

# B7 Family

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B7 family members, as immune checkpoint molecules, can substantially regulate immune responses. Since microRNAs (miRs) can regulate gene expression post-transcriptionally, we conducted a scoping review to summarize and discuss the regulatory cross-talk between miRs and new B7 family immune checkpoint molecules, i.e., B7-H3, B7-H4, B7-H5, butyrophilin like 2 (BTNL2), B7-H6, B7-H7, and immunoglobulin like domain containing receptor 2 (ILDR2).

B7   microRNA   human diseases   cancer   immune checkpoint   immunotherapy   gene therapy

## 1. Introduction

Immune checkpoints can considerably regulate immune responses <sup>[1]</sup>. These molecules are critical for maintaining self-tolerance and preventing the stimulation of immune responses against normal peripheral tissues. Indeed, suppressing inhibitory axes, e.g., the immune checkpoint axis of cytotoxic T lymphocyte antigen 4 (CTLA-4) and programmed death-ligand 1 (PD-L1), has revolutionized cancer immunotherapy <sup>[2]</sup>.

The B7 family is a group of immune checkpoints commonly expressed in different immune cells, such as antigen-presenting cells, T cells, B cells, natural killer cells, and various tissues. They play a crucial role in immune response; for example, they have substantial roles in directing the fate of T cells by binding their receptors. Various members of the B7 family have been identified, e.g., *B7.1* (*CD80*), *B7.2* (*CD86*), *B7-H1* (*PD-L1*, or *CD274*), *B7-DC* (*PD-L2*, *PDC1LG2*, or *CD273*), *B7-H2* (*ICOSL*: inducible T-cell co-stimulator ligand, or *CD275*), *B7-H3* (*CD276*), *B7-H4* (*VTCN1*), *B7-H5* (*VISTA*: V-domain Ig suppressor of T cell activation, *Dies1*: differentiation of embryonic stem cells 1, or *C10orf54*), butyrophilin like 2 (*BTNL2*), *B7-H6* (*NCR3LG1*: natural killer cell cytotoxicity receptor 3 ligand 1), *B7-H7* (*HHLA2*: human endogenous retro virus–H long repeat-associating 2), and immunoglobulin like domain containing receptor 2 (*ILDR2*) <sup>[2][3][4][5][6]</sup>. Indeed, BTNL2 and ILDR2 are introduced as B7-like molecules, and further investigation is needed. B7 family genes have been linked with various pathological conditions, e.g., cancers, infections, autoimmune diseases, and transplantation complications <sup>[6]</sup>. Thus, a better understanding of their biology might pave the way for introducing novel strategies to treat the abovementioned diseases and complications.

MicroRNAs (miRs), as small, non-coding RNAs, can bind to their complementary sequences, which are often the mRNA 3'-untranslated regions (3'UTR) of their targets. Since miRs can cleave their target mRNAs by guiding the

RNA-induced silencing complex (RISC) to target mRNAs, in order to direct the cleavage of mRNA through Argonaute (AGO) endonuclease activity [7], destabilize their target mRNAs via cutting their poly(A) tail, and make the translation of their target mRNA less effective, they are considered potent post-transcriptional gene regulators [8][9][10]. In higher eukaryotes, miRs can regulate the expression of approximately 60% of genes. It is well-established that miRs can contribute to many biological processes, e.g., cell growth, differentiation, metabolism, and immune response regulation [11][12]. Indeed, miRs can modulate the function of immune cells and regulate the expression of immune checkpoints [13][14][15]. Thus, alteration in miR expression is involved in the pathogenesis of various human diseases, like cancers [11][13][16]. Moreover, miRs can regulate the expression of B7 family members in various diseases; thus, there is a need to properly understand the scope and effect of this regulation in human diseases [17][18].

## 2. The Regulatory Cross-Talk between microRNAs and Novel Members of the B7 Family in Human Diseases

### 2.1. B7-H3

*B7-H3*, also referred to as *CD276*, can regulate the stimulation and inhibition of T cells [19][20]. A variety of cells, e.g., natural killer cells, activated T-cells, dendritic cells, macrophages, and non-hematopoietic cells, can express *B7-H3* [21]. Preliminary findings reported that B7-H3 could promote CD4+ and CD8+ T cell proliferation by T cell receptor (TCR) stimulation using immobilized Ig fusion protein [19]. However, it is well-established that B7-H3 can suppress the activation of CD4+ T-cell and the release of effector cytokines [22][23]. This suppression might facilitate the function of transcription factors like nuclear factor of activated T cells (NF-AT), nuclear factor kappa B (NF-κB), and activator protein 1 (AP-1), playing significant roles in T cell function [22]. Moreover, *B7-H3* overexpression has been identified in various cancers, e.g., breast [24], lung [25], kidney, prostate [26], and ovarian cancer [27]. Furthermore, the inhibition of *B7-H3* has decreased angiogenesis in medulloblastoma, indicating its essential role in tumor angiogenesis [28]. As an overexpressed oncogene in various cancers, MYC has a critical role in cancer development, e.g., angiogenesis, apoptosis, proliferation [29][30]. Since MYC inhibition has been associated with the suppressed expression of *B7-H3* in medulloblastoma cells, the MYC-*B7-H3* regulatory axis can play an essential role in regulating angiogenesis [28]. It has been indicated that *B7-H3* knockdown can repress the PI3K/Akt pathway, resulting in decreased STAT3 activity. Since STAT3 can promote the expression of matrix metalloproteinase 2 (*MMP2*) and matrix metalloproteinase 9 (*MMP9*), B7-H3 can regulate the expression of *MMP2* and *MMP9* [31]. Moreover, *B7-H3* can be involved in inflammatory conditions, e.g., sepsis and bacterial meningitis [32]. Since the mRNA expression of *B7-H3* is not as remarkable as its protein expression, the post-transcriptional regulating process might have a considerable effect [21].

### 2.2. B7-H4

*B7-H4*, also known as *B7x*, *B7S1*, and *VTCN1*, can inhibit cytokine production, proliferation, cell cycle progression, and the stimulation of CD4+ and CD8+ T cells [33][34]. Although its transcripts can be found in various tissues, its protein has low expression in most human normal tissues [35]. *B7-H4* expression is positively correlated with cancer

development in patients with gastric cancer [36], glioma [37], squamous cell esophageal carcinoma [38], renal cell carcinoma [39], pancreatic cancer [40], cholangiocarcinoma [18], ovarian cancer [41], and lung cancer [42]. Since *B7-H4* has been associated with cancer development, it can be an appealing target for treating cancer patients [35].

It has been shown that miR-125b-5p has an anti-inflammatory role and can regulate interleukin (IL)-1 $\beta$ -induced inflammatory genes by targeting the TNF receptor associated factor (TRAF6)/mitogen-activated protein kinase (MAPK)/NF- $\kappa$ B pathway in human osteoarthritic chondrocytes [43]. However, miR-125b-5p overexpression in macrophages can increase IL-2 secretion and the proliferation of CD8<sup>+</sup> T cells. Indeed, miR-125b-5p can target *B7-H4* and facilitate inflammation [44]. In line with this, *B7-H4* overexpression has been associated with poor prognosis in colorectal cancer patients [45]. In 24.4% of colorectal cancer patients, single-nucleotide polymorphism (SNP) rs13505 GG of *B7-H4* can confer an alternate binding site for miR-1207-5p, which might result in downregulation of this gene [46]. Furthermore, TGF- $\beta$ 1 can upregulate *B7-H4* and facilitate immune escape via the miR-155/miR-143 axis in colorectal cancer [47].

In 2017, 62 hsa-miRs were identified as regulating *B7-H4* in pancreatic cancer [48]. These miRs were mentioned above in the Results section.

### 2.3. B7-H5

B7-H5, also known as VISTA, C10orf54, Dies1, and PD-1H, is a type-I membrane protein that can stimulate terminal differentiation of embryonic stem cells (ESCs) into cardiomyocytes/neurons via the bone morphogenetic protein (BMP) signaling pathway [49]. It has been reported that miR-125a-5p can directly repress the transcription of *B7-H5* and inhibit ESC differentiation [50]. B7-H5 also plays a pivotal regulatory function in adipocyte differentiation independently from BMP signaling. In particular, the elevated level of *B7-H5* has been shown exclusively in differentiated fat cells and blocked adipocyte differentiation [51]. In *B7-H5* knockout mice, the elevation of inflammatory cytokines can result in chronic multi-organ inflammation, indicating the critical role of B7-H5 in suppressing inflammation [52]. In Crohn's disease, there is a negative association between *B7-H5* expression and hsa-miR-16-1 [53]. B7-H5 can serve as a ligand and receptor on T cells, suppressing the activation of naïve and memory T cells [54][55]. The presence of two PKC binding sites in the cytoplasmic region of B7-H5 might indicate that B7-H5 is a receptor [56][57]. *B7-H5* can be overexpressed in cancer-associated/cancer-adjacent gastric myofibroblasts. However, *B7-H5* expression is generally downregulated in epithelial gastric cancer cells. This can be explained by *B7-H5* promoter methylation, the overexpression of miR-125a-5p, or a combination of both, and even the existence of mutant *p53* [58]. Indeed, the downregulation of *B7-H5* has been associated with de-differentiation and triggered epithelial–mesenchymal transition (EMT) in epithelial cells.

### 2.4. B7-H6

B7-H6, also known as NCR3LG1, is a ligand for the NKp30 [59]. B7-H6 sequence is functionally similar to the other B7 family members. Although *B7-H6* is not found in normal human tissues, it is highly expressed in cancers, e.g., renal cell carcinoma, leukemia, breast cancer, ovarian cancer, and sarcomas [60]. Various factors can regulate *B7-H6* expressions, e.g., protease inhibitors, proinflammatory cytokines, natural killer cells, and miRs. Histone

deacetylase inhibitors (HDACi) and metalloprotease inhibitors can regulate the *B7-H6* expression at transcription and post-transcriptional levels, respectively [61]. Following stimulation of CD14<sup>+</sup>CD16<sup>+</sup> neutrophils and monocytes, B7-H6 can be expressed on these proinflammatory immune cells [62]. Tumoral B7-H6 can be recognized and eliminated via natural killer cells. However, metalloproteases can cleave B7-H6 and shield tumor cells from natural killer-mediated immune responses [63]. Bioinformatics analysis has predicted that miR-93, miR-195, and miR-340 can regulate immune responses by targeting *B7-H6* in breast cancer cells [64].

## 2.5. B7-H7

*B7-H7*, which has previously been referred to as *B7-H5*, is known as the human endogenous retro virus–H long repeat-associating 2 (*HHLA2*) [65][66]. Its receptors can be found on various immune cells, e.g., monocytes, T cells, B cells, and dendritic cells. TMIGD2, which is referred to as CD28 homolog, is one of the identified B7-H7 receptors [67]. In antigen-presenting cells, B7-H7 co-stimulates the proliferation of naïve T cell and cytokine production across TMIGD2 by serine–threonine kinase AKT phosphorylation. However, the second B7-H7 receptor on activated T cells can exert a coinhibitory role, because activated T cells do not express TMIGD2. The identification of the second receptor might clarify the role of B7-H7 in T cell activation and the tumor microenvironment [68]. It has been reported that *B7-H7* is upregulated in lung cancer, osteosarcoma, and breast cancer, and its elevated expression is correlated with a poor prognosis in affected patients [69]. BATF in B lymphocytes and SMAD in monocytes might be involved in the dysregulation of *B7-H7* in kidney clear-cell carcinoma. It has been indicated that hsa-miR-6870–5p and hsa-miR-3116 might have a role in this modulatory mechanism [70].

## 2.6. Bioinformatics Analysis

Based on our results, four potential new interactions between B7 family members and miRs have been identified: (1) the hsa-miR-29b-3p/*B7-H3* axis, (2) the hsa-miR-29a-3p/*B7-H3* axis, (3) the hsa-miR-125a-5p/*B7-H4* axis, and (4) the hsa-miR-486-5p/*B7-H4* axis. Of these four interactions, the association of different isoforms of miR-29 with *B7-H3* has been investigated in previous studies (see above). As mentioned earlier, hsa-miR-125a-5p regulates *B7-H5* expression in gastric cancer, but its association with *B7-H4* has not been studied. Recent findings have shown that miR-125a-5p plays a pivotal role in suppressing the classical activation of macrophages (M1-type) induced by lipopolysaccharide (LPS) stimulation, while promoting IL-4-induced expression of the alternative M2 macrophages by targeting KLF13, a transcriptional factor that is involved in T lymphocyte activation and inflammation [71]. In addition, miR-486-5p is an immunomodulatory tumor suppressor miR that has been reported to have key roles in various oncological and non-oncological disorders [72]. Although our knowledge about the role of miR-125a-5p/*B7-H4* and miR-486-5p/*B7-H4* axes in the immune pathways and the pathogenesis of various diseases is still preliminary, our in silico analysis can pave the way for further investigations.

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