important role of epigenetic inactivation in BC development, even if, compared with female, methylation occurred less often in male BCs. All male tumor cases except one showed methylation of at least one gene, with an average of six genes. Interestingly, genes frequently methylated in female (MSH6, WT1, PAX5, PAX6, and CDH13) were frequently methylated also in male BCs. On the contrary, these genes were not found methylated in normal breast tissues, confirming the important role of methylation in the development of MBC. Other genes, including BRCA1, CDKN2A, VHL, ATM, and CHFR, were rarely found methylated in this study, while ESR1 and GSTP1 methylation was identified to be correlated with high mitotic count, suggesting a role for these two single genes in aggressive male breast carcinogenesis [84]. Compared with FBC, methylation of ESR1, BRCA1 and BRCA2 was less common in MBC [84], evidencing important differences between male and female breast carcinogenesis with regards to gene inactivation by methylation. This was confirmed by the results of a recent study on a cohort of familial BC cases in which we demonstrated that RASSF1A promoter resulted more frequently methylated in familial MBCs than FBCs (76% versus 28%, \( P = 0.0001 \)), and RAR\( \beta \) more frequently methylated in female than male BC (17% versus 8%, \( P = 0.3 \)). Furthermore, RASSF1A and RAR\( \beta \) resulted more frequently overexpressed in familial BC than MBC (RASSF1A: 83% versus 30%, \( P = 0.0001 \); RAR\( \beta \): 55% versus 22%, \( P = 0.012 \)). When we compared methylation data with clinical characteristics, we reported that in familial FBC, a lower RASSF1A expression and higher methylation was associated with a higher positivity of ER, consistently with the role of RASSF1A in downregulating ER\( \alpha \) [85]. In familial MBC however, higher methylation and lower expression of RASSF1A resulted significantly associated with absence of ER expression, thus underlining a different regulation of the ER pathway in the two genders mediated by RASSF1A methylation [86].

miRNA

microRNA (miRNA) are small, highly conserved noncoding RNAs (18–24 nucleotides) that regulate gene expression by targeting RNA degradation or translational inhibition through interaction with the 3’ untranslated region (UTR) of the mRNA target [79], but also the open reading frame (ORF) and the 5’UTR, as evidenced by some authors [87–89]. As a single miRNA can target hundreds of mRNAs and a single mRNA can be targeted by several miRNAs, aberrant miRNA expression can be involved in the initiation of many diseases, including cancer [90, 91]. miRNAs are frequently located in cancer-associated genomic regions that are often subjected to rearrangements, breakpoint regions, loss of heterozygosity, deletions and amplifications in cancer cells. They can act as either oncogenes or tumor suppressors given their inhibition of tumor suppressive or oncogenic miRNAs, respectively [91]. miR27a, miR10b and miR21, promoting cell migration, invasion and cellular proliferation, are examples of oncomiR involved in BC [10]. In particular some authors have defined miR10b as ‘metastomiR’ because of its capacity to induce the development of BC metastasis [92]. On the contrary, let-7, miR17–5p, miR27b, miR125a/b, miR200c, and miR206 act as tumor suppressors in BC as their overexpression causes inhibition of cell growth, migration and invasion [10].

miRNA regulation has been very poorly investigated in MBC. The first miRNA signature was identified by Fassan et al. [93]. It was composed of 34 miRNAs that were differentially expressed between male breast tumors and gynecostias samples, considered a potentially benign counterpart of male breast glands because it represents a condition of increased but benign ductal epithelial proliferation. In particular, 17 miRNAs were upregulated and 26 miRNAs were downregulated in cancers, but the most promising miRNAs of this MBC signature were miR10b, miR126, miR125a–5p, and miR125b [93]. When the authors compared altered miRNA expression between male and female BC samples they demonstrated differences between
diagnostic biomarkers. Patients suggest a potential role for epigenetic alterations as sufficient to understand miRNA regulation in MBC. As in other multifactorial diseases, MBC requires a personalized and comprehensive approach to diagnosis and treatment, in which the knowledge of risk factors such as family history, specific-gender aspects, genetic susceptibility and predisposition, play a key role. Prevention and communication between doctor and patient are also crucial. Recent studies highlight the importance of the development of educational programs to let patient aware of the availability of preoperative and postoperative gender-specific information to relieve psychological problems associated with the BC diagnosis [97]. Furthermore, the absence of specific-gender and preventive treatments leave male patients alone and incapable to have and to give a feedback on their experiences. Because of this absence, a clear marginalization of male patients and disparity of treatment between similar subjects, in both prevention and cure of BC, was observed. At the same time, since the absence of specific-gender information on therapy and cure, several difficulties and concerns were observed also in the relationship between patient and doctor. For instance, these difficulties frequently occur in practicing genetic tests aimed to measure the susceptibility or predisposition to develop BC, where ethical issues involving the right to know and the right to ignore can be relevant in the management of the psychological condition of patients [98]. The absence of gender-specific statistical studies makes more complicated the diagnosis when low-penetration BC genes are observed, preventing an appropriate and adequate genetic counseling and full information to the patient. Furthermore, this uncertainty and difficulties to diagnosis do not contribute to resolve the ethical issues about the extension of genetic testing to family members, which likely do not receive complete information about the utility of such instrument.

Overall, the above summarized problems highlight a clear contrast with the increasing demonstrations of the importance of personalized treatments in therapeutic performance, which take into account the specific differences (sex, age, subtype of pathology, etc.) between a patient and another. The problem of inappropriate medical advancement occurs for several other rare diseases in which medical research and translational medicine are conditioned by cost–benefit considerations, because of large investments required by medical research. Finally, the above questions suggest the necessity to address the management of MBC on a perspective of gender medicine (i.e. prevention screening and adequate adjuvant therapy) in order to guarantee to all individuals, regardless of their specific condition, a personalized cure and care.

conclusions

The identification of BC susceptibility genes, in particular BRCA1 and BRCA2, has changed the management of BC patients with a FH of BC. Several models have been developed and are currently used to assess the pre-test probability of identifying BRCA1/2 germline mutations in individuals at risk for hereditary cancer. Moreover, novel therapeutic strategies specific for BRCA1 and BRCA2 cancers are emerging, including cross-linking agents and PARP inhibitors [99]. Both genetic and epigenetic alterations are frequently associated to specific
biological and clinico-pathological tumor characteristics, allowing the identification of personalized therapies targeting specific molecular pathways. In particular, DNA methylation as well as miRNAs are currently emerging as interesting candidates for the development of therapeutic strategies against BC.

MBC, as well as other multifactorial and rare diseases, suffers from the absence of specific and comprehensive studies that may allow translation of research findings into a personalized management of the disease, particularly when dealing with issues involving complex gene-environmental interactions and implying large numbers of cases, as for studies of low-penetrate BC susceptibility. As demonstrated by the recent GWAS on MBC [77], the ongoing collaborative efforts facilitate research on this rare and peculiar disease and will eventually provide useful information for a more appropriate clinical management of MBC patients.

disclosure
The authors have declared no conflicts of interest.

references


