Understanding the Role of Notch in Osteosarcoma

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Abstract The Notch pathway has been described as an oncogene in osteosarcoma, but the myriad functions of all the members of this complex signaling pathway, both in malignant cells and nonmalignant components of tumors, make it more difficult to define Notch as simply an oncogene or a tumor suppressor. The cell-autonomous behaviors caused by Notch pathway manipulation may vary between cell lines but can include changes in proliferation, migration, invasiveness, oxidative stress resistance, and expression of markers associated with stemness or tumor-initiating cells. Beyond these roles, Notch signaling also plays a vital role in regulating tumor angiogenesis and vasculogenesis, which are vital aspects of osteosarcoma growth and behavior in vivo. Further, osteosarcoma cells themselves express relatively low levels of Notch ligand, making it likely that nonmalignant cells, especially endothelial cells and pericytes, are the major source of Notch activation in osteosarcoma tumors in vivo and in patients. As a result, Notch pathway expression is not expected to be uniform across a tumor but likely to be highest in those areas immediately adjacent to blood vessels. Therapeutic targeting of the Notch pathway is likewise expected to be complicated. Most pharmacologic approaches thus far have focused on inhibition of gamma secretase, a protease of the presenilin complex. This enzyme, however, has numerous other target proteins that would be expected

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E.S. Kleinerman (ed.), *Current Advances in Osteosarcoma*, Advances in Experimental Medicine and Biology 804, DOI 10.1007/978-3-319-04843-7_4, © Springer International Publishing Switzerland 2014

to affect osteosarcoma behavior, including CD44, the WNT/ β -catenin pathway, and Her-4. In addition, Notch plays a vital role in tissue and organ homeostasis in numerous systems, and toxicities, especially GI intolerance, have limited the effectiveness of gamma secretase inhibitors. New approaches are in development, and the downstream targets of Notch pathway signaling also may turn out to be good targets for therapy. In summary, a full understanding of the complex functions of Notch in osteosarcoma is only now unfolding, and this deeper knowledge will help position the field to better utilize novel therapies as they are developed.

Keywords Osteosarcoma • Notch • DLL4 • Jag1 • Angiogenesis • Metastasis • Dormancy • Cancer stem cells

Introduction: The Notch Signaling Pathway

The Notch signaling pathway, a key component in normal bone development that is implicated as a key mediator in a number of various cancers, is initiated when a membrane-bound ligand belonging to the Delta-Serrate-Lag (DSL) family (jagged 1/ Jag1, Jag2, delta-like-1/DLL1, DLL3, and DLL4) on the surface of a cell interacts with a membrane-bound Notch receptor (Notch1-4) on another cell. This interaction induces a two-step proteolytic cleavage of the receptor, first by ADAM10 (also known as Kuz) or ADAM17 (also known as TACE) and then by the γ -secretase complex which is made up of at least four individual proteins: presenilin, nicastrin, anterior pharynx-defective 1 (APH-1), and presenilin enhancer 2 (PEN-2). These cleavage events release the *i*ntracellular domain of Notch (ICN). Now activated, ICN enters the nucleus where it forms a transcriptional complex with Mastermind-like 1 (MAM1) to regulate transcriptional complexes containing the DNA-binding protein CBF1/ RBPjk/Su(H)/Lag1 (CSL). This complex initiates the transcription of Hairy/Enhancer of Split-1 (Hes1), Hes5, Hes7, HES-related with YRPW motif (Hey1/HERP2), Hey2 (HERP1), and HeyL which encode basic helix loop helix (bHLH) transcription factors that perform a range of cellular activities that include promoting progenitor cell survival and suppressing differentiation [1, 2]. This pathway is displayed schematically in Fig. 1. The Notch signaling pathway, via cell-cell contacts, highly regulated feedback loops, and lateral inhibition/induction mechanisms, has been shown to influence multiple cellular processes including cell fate decisions, proliferation, apoptosis, migration, angiogenesis, and plasticity. In terms of bone homeostasis, skeletal cells express Notch1, Notch2, and low levels of Notch3, although Notch1 and 2 are considered responsible for the effects of Notch in the skeleton [3] (Notch signaling reviewed in [4, 5]).

Role of Notch Signaling in Normal Osteoblast Development

Mesenchymal stem cells (MSCs) can give rise to multiple lineages in response to environmental molecular cues: the presence of MyoD leads to the differentiation of MSCs into myocytes, PPAR γ leads to the generation of adipocytes, the Sox family



Fig. 1 Schematic diagram of Notch pathway signaling. Notch ligands, consisting of the jagged (Jag1 and Jag2) and delta-like (DLL1, DLL3, and DLL4) families, typically are presented on the surface of signal-sending cells, though these receptors can be shed by proteolytic cleavage in some circumstances. Prior to ligand binding, the Notch family receptors (Notch1, Notch2, Notch3, and Notch4) remain fixed at the plasma membrane, and the CSL transcription complex remains bound to corepressor elements, shutting off transcription of CSL target genes. Upon binding ligand, Notch1 is subject to a two-step proteolytic cleavage by ADAMS family protease and then γ -secretase. Cleavage by γ -secretase frees the cytoplasmic domain of the Notch1 from the plasma membrane; this fragment is termed *in*tracellular *Notch1* (ICN1). ICN1 binds to CSL, displacing corepressor elements and recruiting coactivator elements, including *Mastermind-Like* (MAML), turning on transcription of CSL target genes, including the Hes, Hey, Herp, NRARP, and Deltex families. Notch1 also mediates transcription of non-CSL target genes, which is termed the noncanonical Notch pathway. Regulation of Notch2, Notch3, and Notch4 is similar

of genes drive chondrocytogenesis, and runt-related transcription factor-2 (RunX2) and osterix lead to osteoblastogenesis [6–8]. Normal osteoblast development and subsequent bone formation are meticulously regulated not only by RunX2 and osterix but also by a cascade of regulatory signaling that includes morphogens, signaling molecules, and transcriptional regulators [9–16]. A partial list of these factors includes the Wnt/ β -catenin, TGF β /bone morphogenic protein (BMP), FGF, Notch and Hedgehog signaling pathways, ATF4, TAZ, RANKL, and NFATc1 transcription factors [16–19]. Signaling molecules like RunX2, BMPs, and the Wnt/ β -catenin canonical pathway are conducive to osteoblastogenesis, while others, such as the Notch signaling pathway, obstruct osteoblast differentiation [20–22]. In osteoblasts, RunX2 regulates the transcription of genes including osteocalcin,

bone sialoprotein, osteopontin, type I collagen, fibronectin, galectin 3, MMP13, osteoprotegrin (OPG), Tram2, Lnx2 (an intracellular scaffolding protein that may play a role in Notch signaling), and Tnfrsf12a (a tumor necrosis factor receptor family member) by binding to sequences that resemble the 5'-ACACCA-3' motif upstream from their transcription start sites [23–28]. Because of its importance in this process, RunX2 is labeled the "master regulator" of osteoblast differentiation; indeed homozygous RunX2 mutant mice have cartilaginous skeletons that fail to mineralize, owing to a complete arrest in osteoblast differentiation [24, 29, 30]. For further details of the role of RunX2 in osteoblast development and in osteosarcoma, please see the chapter on this book entitled "Developmental Pathways Hijacked by Osteosarcoma."

The Notch signaling pathway plays an important and complex role in bone homeostasis [22, 31–34]. In bone marrow, Notch signaling normally acts to maintain a pool of mesenchymal progenitors by suppressing osteoblast differentiation by inhibiting RunX2 [3]. In osteoblasts, the Notch pathway has several mechanisms that inhibit osteoblastogenesis. Notch antagonizes Wnt signaling: ICN2 colocalizes with glycogen synthase kinase-3 β (GSK3 β) to mediate the degradation of β -catenin [22, 35]. It has been shown that NFATc1 and osterix form a complex that activates osterix-dependent transcription [36]; ICN and mastermind form a complex with Foxo1 which inhibits NFAT-mediated osteoblastogenesis, osteoblastic bone formation, as well as osteoclastogenesis and bone resorption [37, 38]. Furthermore, Engin et al. show that Notch both stimulates early osteoblastic proliferation by upregulating cyclin D, cyclin E, and osterix and represses osteoblast maturation through the binding of ICN to RunX2 [31]. Hilton et al. and others demonstrate an additional mechanism by which Notch signaling inhibits RunX2: RunX2 transcriptional activity is inhibited by its direct interactions with the HLH and Orange domains of Hey1 [3, 34]. The enzyme necessary for Notch receptor cleavage and activation, ADAM10, is expressed in cells of the osteoblast lineage and is localized at sites of active bone formation. Catalytically active ADAM10 was found to colocalize with Notch2 at these bone-forming sites [39]. This suggests that ADAM10 may play a role in controlling osteoblast differentiation; alternatively, it has been suggested that ADAM10 may work rather to cleave Notch receptor ligands to provide soluble activators of the receptor [39, 40].

Osteosarcoma and Differentiation. Osteosarcoma (OS) may be thought of as a disease of disrupted osteogenic differentiation [8, 10, 41–43]. With the prevention of the differentiation of MSCs into mature osteoblasts, there is an increased risk for malignant transformation as cells continue to proliferate uncontrollably [8, 44]. Osteosarcoma cells display similar characteristics to undifferentiated osteoblasts: early osteogenic markers like CTGF are high in OS cell lines, while markers of differentiation like RunX2, alkaline phosphatase, osteopontin, and osteocalcin are low [10, 41, 42, 45]. Interestingly, the aggressiveness of OS may depend on the stage of differentiation that was disrupted: more aggressive OS may develop from disruptions in the differentiation of early osteoblast progenitors, while benign tumors may arise from disruptions in late-stage osteoblasts [8, 41]. Considering the

importance of Notch in normal osteoblast development, the Notch signaling pathway has become increasingly interesting to those studying the progression of osteosarcoma [46–52].

Notch and the Vasculature

Introduction. Blood vessels comprise an extensive tubular network that delivers oxygen and nutrients to all organs and tissues. Vital processes such as embryogenesis, wound healing, body temperature stabilization, and homeostatic balance maintenance all require highly adjustable blood supply and nutrient delivery. These demands are met through the meticulously regulated growth and expansion of the vascular network by angiogenesis. The process of sprouting angiogenesis is highly dynamic and requires a multitude of individual processes such as the proliferation of endothelial cells (ECs), selection of leading cells that develop filopodia and promote endothelial motility, elongation of the new sprout, formation of new cell–cell junctions, conversion into endothelial tubules, specification into arteries, veins, and capillaries, recruitment of mural cells (smooth muscle cells, SMCs, and pericytes), anastomosis with other vessels, remodeling and pruning, perfusion, and stabilization of the newly formed vessel.

The Notch signaling pathway is evolutionarily conserved and is an important mediator of cell–cell communication during the formation of new blood vessels [53]. Major components of the Notch pathway are expressed in the vasculature [54, 55], and genetic deletion of Notch pathway components, including Notch1 [56–58], Notch2 [59], Jag1 [60], DLL1 [61, 62], DLL4 [63, 64], Hey1/Hey2 [65], CSL [66], or presenilins which make up the γ -secretase complex [67, 68], as well as the ectopic activation of Notch1/Notch 4 [69, 70], results in embryonic lethality associated with defects in sprouting angiogenesis, arterial/venous specification, vascular remodeling, and vascular SMC organization (Table 1).

Role of Notch Signaling in Normal Vascular Development

Notch and Arterial/Venous Specification

One of the earliest roles for Notch is in the developing embryo; Notch functions in early vascular development to drive endothelial identity while suppressing venous identity [64, 71]. Later in development, arterial endothelial cells have been shown to require DLL1 to maintain their cellular identity [61]. A more detailed review of this subject has been published recently [72].

Knockout	Major effect	Author, Year
Notch ligands		
Jagged 1	Embryonic lethal; severe vascular defects	Xue et al. [60]
Jagged 2	Defects in limb, craniofacial, thymic development	Jiang et al. [207]
Delta-like ligand 1	Embryonic lethal; defects in the formation of somite borders; defects in arterial identity	Hrabe de Angelis et al. [62]; Sorensen et al. [208]
Delta-like ligand 3	Highly disorganized vertebrae and costal defects; disruption of the segmentation clock	Dunwoodie et al. [209]
Delta-like ligand 4	Embryonic lethal; defects in arterial development	Duarte et al. [64]; Gale et al. [63]
Notch receptor:	5	
Notch1	Embryonic lethal; severe defects in angiogenic vascular remodeling	Swiatek et al. [58]; Krebs et al. [57]; Limbourg et al. [56]
Notch2	Embryonic lethal; defects in postimplantation development	Hamada et al. [59]
Notch3	Defects in arterial identity and maturation of vascular smooth muscle cells	Domenga et al. [210]
Notch4	No apparent deficiencies	Krebs et al. [57]
Notch1 and 4	More severe than Notch1 KO only	Krebs et al. [57]
Downstream no	otch targets	
Hes1	Death occurs in utero or neonatally	Blake et al. [206]
Hey1	No apparent deficiencies	Fischer et al. [65]
Hey2	Postnatal lethality; cardiac defects	Fischer et al. [65]
Hey1 and 2	Embryonic lethal; global lack of vascular remodeling	Fischer et al. [65]
Notch-related g	enes	
γ-secretase complex		
Presenilin 1	Skeletal and CNS defects	Shen et al. [211]; Nakajima et al. [68]
Presenilin 2	Mild pulmonary fibrosis	Herreman et al. [67]
CSL	Vascular defects	Krebs et al. [66]

Table 1 Notch signaling pathway knockout mice

The major effects observed in mice with each of the Notch family ligands, receptors, and downstream signaling molecules are summarized, together with the relevant publication referenced

Notch and Sprouting Angiogenesis

Vascular endothelial growth factor (VEGF/VEGF-A) is the key regulator that promotes sprouting angiogenesis. In normal/physiologic angiogenesis, VEGF-A is secreted by astrocytes in the avascular region leading to the formation of a VEGF gradient [73, 74]. VEGF-A binds to the tyrosine kinase receptors VEGFR1 (Flt1) and VEGFR2 (KDR/Flk1/Flt2) expressed on the cell surface of nearby ECs.

VEGFR2 is the primary receptor transmitting VEGF signals in ECs [75, 76], while VEGFR1, with weaker kinase activity, acts as a VEGF decoy [77, 78]. Newly sprouting blood vessels are made up of two important endothelial cell types: *tip cells*, which initiate new sprouting, and stalk cells which maintain connection with the parent vessel [79–83]. In response to VEGF-A/VEGFR2-mediated signaling, ECs at the leading front of angiogenic sprouts develop protruding filopodia and become tip cells that extend toward sources of pro-angiogenic growth factors. These tip cells respond to positive/negative guidance cues to allow for directional growth while preventing unorganized and random vessel development [84, 85]. Once such negative guidance cue involves VEGF-mediated induction of DLL4 as a negative feedback regulator, which acts to prevent uncontrolled angiogenic sprouting while promoting the timely formation of a well-differentiated vascular network [83, 86]. Expression of DLL4 stimulates Notch1 activation in adjacent ECs that trail tip cells and form the base of the protrusion and become stalk cells [87]. Whereas tip cells mainly express DLL4, stalk cells primarily express Jag1 which consequentially antagonizes DLL4 activity by competing for Notch receptors via DLL4/Notch1/Jag1-mediated lateral inhibition [82-84, 88-90]. Stalk cells are important in that they proliferate when stimulated with VEGF-A, form the vascular lumen, establish adherins and tight junctions to maintain integrity of the new sprout, and maintain connection with parental vessels so as to establish luminal/abluminal polarity which leads to basal lamina deposition and mural cell recruitment and attachment [84, 91, 92]. In stalk cells, Notch signaling potently inhibits VEGFR3 [93, 94]; VEGFC/VEGFR3 signaling activates PI3K and its downstream target FoxC2, which results in the downregulation of DLL4 in the stalk cell [95, 96]. High levels of activated Notch (ICN) lead to the production of soluble VEFGR1 which acts to enhance the steepness of the VEGF-A signaling gradient by sequestering VEGF-A and inhibiting its action with VEGFR2 in stalk cells [97]. Stalk cells express Hes1 and Hey1 which act to downregulate the levels of VEGFR2, VEGFR3, and DLL4, thereby transiently decreasing the responsiveness to VEGF-A and further enhancing the stalk cell phenotype [81, 82, 93]. This allows new tip cells to form along the front to form branching vessels [98, 99]. Vessel branching within the developing vascular network is also the consequence of another downstream Notch target, Notch-regulated ankyrin repeat protein (Nrarp), which counteracts Notch signaling and is expressed in stalk cells at the branch points [100, 101].

Considering that local changes in VEGF/Notch signaling can trigger the conversion of stalk cells into tip cells, and that the Notch pathway can act in a highly transient and oscillating manner [102], tip and stalk cell phenotypes are remarkably transitory and interchangeable as ECs dynamically shuffle position along the angiogenic sprout competing for the tip cell position [103]. This leads to highly regulated and organized vessel formation. In normal vascular development, these mechanisms work together to balance the numbers of tip cells and stalk cells required for effective sprouting and network formation [82, 104–107]. Tissue oxygenation eventually downregulates paracrine VEGF-A production and thus helps establish a quiescent state for the new vessels [108]. This process has been reviewed in detail [87, 109]. The role of Notch pathway signaling in regulating normal vascular development is shown schematically in Fig. 2.



Fig. 2 Normal angiogenesis and the role of Notch pathway signaling. (a) Tip cell development through tubulogenesis. Upon exposure to VEGF-A, endothelial cells respond by taking on a tip cell signaling phenotype. The initial response is stochastic and cyclical, eventually allowing some cells to acquire the full tip cell phenotype, while adjacent cells are prevented from acquiring this phenotype through lateral inhibition, which is Notch mediated. Initial sprouting of tips is also a cyclic process, with individual tips extending and retracting back into the tip cell, leaving behind empty matrix sleeves that help to repattern the extracellular matrix needed in the sprouting blood vessel. Cells adjacent to tip cells become stalk cells, extending outwards toward the VEGF-A gradient, pushing the tip cell outward from the parent vessel. As the filopodia of nearby tip cells contact each other, macrophages are recruited to the site of anastomosis, facilitating fusion of tubes, with subsequent extension of these tubes. (b and c) Notch/VEGF signaling during activation, selection, and sprouting. VEGF-A binds to both VEGFR-1 and VEGFR-2 on adjacent endothelial cells, signaling through both receptors. Predominance of VEGFR-2 signaling favors a tip cell phenotype, which VEGFR-1 favors a stalk cell phenotype. VEGFR-2 signaling mediates upregulation of DLL4 which, in turn, activates Notch1 on the cells to either side of the endothelial cell. DLL4 reduces transcription of VEGFR-2 and promotes secretion of a soluble VEGFR-1 that serves as a ligand trap and reduces the ability of stalk cells to respond to VEGF-A. (d) Notch/ VEGF signaling during anastomosis and the role of macrophages. Normal macrophages, without activation, express cell surface DLL4, Jag1, and Jag2 as well as Notch1, Notch2, and Notch4. Notch receptors, especially Notch2, allow macrophages to be recruited to the sites of tip cell anastomosis, where the high levels of DLL4 activate these macrophages. Through a process that is not fully understood, the activated macrophage then helps two tip cells to form a stable bridge that develops into a full vascular loop

Notch and Vascular Mural Functions

Notch signaling also plays an important role in vessel stability by regulating vascular mural cell function. Mural cells (SMCs and pericytes) are attached to the basal surface of certain vessels and help to stabilize the vessel wall, signal to ECs to inhibit their proliferation, promote survival, and regulate blood pressure [110, 111]. Mural cells express Notch1-3, Jag1, and DLL4 [112]. In vitro, it has been shown that endothelial Jag1 activates Notch3 on SMCs to induce Notch3 expression and regulate SMC differentiation [113]. Notch1 signaling is critical for mural cell recruitment to new vessels, whereas Notch3 plays a role in pericyte/SMC maturation once it arrives at its final destination. This process has been reviewed recently [72]. Notch pathway activity is essential for recruitment of bone marrow-derived pericytes to the blood vessels of Ewing sarcoma tumors, and inhibition of the Notch pathway with either shRNA or antibodies impeded Ewing sarcoma tumor growth in vivo and caused impaired vasculogenesis [114, 115]. Perivascular cells, in addition to the endothelium, also have been shown to play an important role in angiogenesis and are deregulated in pathological angiogenesis [110, 115].

Notch and Macrophage-Mediated Angiogenesis

Macrophages have been recognized as key angiogenic effector cells [116, 117]. Macrophages are closely associated with sprouting endothelial cells during retinal angiogenesis [118]. Importantly, tissue macrophages act as cellular chaperones during VEGF-mediated endothelial tip cell induction and anastomosis, allowing for the bridging of tip cells to form stable, perfused vessels [117, 119]. Inactive macrophages express Notch1, -2, and -4, DLL4, and Jag1-2; once activated, macrophages increase their expression of Notch1 and Jag1 [120-122]. Though it is known that VEGFR1 recruits macrophages to sites of inflammation and active angiogenesis [123], macrophage recruitment to sites of anastomosis remains an active area of research. It has been hypothesized that DLL4 expressed in tip cells attracts macrophages via Notch1–DLL4 signaling [117]. Mice with heterozygous mutations for Notch1 have decreased macrophage recruitment and, interestingly, also have decreased expression of VEGFR-1 [124]. Through these studies and others, it is clear that both VEGFR1 and Notch1 play an important role in macrophage recruitment to sites of angiogenesis. Recent publications are available with more complete reviews of the role of macrophages in angiogenesis [72, 125].

Role of Notch Signaling in Tumor Vascular

Notch Signaling at the Primary Tumor

Tumor angiogenesis relies on many of the same mechanisms involved in physiological angiogenesis. Tumors, restricted to 1–2 mm³ without an oxygen and nutrient source, release large amounts of VEGF in response to their hypoxic environment. Unlike normal angiogenesis, however, tumors continuously release pro-angiogenic factors despite the ever-growing expansion of blood vasculature into the welloxygenated portions of the tumor. This vasculature not only feeds the tumor and allows for uncontrolled proliferation, but it also allows for the metastatic spread of the disease to distant loci, since osteosarcoma spreads almost exclusively via the hematogenous route.

VEGF-A has been shown to be over-expressed in many tumor types [126–128]. Although not much is known about the process of vasculogenesis in osteosarcoma, multiple studies have shown that VEGF overexpression in osteosarcoma unfavorably impacts the overall survival [129–131]. Similarly, the role of Notch has been well documented in other tumor types [115, 132, 133] but continues to be an active area of study in osteosarcoma. In multiple tumor types, it has been shown that either blockade [105, 106, 134–136] or forced activation of the Notch pathway [137–142] can inhibit angiogenesis. Genetic or pharmacologic inactivation/inhibition of either DLL4 or Notch1 signaling leads to an increase in the number of filopodia and sprouting tip cells at the angiogenic front which, together with EC proliferation, results in the formation of a hyperdense vascular network with immature, hyperplastic, and nonfunctional characteristics [81, 83, 86, 104, 107, 143]. Chronic blockade of the pathway, however, results in the formation of vascular neoplasms [144]. Conversely, activation of Notch signaling leads to a reduced number of tip cells and less dense vascular network [86, 107]. A schematic model of the role of Notch in tumor angiogenesis is shown in Fig. 3.

Notch Signaling at the Metastatic Site

Judah Folkman first championed the concept that tumors require an "angiogenic switch" in the balance between pro- and anti-antigenic signals to establish a robust blood supply capable of supporting rapid tumor growth [145]. By extension, this model would suggest that, for dormant tumors, there is a balance between signals that increase angiogenesis and those that impede angiogenesis and that dormant micrometastases of osteosarcoma would be relatively poorly vascularized. Indraccolo and colleagues showed that expression of DLL4 on blood vessels in close proximity to colon cancer cells was necessary for these tumor cells to awaken from dormancy [146]. The same group had shown already that a short-term "spike" in angiogenesis was sufficient to awaken dormant tumors [147]. This awakening is associated with a transcriptional switch from expressing anti-angiogenic proteins to secreting



Fig. 3 Tumor angiogenesis. (a) Heterogenic distribution of vasculature and O_2 in a tumor. Because oxygen diffusion is limited in tissues to ~1 mm from capillaries, rapidly growing tumors will have regions of relative normoxia and other areas of profound hypoxia, with an oxygen gradient between these regions. The extremely high levels of VEGF-A secreted in the areas with the worst hypoxia override normal angiogenic controls, leading to large numbers of small, dysfunctional, and leaky blood vessels that can be observed on arteriograms (a, right hand panel) as a "vascular blush." Other areas of the tumor do not appear to have any blood supply at all and often are necrotic when examined pathologically. (The *right hand panel* in (a) is taken from an osteosarcoma patient receiving an arteriogram prior to the delivery of intra-arterial chemotherapy. The method is exactly as described previously [205].) (b) Tumors hijack empty matrix sleeves for migration/invasion. As described above and in Fig. 2, normal angiogenesis involves cyclical extension and retraction of tips, repatterning the extracellular matrix, including spreading laminin away from the basement membrane toward the VEGF-A source. In tumors, these empty sleeves left behind by tip cell extension and retraction become pathways in which the extracellular matrix ceases to be a barrier to tumor cell migration, but rather a guide for tumor cells to "find" blood vessels. (c) Tumors promote uncontrolled angiogenesis. Growing tumors provide a sustained source of VEGF-A, either directly through their own secretion or by inducing hypoxia, thereby promoting VEGF-A secretion from nonmalignant cells within the tumor, such as tumor-associated fibroblasts. Unlike normal angiogenesis, in which VEGF-A levels eventually decline and new vessels are allowed to mature and stabilize, the sustained VEGF-A secretion in the tumor microenvironment causes uncontrolled, sustained angiogenesis, without the maturation and stabilization found in normal angiogenesis. (d) High expression of VEGF promotes an all tip cell phenotype. In areas with the highest VEGF-A secretion, the concentration of VEGF-A is sufficient to override the cellular processes that induce lateral inhibition and organized vessel formation. In this environment, endothelial cells may take on an "all tip cell" phenotype, leading to vascular leak and highly disorganized blood vessels that completely lack vessel wall components. Note that in any given tumor, aspects of abnormal blood vessel development shown in panels A–D may all be taking place, each in different regions of the tumor

pro-angiogenic ones [148]. While there is no direct experimental evidence in osteosarcoma models to support this role of the vasculature in osteosarcoma metastasis, it certainly seems plausible that a similar effect operates in these patients' lungs.

There is a conception among some patients and families that major operations for osteosarcoma patients "spread the tumor." While this has not been scientifically validated, it has been observed that pulmonary metastasis sometimes develops shortly after resection of the primary tumor or lung metastases. Since the healing of large wounds results in high levels of circulating growth factors and cytokines such as EGF and its related ERBB family ligands, these growth factors and angiogenic cytokines could stimulate the expansion of tumor vessels in micrometastases. The transient upregulation of Notch ligands on vessels near the dormant micrometastases may initiate the angiogenic response that facilitates growth. A more comprehensive review of the putative roles of the Notch pathway in regulating tumor escape from dormancy in the metastatic site has been published recently [149].

Notch Signaling in Osteosarcoma

The Notch pathway has been called "the stem cell master switch" [53, 150] because it influences multiple processes that drive morphogenesis, lineage specification, apoptosis, and proliferation, not only in normal tissues but also in some cancers [151]. Notch dysregulation serves as an oncogene for many cancers including T-cell leukemia [152] and solid tumors of pancreas, breast, prostate, melanoma, and colon [151, 153–157]. In these malignancies, it contributes to malignancy by promoting growth, survival, motility, neo-angiogenesis, drug resistance, invasion, and metastasis [158–163]. In other cancers, Notch functions as a tumor suppressor, impeding growth or causing apoptosis in B-lineage ALL [164], myeloid malignancies [165], squamous cell carcinomas [166], neuroblastoma [167], other neural crest-derived cancers [168], and the GI stromal tumor [169]. It was recently suggested that Notch1 signaling is activated in human OS and may play a role in tumor invasion and metastasis [47, 52, 170]. One possible reason for this association is the reported link between Notch pathway activity and behavior of tumor-initiating cells or the putative cancer stem cells [171–177].

Two popular models for tumorigenesis include the stochastic model and the cancer stem cell model. The traditional stochastic model presumes that cancer arises from a single cell which has become genetically unstable and initiates tumor growth. The cancer stem cell model proposes that tumor-initiating cells share important properties with normal stem cells, including self-renewal and resistance to stress [42]. Over the past 5 years or more, the theory of cancer stem cells in osteosarcoma has gained a great deal of acceptance, with numerous publications in recent years describing phenotype, behavior, and therapeutic potential [178–194]. Logically, cells with stem cell-like properties should be superior at tumorigenesis and metastasis.

This concept was studied recently using two murine cell lines, K7M2 and K12, which were derived from the same spontaneously occurring murine osteosarcoma. K7M2 metastasizes with high frequency to the lung in mouse models, whereas K12 is much less metastatic [195].

Several groups have published that K7M2 and K12 cells produce different quantities of cytokines and that inhibition of these cytokines alters OS cell behavior in vitro [195–198]. For example, we have demonstrated that highly metastatic K7M2 cells express and produce more bone morphogenetic protein-2 (BMP-2) and VEGF than less metastatic K12 cells. Additionally, we observed that the inhibition of these factors diminished the motility and viability of K7M2 cells [197, 198]. More recently, we have demonstrated important differences between K7M2 and K12 in terms of Notch1 expression and function [50].

To evaluate the role of Notch in regulating stemness behaviors, we first compared K7M2 and K12 cells with reverse transcription polymerase chain reaction (RT-PCR). We analyzed differences in the expression of Notch1, its downstream targets, and other important genes in OS biology. We observed a significant upregulation (nearly twofold) of Notch1, Notch2, and Notch4 expression [50]. We also observed the upregulation of the Notch1 target genes Hes1 and Stat3 in highly metastatic K7M2 cells compared with less metastatic K12 cells. Notch pathway inhibition using an inhibitor of γ -secretase (GSI) in K7M2 cells reduced expression of these genes down to levels similar to K12 and also reduced migration and invasiveness of K7M2. Activation of Notch in K12 using an exogenous ligand increased invasiveness and migration, confirming the vital role of the Notch pathway in regulating these processes in this model [50].

Aldehyde dehydrogenase (ALDH) is another putative cancer stem cell factor [199–202] that has been implicated in a variety of human cancers. ALDH is a tetrameric protein that oxidizes aldehydes to carboxylic acids and thus enables cells to withstand oxidative stress. Its activity has been associated with metastasis, drug resistance, and poor prognosis [199–203]. We have shown that K7M2 cells possess greater mean ALDH activity and a higher percentage of ALDH-positive cells than the less metastatic K12 cells [204]. GSI treatment of K7M2 cells reduced the expression of ALDH and rendered the cells less tolerant of oxidative stress (Fig. 4), while treatment of K12 cells with the Notch ligand jagged 1 increased ALDH expression and rendered cells more tolerant of oxidative stress (Fig. 5), confirming that Notch pathway signaling is upstream of ALDH expression [50].

Conclusions

These studies, taken together, support the concept that Notch pathway signaling plays a key role in maintaining a stem cell-like phenotype for osteosarcoma and highlights the importance of Notch in osteosarcoma growth and metastasis. It is



Fig. 4 K7M2 cells are resistant to H_2O_2 but become sensitive after treatment with DAPT. (**a**) K7M2 cells were treated with or without the γ -secretase inhibitor DAPT (10 μ M) for 4 days and were then cultured with media containing H_2O_2 (0, 250, or 500 μ M) for 6 h. Cell death was analyzed using PI exclusion assay. (**b**) The percentage of PI+ cells was determined for each group in (**a**). *Asterisk* indicates that the difference is significant comparing DAPT-treated or non-treated samples (p < 0.05). Figure taken from [50], used with permission

interesting to note, however, that the phenotype associated with Notch pathway expression could be induced by exposure to exogenous Notch ligand, calling into question the concept that tumor stem cells represent a discrete subpopulation in osteosarcoma. Given the importance of Notch signaling in tumor blood vessels and the high level of expression of Notch ligands in the vasculature, it is possible that the phenotype we associate with stemness in osteosarcoma really reflects proximity to tumor blood vessels and, therefore, exposure to Notch ligands. As therapies are developed to target Notch in cancer patients, the role of Notch in tumor vessel formation and expansion must also be considered.



Fig. 5 Notch1 activation with jagged 1 increases K12 cells' resistance to oxidative stress. (**a**–**d**) K12 cells, which have low levels of Notch activation, were treated with soluble Jag1 to activate Notch pathway signaling. After Notch1 activation, K12 cells exhibited greater resistance to oxidative stress than untreated K12 cells. These images are presented as in Fig. 4. (e) K12 cell invasiveness increases with jagged 1 treatment. Jagged 1 treatment of K12 cells increased the in vitro invasion capacity of the cells through a semisolid matrigel matrix, suggesting that enhanced Notch expression contributes to metastatic potential in OS cells. Graphs depict the quantified mean invasion of tumor cells into matrigel over time. (f) Gene expression with Notch1 activation in less metastatic K12 cells. RT-PCR showed that the expression of Notch1, Hes1, and ALDH was upregulated in K12 cells with jagged 1 treatment, indicating a more aggressive phenotype. This figure is adapted from [50] and is used with permission

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