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Exploring genetic and immune underpinnings of the sexual dimorphism in tumor response to immune checkpoints inhibitors: A narrative review

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ABSTRACT

Introduction: In spite of the undisputed relevance of sex as critical biologic variable of the immune landscape, still limited is our understanding of the basic mechanisms implicated in sex-biased immune response thereby conditioning the therapeutic outcome in cancer patients. This hindrance delays the actual attempts to decipher the heterogeneity of cancer and its immune surveillance, further digressing the achievement of predictive biomarkers in the current immunotherapy-driven scenario. **Body:** The present review concisely reports on genetic, chromosomal, hormonal, and immune features underlying sex-differences in the response to immune checkpoint inhibitors (ICIs). In addition to outline the need of robust data on ICI pharmacokinetics/dynamics, our survey might provide new insights on sex determinants of ICI efficacy and suggests uncovered pathways that warrant prospective investigations.

Conclusion: According to a sharable view, we propose to widely include sex among the co-variables when assessing the clinical response to ICI in cancer patients.

1. Introduction

In the last decade, immune checkpoint inhibitors (ICIs) have prompted a paradigm shift in the treatment of several solid and hematologic malignancies, including non-small cell lung cancer (NSCLC) (Ribas and Wolchok, 2018), malignant melanoma and genitourinary cancers (Lin et al., 2022; Lalani et al., 2022). At present, ICIs are approved for the first and more-line treatment in advanced NSCLC (Pasetto et al., 2020), with the notable exception of consolidation durvalumab, which is employed in unresectable locally-advanced NSCLC after radical chemoradiation (CRT) (Gray et al., 2020). Nonetheless, the profound and long-lasting benefit derived from ICIs in metastatic setting (Gadgeel et al., 2020; Paz-Ares et al., 2020) is still achieved in a limited fraction of patients, thus making imperative the identification of prognostic and predictive biomarkers able to guide patient selection (Tray et al., 2018).

The central role of tumor immune microenvironment (TIME) has been repeatedly demonstrated (Altorki et al., 2019; Binnewies et al., 2018; Mazzaschi et al., 2018), mainly involving the assessment of PD-L1 status, that is currently the only approved ICI-biomarker, tumor infiltrating lymphocytes (TILs) density and phenotype, and activating (i.e. interferon- γ) or inhibitory (i.e. CD38, transforming growth factor- β)

signalling pathways. Moreover, as cancer immunoeediting and immune response also engage the peripheral circulation, the contribution of circulating immune cells, cytokines, growth factors and chemokines has been intensively investigated (Buder-Bakhaya and Hassel, 2018; Nixon et al., 2019; G. Mazzaschi et al., 2020).

Genomic and RNA-based studies exploring predictors of ICIs responsiveness have designated tumor mutational burden (TMB) and neoantigen signature as potential biomarkers in NSCLC patients (Rizvi et al., 2015; Fumet et al., 2020; Anagnostou et al., 2017). Other currently explored relevant factors are embodied by human leukocyte antigens (HLAs) (McGranahan et al., 2017) and distinct somatic mutations (i.e., serine/threonine kinase 11, *STK11*) (Skoulidis et al., 2018). Recently, a 18-gene pan-tumor signature (Tumor Inflammation Signature, TIS) associated with high response to PD-1 inhibitors, was proposed (Danaher et al., 2018).

Multiple clinical aspects, including age, performance status (ECOG PS), number and sites of metastatic involvement, concomitant interfering drugs (i.e. corticosteroids, proton pump inhibitors, antibiotics) or the occurrence of immune-related adverse events (irAEs) have shown to significantly affect the response to ICIs (Brueckl et al., 2020; L. Huang et al., 2020; Buti et al., 2021).

How sex impacts on the actual immunotherapy scenario and on the

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urgent need of predictive biomarkers of ICI efficacy remains largely uncovered. Thus, the aim of the present review is to provide a concise survey on sex related genetic and immune features implicated in the response to ICIs.

2. Current knowledge on sex and response to immune checkpoint inhibitors

Sex differences in cancer biology are well documented and may be responsible for a greater risk of cancer development and mortality in man, reaching up to twice that of women in specific tumor subtypes (Cook et al., 2009, 2011). It is a long-standing notion that sex, meaning the biological differences between men and women, and gender, implying behavioural differences derived from being male or female, represent variables potentially affecting immune responses to both foreign and self-antigens (Roved et al., 2017). However, whether sex difference (Márquez et al. 2020; Roved et al., 2017) is a relevant determinant of clinical outcome in cancer patients treated with immunotherapy remains unclear.

ICIs are humanized or human monoclonal antibodies whose therapeutic task is essentially addressed to the reinvigoration/rejuvenation of the immune mediated anti-tumor cytotoxic response (Huang et al., 2017). This is achieved mainly by antibody-dependent cellular cytotoxicity (ADCC) and complement-dependent cytotoxicity (CDC) or true receptor blockade resulting in cleavage of either the ligand (i.e. PD-L1) or the receptor (i.e. PD-1) at cancer-immune synapse (Ribas and Wolchok, 2018). On one side, targeted drug-receptor affinity as different IgG class of therapeutic antibodies (mostly IgG1 while IgG4 for anti PD-1) are undoubtedly crucial to trigger the immune response and represent important variables potentially conditioned by sex. On the other side, the different immune background in male and female might critically train the quantitative and functional state of relevant effector and suppressor cells both at tumor sites and in the circulation. The fine molecular mechanisms by which sex-related genetic, hormonal, and environmental cues act on each of these steps responsible for ICI efficacy are currently not elucidated.

2.1. Sex differences in ICI pharmacokinetics and pharmacodynamics

Before addressing the question whether a distinct outcome occurs in male and female cancer patients following ICIs, a necessary pre-requisite is to provide a succinct description of sex-associated pharmacokinetics (PK) and pharmacodynamics (PD) of this class of therapeutic agents.

PK and PD studies focused on ICI and data on relationships between exposure and response are still inconsistent. Patient- (i.e. age, sex, ethnicity, body mass index, liver and renal function, ECOG PS) and tumor-associated (i.e. tumor burden, immunogenicity) factors are known to affect drug clearance, however their effect on ICI PK has been estimated to reach at most 30% (Desnoyer et al., 2020). Intriguingly, sex does not uniformly impact on ICI clearance as male sex is associated with faster clearance of the anti-CTLA4 tremelimumab and the anti-PD-1 nivolumab, while that of the anti-PD-L1 durvalumab decreases in female patients (Desnoyer et al., 2020). Observations on differential PKs of other analogous (Centanni et al., 2019) or recently introduced (Melhem et al., 2022) ICI agents according to sex are inconclusive. Overall, PD and PK studies strongly suggest to incorporate sex among the clinical covariates to assess ICI efficacy in cancer patients (Bajaj et al., 2019).

2.2. Sex differences in the response to ICI: clinical evidence

Based on large-scale meta-analyses and systematic reviews (Conforti et al., 2018; Wallis et al., 2019; Grassadonia et al., 2018; Pala et al., 2022), an intense and open debate on whether cancer immunotherapy efficacy is different between male and female patients is still ongoing. In a meta-analysis of randomized clinical trials including 11,351 ICI-treated patients (67% men and 33% women, with a predominance of melanoma

[32%] and non-small cell lung cancer [31%]), Conforti et al. reported that the magnitude of ICI response was sex-dependent, as male patients achieved greater benefit than females (Conforti et al., 2018). Conversely, a more recent meta-analysis of all available ICI-based clinical trials across several cancer types (13,721 patients, 67.9% men and 32.1% women) did not document any significant difference in overall survival (OS) when comparing the effectiveness of these treatments between the sexes (Wallis et al., 2019). Moreover, performing subgroup analyses, including disease site, line of therapy, class of immunotherapy, and study methodology, no meaningful sex-associated differences in clinical outcome were observed (Wallis et al., 2019). An additional meta-analysis of phase III randomized clinical trials showed better results from immunotherapy in man for all advanced cancers with the exception of melanoma (Grassadonia et al., 2018). Accordingly, by a machine learning algorithm on a multiscale analysis on more than 1000 patients with different tumor types, male sex resulted a positive predictor among the 12 biomarkers enclosing a score for the response to immunotherapy (Litchfield et al., 2021). These contrasting findings are based on subgroup hazard ratios (HR) of published clinical trials lacking the analysis of individual patients, and/or the differential distribution of age, smoking habits and clinicopathological characteristics, such as PD-L1 expression and TMB, thus further clouding the significance of the obtained results. In an attempt to shed new light on sex-related difference in ICI efficacy according to well-known biomarkers, a post hoc analysis of prospective individual patient data from five clinical trials (OAK, POPLAR, IMvigor210, KEYNOTE-001, and CheckMate-012), and a meta-analysis of nine randomized controlled trials (RCTs) have been also conducted stratifying patients according to PD-L1 status (Li et al., 2020). The authors documented that survival benefits from ICI in male and female were greatly influenced by PD-L1 expression, especially in NSCLC, thus recommending to jointly consider sex and PD-L1 in the clinical decision-making in the setting of ICI treated cancer. Concerning tumor mutational status, it has been reported that several solid neoplasms in women display a lower TMB (Xiao et al., 2016) which is associated to a lower response rate to immunotherapy in melanoma (Van Allen et al., 2015). Nonetheless, more recent receiver operating characteristic-based analyses to define high vs low TMB on three datasets of NSCLC patients showed a better performance in predicting a greater benefit from ICI in female tumors with high TMB (Wang et al., 2019).

2.3. Sex differences in immune related adverse events

An additional important aspect with biological and clinical implications arisen from the advent of immunotherapy is represented by the occurrence of irAEs. Not surprisingly, therapeutic inhibition of CTLA-4 or PD-1/PD-L1 checkpoints, the natural machinery instrumented to survey non-self antigens, may result in autoimmune manifestations (Shankar et al., 2020). Although irAEs have been repeatedly reported to positively impact on ICI response in NSCLC (Shankar et al., 2020; Hussaini et al., 2021; Grangeon et al., 2019), the biological basis of this phenomenon requires to be deeply investigated. Even more limited is the documentation on whether female patients, carrying a natural propensity for autoimmunity, are more (Kitagataya et al., 2020) or less (Triggianese et al., 2020) prone to develop irAEs. A recent analysis on a large cohort (n = 23,296) of cancer patients disclosed a 49% increased risk of AEs in female receiving immunotherapy compared with males (Unger et al., 2022), reinforcing the notion of sex-driven pharmaco-kinetics, -dynamics and -genomics differences with relevant implication on clinical outcome.

3. Sexual dimorphism in immune response

Genetic, behavioural, environmental and hormonal factors are implicated in sexual dimorphism of the immune system (Naqvi et al., 2019). Estrogen and androgen responsive elements are present in promoter regions of a consistent number of immune related genes (Hannah et al., 2008), as sex hormones receptors are expressed by a variety of

immune cells (Mantalaris et al., 2001; Arruvito et al., 2008; Dosiou et al., 2008). The understanding of such sex related diversities may benefit from the advanced knowledge achieved on the role of microbiome in shaping the immune response. The microbiome has been implicated in the development of inflammatory, autoimmune and neoplastic (Huang et al., 2018) diseases in humans (Yatsunenkov et al., 2012; Haro et al., 2016; de la Cuesta-Zuluaga et al., 2019) and mice (Sheng et al., 2021; Markle et al., 2013). Due to the ability of microbes to process and/or synthesize estrogen and androgen metabolites (Taneja, 2018), gut microbiota regulates immune functions in a sex-specific manner. The gender dimorphic microbiome is under intense biological and clinical scrutiny, leading the scientific community to coin the term 'micro-genderome' (Vemuri et al., 2019; Flak et al., 2013).

Evidence of a sexual dimorphism in the modulation of cholesterol homeostasis, mainly exerted by proprotein convertase subtilisin kexin-like 9 (PCSK9) (Ghosh et al., 2015), reinforces the notion of a sex/gender-dependency of immune metabolic pathways, ultimately conditioning tumor immune landscape (Ma et al., 2019) and response to ICIs.

3.1. Genetic basis of sex differences in immunity

Sexual dimorphism of the human immune system is detectable as early as within the first 6 months after birth, as genetic-transcriptional analysis of the thymus have documented that sex hormones and XX and XY genomic backgrounds condition autoimmune regulator (AIRE) interactors (Moreira-Filho et al., 2018). AIRE is a transcription factor expressed by thymic (Anderson et al., 2002) and extrathymic (Poliani et al., 2010) cells, including stromal (Bergström et al., 2019) and circulating (Suzuki et al., 2008) elements, displaying features shared with dendritic cells (DCs) and therefore critically implicated in central tolerance. Intriguingly, animal models (Zhu et al., 2013) and human studies (Nguyen et al., 2020; Kalra et al., 2018) have pointed to a regulatory role of AIRE in cancer immune surveillance. However, this contention cannot be widely applied to a variety of neoplastic diseases since conflicting results have been reported (Klamp et al., 2006). Keeping on the immunotherapy scenario, unveiling the distinctive clinical significance of AIRE expression in cancer and/or immune cells in female and male patients, represents an area of prospective studies with potential therapeutic spill-over.

Importantly, sex-associated dichotomic immune response can be elicited because immune relevant genes, as *interleukin 2 RG (IL2RG)*, *IL-13RA2* and *TLR7-8*, coding for cytokine receptors, or androgen receptor (*AR*) and *forkhead box P3 (FOXP3)* for transcription factors (Kawai and Akira, 2006; Kleina et al., 2015; Lubahn et al., 1988; Su et al., 2009; Souyris et al., 2019; Zhao et al., 2020), are X-linked. Of note, sex biased expression patterns are generated by the escape from X chromosome inactivation (XCI) in nearly 1/4 (23%) of X-linked genes (Tukiainen et al., 2017). In addition to their largely documented role in female proneness to develop autoimmune diseases (i.e. lupus erythematosus), numerous XCI-escaped genes have also been implicated in tumor-suppressing functions (Clocchiatti et al., 2016; Dunford et al., 2017). As an example, the protection of females from bladder cancer has been associated with the biallelic expression of *KDMA6*, a sex-biasing tumor suppressor gene that escaped XCI in females (Dunford et al., 2017; Kaneko and Xue, 2018; Ntziachristos et al., 2014). Although not peer reviewed, a very recent study identified *KDM6A* as the most differentially regulated gene escaping XCI and conditioning sex differences in number and function of natural killer (NK) cells. Independently from sex hormones, *KDM6A*, through its encoded histone demethylase UTX, was found to be responsible for the decrease frequency and increased IFN γ expression characterizing the female NK phenotype (Cheng et al., 2022). For completeness, additional immune-related XCI-escaped genes include *CD99*, *TLR8*, *TASL*, *DDX3X*, *USP27X*, *CXCR3*, *LAMP2*, *XIAP*, *CD40LG*, *IRAK1*, and *IL9R* (Carrel and Willard, 2005; Mousavi et al., 2020; Oghumu et al., 2019; Vermeesch et al.,

1997).

A seminal work addressing the impact of sex on the genomic landscape of multiple cancers disclosed sex-biased molecular patterns in more than 50% of clinically targetable genes (Yuan et al., 2016). Specifically, *IL2*, *IL6*, *STAT5*, *JAK*, *STAT3*, *IFN α* and *IFN γ* , *TNF- α* and complement, involved in signalling pathways implicated in immune responses, emerged as differentially expressed genes.

These chromosomal and genetic contexts driving a differential immune response to cancer in the two sexes are listed in the visual abstract. However, the translational significance of the indicated groups of immune-related genes which are differentially regulated among the two sexes is still unveiled and necessitates prospective studies.

3.2. Sex hormones and immune profile

The immunomodulatory effect of sex hormones is a long-standing notion. By inhibiting pro-inflammatory (including TNF α , IL-1 β and IL-6) (Straub, 2007) and stimulating anti-inflammatory (including IL-4, IL-10 and TGF β) pathways, estrogens establish a sort of an unbalanced immune response favouring T helper (Th) type 2 vs Th1 activity (Roved et al., 2017) and partly explaining the predominance of Th1- and Th2-dependent autoimmune diseases in male and female, respectively (Whitacre, 2001). However, the effects of female hormones are context-dependent as, mainly after menopause, estrogen stimulates NK cell mediated responses (Giglio et al., 1994). Similarly, the decreased NK cytotoxic activity observed during pregnancy (van Nieuwenhoven, et al. 2003) disappears after menopause (Giglio et al., 1994).

While estrogens are associated with enhanced immune reactivity, testosterone has been widely ascribed as immunosuppressive (Foo et al., 2017). This contention is supported by evidence that T cells express androgens receptors (AR), which upon activation suppress IFN γ production, negatively conditioning ICI activity (Guan et al., 2022). Accordingly, clinical trials have documented an increased response rate in patients with advanced prostate cancer treated with AR inhibitors plus PD-1 blockade (Graff et al., 2016, 2020). As programmed exhaustion of CD8 $^{+}$ T cells within the TIME is critically regulated by T cell-intrinsic AR signalling (Kwon et al., 2022), the mechanism underlying the positive outcome from immunotherapy might reside in the synergistic effect of AR and PD-1 blockade, respectively preventing CD8 T cells anergy and unleashing their cytotoxic activity (Guan et al., 2022).

Sexual dimorphism in immune response resides also in the differential impact exerted by sex hormones on blood immune cell populations in a quantitative and qualitative manner. In large cohorts of healthy adults, females displayed higher number of CD4 $^{+}$ T cells and macrophages, higher CD4/CD8 ratio and lower NKs and T regulatory cells (Tregs) than males (Abdullah et al., 2012; Ahnstedt et al., 2018; Lee et al., 1996; Scotland et al., 2011). Healthy females also carry more activated CD8 T phenotypes (IFN γ , TNF α , G α ZB) and increased B cells number (Abdullah et al., 2012). Higher baseline levels of immunoglobulin M (IgM) (Butterworth et al., 1967) and greater antibody response to vaccination against seasonal and pandemic viruses (influenza, yellow fever, rubella, measles, mumps, hepatitis A and B, herpes simplex 2, rabies, smallpox, and dengue viruses) (Klein et al., 2010), including Sars-Cov2 (Bignucolo et al., 2021), compared to males also characterize female immunity.

In conventional DCs, as opposed to testosterone, estrogens enhance type 2 (IL-4, IL-10, and IL-13) cytokines and may also upregulate the expression of major histocompatibility complex (MHC) class II receptors and co-stimulatory molecules (Hepworth et al., 2010). While both testosterone (Corrales et al., 2009) and estrogens (Relloso et al., 2012) similarly suppress Th17 responses in conventional DCs, estrogens favour the release of type 1 cytokines in plasmacytoid DCs (Laffont et al., 2014; Seillet et al., 2012). Additionally, a higher production and receptor expression of type I IFNs was seen in female plasmacytoid DCs (Mocikat et al., 2003). Of note, single cell RNA sequencing documented upregulation of type I IFN stimulated genes in circulating neutrophils from healthy females as compared to male subjects (Gupta et al., 2020). Thus,

the identification of a sex-specific *IFN*-gene signature involving multiple immune-inflammatory phenotypes may offer important insights for personalized therapeutic strategies including immunotherapy.

The notion that estrogens are potent inducers of FOXP3 resulting in expansion of Treg compartment is well recognized (Polanczyk et al., 2004; Polanczyk et al., 2005). Sexual dimorphism on Treg population has been also experimentally documented in melanoma as improved anti-tumor immunity conferred by a reduced Treg function was observed in females (P.-Y. Lin et al., 2010).

Finally, aging in humans is associated with a decline in naive T cells and CD8⁺ T cells and a rise in CD3⁺CD45RA-CCR7+ effector memory, CD4+FOXP3+ Treg and NK cells (Márquez et al., 2020; Yan et al., 2010). However, this effect of aging is attenuated in women which display a relative increased immune reactivity (Takahashi and Iwasaki, 2021). More recently, an age-associated increase in CD8⁺ T effector memory (TEM) Granzyme K+ (GnZK) and PD-1+ circulating lymphocytes has been reported in humans (Mogilenko et al., 2021), although the impact of sex on this cell population was not investigated.

3.3. Sex differences in PD-1/PD-L1 immune checkpoint

Limited reports are available on the differential expression of PD-1 and PD-L1 in lung cancer according to sex (Pan et al., 2017; Moutafi et al., 2021; Ye et al., 2020). Interestingly, these studies concordantly documented higher PD-L1 levels in tumors from male patients potentially leading to a higher sensitivity to ICIs. Conversely, a lower fraction of PD-1+ CD8⁺ lymphocytes in female melanoma patients was associated with a lower rate of response to combined ICIs (Loo et al., 2017). Intriguingly, a multiomic molecular analysis conducted on a variety of tumor types, identified a female-bias immune signature in lung squamous carcinoma characterized by higher cytotoxic CD8 T cell activity and PD-1 expression (Ye et al., 2020).

However, in both aforementioned studies the potential confounding role of smoking habit was not evaluated.

Experimental observations made in an animal model revealed that female Tregs display an estrogen-insensitive lower expression of PD-L1 compared to male cells and this phenomenon appears to be coupled with a better response to PD-1 blockade (Lin et al., 2010). Moreover, the potency of Treg-mediated suppressive function has been linked to an increased estrogen-sensitive intracellular expression of PD-1 (Polanczyk et al., 2007; C. Wang et al., 2009) which is translocated to the cell surface upon Treg activation (Raimondi et al., 2006).

Finally, an often disregarded aspect when exploring sex-associated differences in immunity is the transient tolerogenic state that only women intrinsically experience during pregnancy (Barnet et al., 2018). However, this unique immune state engendered by both fetal (Rackaityte and Halkias, 2020) and placental (Murata et al., 2021) cues may evolve during life as chimerism (Bianchi et al., 1996; Jeanty et al., 2014), resulting from long term persistence of fetal DNA in mothers, may constitute an underlying mechanism of the increased incidence of auto-immunity in women (Fugazzola et al., 2011). Most clinical and experimental observations have suggested a rather protective action exerted by fetal microchimerism on the development of cancer, however conflicting results persist on such issue (Sedov et al., 2022; Kallenbach et al., 2011). How immunogenic and tolerogenic pathways in women who have been pregnant are differentially informed with the advent of cancer remains unknown and represent a fascinating area of future investigations in the era of immunotherapy.

4. Concluding remarks

Profound sex differences exist in immune response which are in part constitutive or take place during life as a result of adaptive measures of the organism (Murphy and Weaver, 2016). Genetic, hormonal and environmental factors contribute throughout life to create a divergent metabolic substrate and cytokines/chemokines networking, ultimately

conditioning sex specific immune profiles.

How this sexually determined immune dynamic is translated into differential tumor microenvironmental features and ICI response remains largely unknown and prospective data on sex differences in TIME composition are warranted.

Sex intersects with multiple biological, genetic and environmental factors implicated in the onset and evolution of cancer as well as its immune surveillance. So far, studies aimed at predicting ICI efficacy by the adoption of sex as a co-variate to be integrated with age, pregnancy or easily accessible blood immune descriptors are lacking and should represent the focus of shortcoming clinical and experimental observations.

CRedit authorship contribution statement

Giulia Mazzaschi: Writing – original draft. **Federico Quaini:** Writing – original draft, Writing – review & editing. **Sebastiano Buti:** Writing – review & editing, Supervision.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

No data was used for the research described in the article.

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