

Review

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Review

Do ERBB Receptors Serve as a Nexus for Oncogenic Signals in Uveal Melanoma?

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Abstract

Uveal melanomas (UMs) metastasize at a high frequency, and metastatic UMs are associated with very poor clinical outcomes. Consequently, there is considerable interest in the genetics and biochemistry of UM and how these insights may lead to novel and effective approaches for treating UM. This work reviews evidence that elevated signaling by the CYSLTR2/Gaq/Ga11 pathway drives UM. This work focuses on the large number of signaling pathways that appear to be activated by the CYSLTR2/Gaq/Ga11 pathway in UM, including pathways not thought to be effectors of canonical CYSLTR2/Gaq/Ga11 signaling. This work reviews evidence suggesting that ERBB receptor tyrosine kinases may mediate CYSLTR2/Gaq/Ga11 signaling in UM, thereby accounting for the non-canonical CYSLTR2/Gaq/Ga11 signaling observed in UM. Thus, this work describes novel targets for UM therapy.

Keywords: uveal melanoma; targeted therapy; signal transduction; Galphaq; Galpha11; PI3K/AKT/mTOR; RAS-MAPK; GPCR-EGFR crosstalk; ERBB heterodimerization

1. Introduction to Uveal Melanoma

Uveal melanoma (UM) is the most common primary intraocular malignancy in adults, accounting for approximately 4-5% of all melanomas. Its worldwide incidence is reported to range from 4 to 7 cases per million individuals annually [1–13]. UM consists of any malignant lesion derived from melanocytes of the uveal tissues (choroid, ciliary body, and iris). UM most frequently arises in choroid tissues (90%) and less frequently in the ciliary body (6%) and iris (4%) [4,11,14–18].

UM typically presents in adulthood, with a peak incidence around the age of 60 [4,14,16]. The goals of UM treatment are to prevent metastatic spread and conserve the eye and vision [4,15,19]. As noted elsewhere in this review, the primary tumor treatment options are considered relatively effective. Nonetheless, the prognosis for UM patients is often poor, as UM frequently metastasizes to the liver, presumably before or during the treatment of the primary tumor. This challenge is exacerbated by the fact that effective targeted therapies for metastatic UM have yet to be discovered [4,6,11,13,17,18,20–31]. In fact, the 2025 NCCN guidelines indicate that the preferred therapy for metastatic UM is a clinical trial [4,32].

UM is more common in Caucasian populations, particularly at higher latitudes, and among individuals with light-colored skin and irises, suggesting that solar ultraviolet light exposure contributes to the pathogenesis of UM [2,6,7,17,33–39]. Thus, it is somewhat surprising that UM most frequently arises in choroid tissues, as these tissues are relatively protected from sunlight [11,40–42]. UM does not typically exhibit the same genetic changes as cutaneous skin melanoma (CM), which is also strongly associated with sunlight exposure [3,4,6,11,30,43–47]. Nonetheless, like CM, UM is

more common among men than women [2,4,14,16]. Moreover, epidemiologic studies of CM predict that UM is more common among military service members and retirees than among civilians [48]. In this review, we propose that ERBB receptor signaling may act as a critical intermediate in CYSLTR2/G_{αq}/G_{α11}-driven oncogenic signaling in uveal melanoma.

2. Treatment of Uveal Melanoma

The typical treatment for primary UM includes radiotherapy (either plaque brachytherapy or external radiation therapy), photocoagulation, transpupillary thermotherapy, and various forms of tumor removal, such as transscleral resection, endoresection, and removal of the entire eye (enucleation). Thus, UM treatment is commonly associated with visual handicap or facial disfigurement [11,18,26,49]. The treatment of primary UM is typically effective, as relatively few patients experience recurrence at the primary tumor site. However, approximately 50% of UM patients eventually develop metastatic disease. Roughly 90% of metastatic melanomas target the liver, whereas the lung and bone are targeted to a lesser extent [3,4,9,11,13,21,26,27,30,50].

Metastatic UM appears to arise from hematogenous spread of micrometastases before or during treatment of the primary tumor; even enucleation or exenteration (removal of the eye and surrounding tissues) has little effect on the progression to metastatic disease [4,6,8,17–19,51–56]. Metastatic UM is typically fatal, and has a median overall survival of 4 to 15 months [3,4,8,9,11,18,24–27,30,56–61]. However, the median time to progression to metastatic UM is measured in years [18,20,21,29,62], as the mortality rate at 10–15 years after diagnosis of the primary tumor is approximately 40–50% [8,18,20,21,62]. The long latency of progression and mortality suggests that the latent micrometastases must acquire additional genetic changes (relative to the primary tumor) to become clinically relevant.

Circulating tumor DNA (ctDNA) is a biomarker of UM progression to metastatic disease [18,63–65]. Hence, strategies for targeting metastatic UM should be reserved for patients with ctDNA harboring alterations characteristic of UM with high metastatic potential [13,26,66,67], as the benefits of therapy are more likely to outweigh any adverse effects in these patients.

Unfortunately, as noted earlier, there is no effective standard treatment for metastatic UM [4,11,17,31,32]. Nonetheless, several advances in treatment paradigms have been made, particularly those aimed at reducing tumor cell immune evasion [4,13,17].

Immune checkpoint inhibitors (ICIs), including antibodies against PD-1 (e.g., pembrolizumab, nivolumab), PD-L1 (e.g., atezolizumab), and CTLA-4 (e.g., ipilimumab), are effective against CM and other tumors [4,68–86]. Single ICI agents exhibit limited therapeutic efficacy against metastatic UM. Combinations of ICIs have elicited surprisingly modest responses, presumably due to the relatively low mutational and neoantigen burden of these tumor cells, particularly those that harbor wild-type *MBD4* alleles [4,7,17,32,47,87–99]. Thus, future experimentation may identify those metastatic UM subtypes that exhibit more robust responses to combinations of ICIs.

Tumor-infiltrating lymphocyte (TIL) therapy has shown promising activity against metastatic UM [4,100]. However, this approach requires preparing TILs for each patient, which limits scalability and makes it relatively expensive [4,101]. Nonetheless, given that TILs appear to be more effective than ipilimumab against metastatic CM [101–103], further investigation of TIL therapy seems warranted, particularly if TIL therapy can overcome the limitation of ICI effectiveness in low-mutational burden tumors.

Uveal melanomas and CMs commonly overexpress gp100, a 100 kDa glycosylated transmembrane protein involved in melanosome maturation [104,105]. Moreover, gp100 is a target for anti-CM TILs and anti-CM vaccines [104,106–108]. Consequently, agents targeting gp100 have been extensively studied as potential anti-UM therapies.

Anti-GP100 agents include tebentafusp, an ImmTAC (immunomobilizing monoclonal T-cell receptor) targeting cancer. Tebentafusp consists of a modified T cell receptor (TCR) that recognizes a gp100 peptide in the context of a specific human leukocyte antigen (HLA-A*0201). This modified TCR is fused to a single-chain antibody against CD3, a molecule expressed by T lymphocytes that

plays a crucial role in their activation. Thus, tebentafusp binds tumor cells that present the gp100 peptide in the context of HLA-A*0201; tebentafusp then recruits and activates T lymphocytes, ultimately resulting in the formation of a “lytic immune synapse” of the target tumor cell and the cytotoxic T lymphocyte [4,104,109].

Some of the earliest data emerging from the pivotal tebentafusp phase III clinical trial (NCT03070392 [110]) reported that HLA-A*0201 metastatic UM patients treated with tebentafusp exhibited 73% overall survival at 1 year, whereas control patients treated with the investigators’ choice of therapy (pembrolizumab, dacarbazine, or ipilimumab) showed 59% overall survival at 1 year. Likewise, progression-free survival at 6 months was higher in the tebentafusp group (31%) than in the control group (19%). Adverse cytokine-mediated or skin-related events occurred infrequently (2%) and led to trial discontinuation [109]. Thus, in January 2022, tebentafusp was granted Breakthrough Therapy designation by the United States Food and Drug Administration [7,11,17,30,47,111–113].

Additional data from NCT03070392 indicated that the median overall survival of HLA-A*0201 metastatic UM patients was 21.6 months in the tebentafusp group and 16.9 months in the control group (0.68 hazard ratio [95% confidence interval of 0.54 – 0.87]). The three-year survival was 27% in the tebentafusp group and 18% in the control group. By approximately 64 months, all control patients had died, while approximately 15% of the patients in the tebentafusp group were alive [110,112]. This modest effect on survival highlights the need for additional innovation in metastatic UM therapy, particularly since only approximately 50% of Caucasians and fewer Hispanics and African-Americans are HLA-A*0201 positive [4,17,18,104,113–117].

Most CMs harbor mutations in genes (e.g., *BRAF*, *NF1*, *NRAS*) that encode proteins involved in the RAF/RAS/MAPK signaling pathway, leading to increased signaling through this pathway. These molecular insights have driven the use of BRAF and MEK inhibitors to treat *BRAF*-mutant CMs [70,78,83–86,118–122]. The most commonly mutated genes in UMs are *GNAQ*, *GNA11*, and *BAP1*. Unfortunately, these insights have not yet yielded strategies to prevent or treat metastatic UMs [6,7,11,17,18,30,32]. Thus, in the next section, we will discuss how molecular characterization of UMs has revealed potential future strategies for preventing or treating metastatic UMs.

3. CYSLTR2/ $G_{\alpha q}$ / $G_{\alpha 11}$ Signaling in UM

A. CYSLTR2, $G_{\alpha q}$, and $G_{\alpha 11}$

CYSLTR2 encodes cysteinyl-leukotriene receptor 2, a G protein-coupled receptor that signals through heterotrimeric G proteins containing $G_{\alpha q}$ or $G_{\alpha 11}$ subunits (Figure 1) [123–125]. The most common genetic alterations in UM involve mutations in the *GNAQ* or *GNA11* genes [4,6,11,13,18], resulting in constitutive canonical GPCR/ $G_{\alpha q}$ / $G_{\alpha 11}$ signaling through loss of $G_{\alpha q}$ or $G_{\alpha 11}$ GTPase activity [13]. Likewise, mutations in *CYSLTR2* that stimulate $G_{\alpha q}$ or $G_{\alpha 11}$ signaling appear to drive UM [4,6,11,13,30,126,127].

B. *PLCb4*

Phospholipase C beta 4 (*PLCb4*) cleaves the membrane lipid phosphatidylinositol 4,5 bisphosphate (PIP₂), producing inositol 1,4,5-trisphosphate (IP₃) and diacylglycerol (DAG). $G_{\alpha q}$ and $G_{\alpha 11}$ directly stimulate *PLCb4* [128]. This suggests that *PLCb4* may mediate *CYSLTR2*/ $G_{\alpha q}$ / $G_{\alpha 11}$ signaling in UM. Indeed, activating mutations in *PLCb4* are found in UM [3,4,6,11,129,130]. Activating mutations in *GNAQ*, *GNA11*, *CYSLTR2*, and *PLCb4* are mutually exclusive [4,13,30], suggesting that these genes encode components of a single signaling pathway that drives UM by activating RAS-MAPK and PKC signaling [11,131,132].

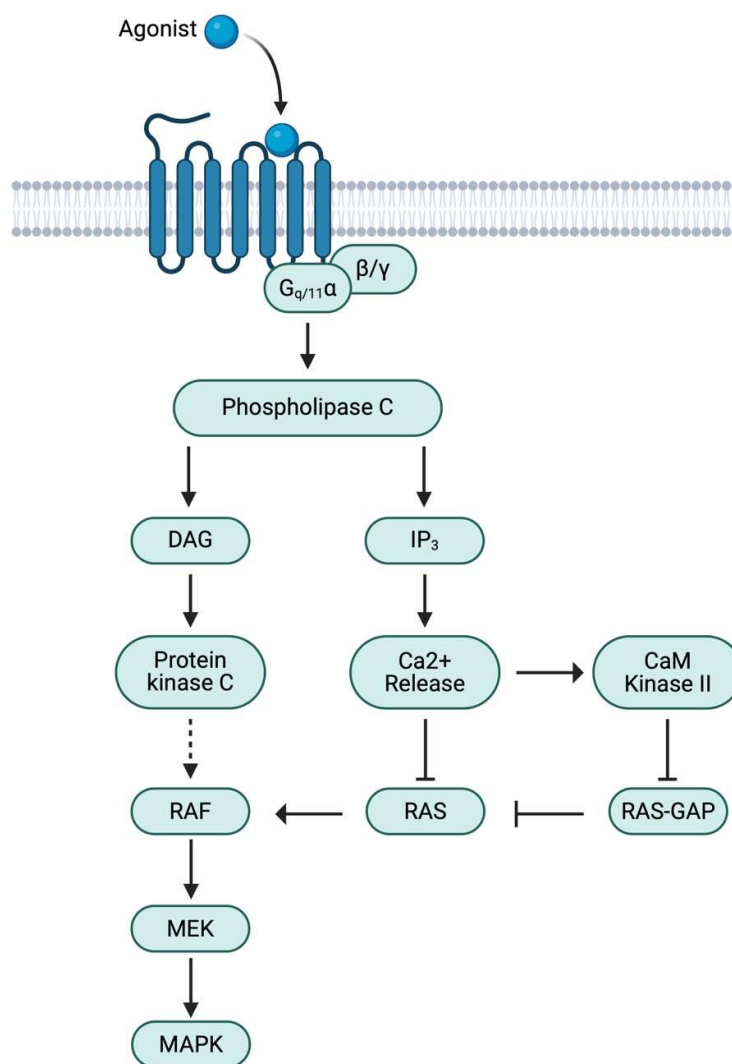


Figure 1. GPCR/Gαq/Gα11 Coupling to the RAS/MAPK Pathway.

Taken from [125].

C. RAS-MAPK

The RAS-MAPK (mitogen-activated protein kinase) signaling pathway is a major regulator of cellular proliferation. This pathway is commonly activated in UM by *CYSLTR2/Gαq/Gα11/PLCβ* signaling (Figure 1) [11,13,125,131,133,134]; one mechanism may involve the phosphorylation of Thr133 in the RAS guanine nucleotide exchange factor RasGRP3, leading to GTP loading onto all three RAS isoforms. PKC may be responsible for this phosphorylation; however, the cited work did not demonstrate that PKC directly phosphorylates RasGRP3 [13,134]. Another mechanism may involve IP₃-stimulated Ca²⁺ release, which activates CaM kinase II. CaM kinase II phosphorylates and inhibits the activity of the RAS GTPase-activating protein (RAS-GAP), resulting in decreased GTP hydrolysis by RAS and increased RAS signaling activity [124]. *MAPKAPK5*, which encodes the MAPK-activated protein kinase 5, is mutated in approximately 2% of UM cases. These mutations support the hypothesis that the RAS-MAPK pathway contributes to UM. However, frameshift mutations are most common among the predominant *MAPKAPK5* alterations in UM, suggesting that *MAPKAPK5* may negatively regulate signaling by the RAS-MAPK pathway in UM [11,66].

D. PKC

Protein kinase C (PKC) is a serine-threonine kinase, and DAG and Ca²⁺ activate many PKC isoforms. Thus, PKC signaling is elevated in UM, presumably due to elevated CYSLTR2/G_{αq}/G_{α11}/PLCβ4 signaling [30]. PKC inhibitors have exhibited only modest effects in UM [30,135–137], suggesting that additional signaling pathways are activated in these tumors. Indeed, the combination of a PKC inhibitor and a MEK inhibitor exhibited greater effects than either drug alone in a preclinical model system [30,138]. Moreover, these data suggest that the MEK pathway is stimulated independently of PKC.

E. PI3K/AKT/mTOR

Phosphatidylinositol 3-kinase (PI3K) is a lipid kinase that phosphorylates the membrane phospholipid phosphatidylinositol (4,5) biphosphate (PIP₂), yielding phosphatidylinositol (3,4,5) trisphosphate (PIP₃). PIP₃ recruits Protein Kinase B (PKB/AKT) to the membrane, enabling AKT phosphorylation (at Thr308 and Ser473) and signaling activity. PIP₃ also stimulates signaling by PDK1 (phosphoinositide-dependent kinase-1), which phosphorylates AKT at Thr308. Ser473 of AKT is phosphorylated by a multiprotein complex (mTORC2) that features mTOR (mammalian target of rapamycin). The canonical PI3K/AKT/mTOR signaling pathway ultimately regulates the biochemical activity of GSK-3β (glycogen synthase kinase 3-beta), FOXOs (forkhead box O proteins), TSC1/2 (tuberous sclerosis complex 1/2 proteins), S6K (ribosomal S6 kinase), and other effectors [11,139].

Elevated signaling by the PI3K/AKT/mTOR pathway is a characteristic of UMs that exhibit elevated CYSLTR2/G_{αq}/G_{α11} signaling [11,30,140]. For example, the GNAQ-mutant Mel270 and 92-1 uveal melanoma cell lines exhibit elevated PI3K/AKT/mTOR signaling, as evidenced by phosphorylation of AKT and GSK3. Likewise, the PI3K inhibitor LY294002 inhibits the proliferation of the Mel270 and 92-1 cell lines. However, LY294002 does not inhibit ERK1/2 phosphorylation in these cell lines, suggesting that the PI3K/AKT/mTOR and MAPK signaling pathways independently drive UM proliferation. Indeed, combinations of PI3K and MEK inhibitors are more effective in inhibiting the proliferation of UM cell lines than either class of inhibitor alone [18,133,141]. However, the combination of the MEK inhibitor trametinib and the AKT inhibitor GSK2141795 (GSK795) did not significantly improve the survival of metastatic UM patients [18,142–144]. Additional signaling events may contribute to UM proliferation. The discrepancy may also be due to tumor heterogeneity and adaptive resistance mechanisms *in vivo*.

F. Hippo/YAP

The Yes-Associated Protein (YAP) is a component of transcription factor complexes that include the TAZ (Transcriptional co-Activator with PDZ-binding motif) protein and TEAD transcription factors. These complexes regulate cellular homeostasis in part by preventing abnormal cell proliferation. YAP/TAZ/TEAD complexes are regulated by the Hippo pathway, also known as the Salvador/Warts/Hippo (SWH) pathway. This pathway was initially discovered in *D. Melanogaster* and named after one of its major components, the Hippo protein kinase. However, this pathway exhibits substantial evolutionary conservation through mammals. Additional components downstream of Hippo include the mammalian STE20-like protein kinases (MST1/2) and the large tumor suppressor kinases 1/2 (LATS1/2) [145,146].

The Hippo/YAP pathway can be regulated by a variety of intracellular and extracellular signals, including GPCR- and receptor tyrosine kinase-mediated signaling. Hippo signaling initiates the MST/LATS kinase cascade, resulting in the phosphorylation of YAP/TAZ. Phosphorylated YAP/TAZ is retained in the cytoplasm and is degraded. Conversely, low levels of Hippo signaling cause reduced YAP/TAZ phosphorylation. Unphosphorylated YAP/TAZ translocates to the nucleus, driving cell proliferation [145,146]. The overexpression of YAP/TAZ is associated with poor clinical outcomes in breast, colorectal, and liver cancers [146].

Activating mutations in GNAQ or GNA11 are associated with the dephosphorylation of YAP and TAZ in UM cells. Verteporfin, a drug that disrupts YAP/TEAD interactions, inhibits the proliferation of GNAQ/GNA11-mutant UM cells [30,147]. Focal adhesion kinase (FAK) stimulates

YAP dephosphorylation via canonical and non-canonical pathways. Likewise, genetic ablation or pharmacological inhibition of FAK reduces proliferation in a *GNAQ*-mutant UM cell line [30,148]. Moreover, due to compensatory signaling, simultaneous inhibition of the RAS-MAPK and FAK/Hippo/YAP pathways may yield more favorable clinical responses than inhibiting either pathway individually [30,149].

G. JAK/STAT

Signal Transducers and Activators of Transcription (STAT proteins) are a family of transcription factors that regulate gene expression. Like many transcription factors, they reside in the cytoplasm and nucleus. The translocation of STAT proteins into the nucleus is required for them to function as transcription factors. STAT dimerization and translocation to the nucleus are commonly induced by STAT phosphorylation by members of the Janus kinase (JAK) family of non-receptor tyrosine kinases. Cytokine receptors and receptor tyrosine kinases are typically upstream stimuli of the JAK-STAT signaling pathway. Some STAT proteins stimulate the transcription of genes that encode proteins that inhibit apoptosis or stimulate cell proliferation, including Bcl-xL, cyclin D1, and c-myc. Likewise, elevated activity of a JAK/STAT pathway drives numerous cancers [150–153], and increased signaling by STAT3 [6,11,18,27,46] and STAT5 [11] is observed in UM. Because GPCR signaling is not typically directly coupled to JAK/STAT signaling, GPCR-ERBB receptor crosstalk may be responsible for the elevated JAK-STAT signaling observed in UM.

4. Could GPCR-ERBB Receptor Crosstalk Contribute to UM Tumorigenesis?

A. Overview of GPCR-ERBB Receptor Crosstalk

Epidermal growth factor receptor (EGFR/ERBB1) is a receptor tyrosine kinase (RTK) that is closely related to three other ERBB receptor tyrosine kinases (ERBB2/HER2, ERBB3/HER3, and ERBB4/HER4). Crosstalk between GPCRs and ERBB receptors has been observed in numerous contexts and appears to occur via multiple mechanisms [128,154–159]. (a) Some GPCRs stimulate the activity of the Src non-receptor tyrosine kinase. Src directly phosphorylates EGFR tyrosine residues, thereby coupling EGFR to downstream signaling effectors [128,154–163]. (b) Some GPCRs complex with EGFR and stimulate EGFR tyrosine phosphorylation, presumably by stabilizing EGFR dimerization [154,155,164–166]. (c) A well-explored mechanism of GPCR-ERBB receptor crosstalk (Figure 2) appears to involve Src stimulation of the expression or activity of a matrix metalloproteinase (MMP) or an ADAM (a disintegrin and metalloproteinase). The metalloproteinase cleaves the transmembrane precursor form of an epidermal growth factor (EGF) family peptide hormone, releasing the mature hormone into the extracellular milieu. This enables ligand binding to ERBB receptors, and ligand-induced ERBB receptor dimerization and signaling [128,154–159,163,167–175]. (d) Stimulation of ERBB ligand maturation by MMP/ADAM activity by GPCRs may also be mediated by reactive oxygen species [170,172]. Direct evidence of CYSLTR2 and EGFR crosstalk has been observed in primary human bronchial fibroblasts, as the CYSLTR2 agonist leukotriene C₄ (LTC₄) potentiates the mitogenic effect of EGF in these cells [176]. However, the first-generation EGFR tyrosine kinase inhibitor gefitinib failed to yield a significant benefit in a small number (n = 6) of unselected patients with metastatic choroidal melanoma [13,177]. Of course, this negative result may be due to the small sample size and a lack of biomarker-based patient selection. Moreover, EGFR inhibition alone may not adequately target ERBB family receptor signaling.

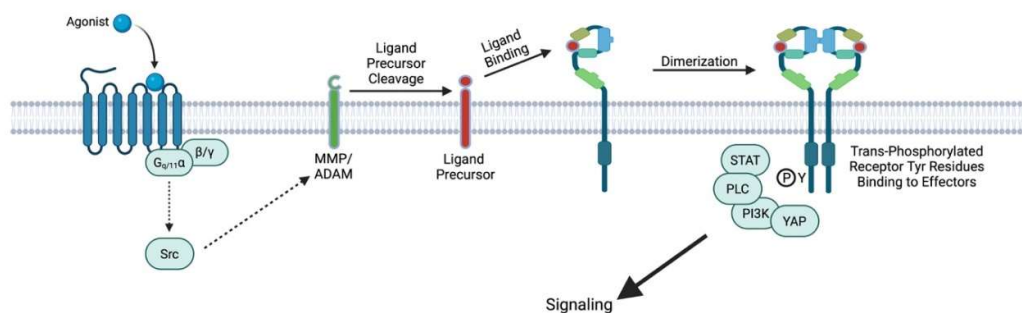


Figure 2. GPCR-EGFR Crosstalk.

Taken from [178].

B. Mechanism of Ligand-Dependent ERBB Receptor Signaling

Ligands for ERBB receptors include amphiregulin, betacellulin, EGF, epigen, epiregulin, heparin-binding EGF-like growth factor, neuregulin isoforms, and transforming growth factor alpha. As noted earlier, ERBB ligands are initially expressed as transmembrane precursor proteins that must be cleaved to enable the soluble form of the ligand to bind the extracellular region of the cognate receptor. Ligand binding stabilizes the ERBB receptor extracellular domains in a conformation that is competent for symmetrical dimerization of the ERBB receptor extracellular domain. Because a small fraction of EGFR that is present on the cell surface exists in the conformation that is competent for dimerization, overexpression of EGFR (and other ERBB RTKs) can cause ligand-independent symmetrical dimerization of the receptor extracellular domain. In both ligand-dependent and -independent signaling, this symmetrical dimerization of the ERBB extracellular domains is accompanied by asymmetrical dimerization of the ERBB intracellular domains. Consequently, within an ERBB receptor dimer, the kinase domain of one ERBB monomer phosphorylates tyrosine residues of the other ERBB monomer. Therefore, mechanistically, ERBB receptors do not undergo autophosphorylation; instead, transphosphorylation occurs within the dimer. ERBB receptors contain multiple tyrosine phosphorylation sites, each of which can bind distinct effector proteins via their SH2 or PTB domains. Thus, ERBB receptor phosphorylation stimulates numerous signaling pathways and biological responses, and differences in the sites of tyrosine phosphorylation for a given ERBB family receptor enable signaling specificity. [179–185].

C. Specificity of Ligand-Induced ERBB Receptor Signaling

This signaling specificity appears to be regulated by the juxtaposition of ERBB monomers within the dimer; the specificity of ERBB dimer conformations is likely to underlie many of the functional differences among the various ligands for a particular ERBB receptor [186–195]. Specificity also arises through heterodimerization by ERBB family receptors. This heterodimerization enables ligand-dependent signaling by ERBB2, which does not bind any EGF family member; heterodimerization also facilitates signaling by ERBB3, which possesses little tyrosine kinase activity. Hence, ligand-binding to EGFR, ERBB3, or ERBB4 may also elicit signaling by the other three ERBB receptors. Heterodimerization greatly diversifies ERBB receptor signaling, as the four ERBB receptors do not activate identical downstream signaling events. For example, EGFR and ERBB2 phosphorylation sites couple to the RAS/MAPK pathway via GRB2 and SOS [181,183,184,194]. Phosphorylated ERBB3 and ERBB4 each possess at least one PI3K binding site, whereas phosphorylated ERBB4 also possesses binding sites for YAP, STAT5a, STAT1, and PLCg [179,181,196–201].

One consequence of this specificity is that receptor homodimers and heterodimers may exhibit distinct signaling properties and may stimulate distinct biological effects. For example, ERBB4 homodimers commonly function as tumor suppressors by stimulating apoptosis or growth arrest.

In contrast, ERBB4-EGFR or ERBB4-ERBB2 heterodimers function as oncoproteins by stimulating cell proliferation and suppressing apoptosis [179,200,202–204]. The mechanism of this specificity is unclear, although context-specific sites of ERBB receptor tyrosine phosphorylation confer other forms of ERBB receptor signaling specificity [179,186–195,205–208].

D. Non-Canonical Mechanisms of ERBB4 Signaling

ERBB4 exhibits signaling mechanisms distinct from those of canonical RTK signaling. Following ligand binding to ERBB4, the transmembrane metalloprotease tumor necrosis factor alpha (TNF α) converting enzyme (TACE) cleaves the ERBB4 extracellular domain near the transmembrane domain. This releases the 120 kDa extracellular domain into the extracellular milieu, where it can function as a ligand sink [179,209–218]. Then, the gamma-secretase complex cleaves the ERBB4 cytoplasmic domain near the transmembrane domain. This releases the 80 kDa cytoplasmic region of ERBB4 (4ICD) from the plasma membrane [179,211–214,216,219–223].

The cytoplasmic region of ERBB4 contains a Bcl2 homology 3 (BH3) domain, which can bind pro- or anti-apoptotic proteins of the BAX/BAK or BCL-2 families. Homotypic 4ICD signaling triggers apoptosis by stimulating BAK oligomerization within the outer mitochondrial membrane (OMM). This may occur via 4ICD binding to BAK or through binding and sequestration of BCL-XL or other anti-apoptotic proteins [179,224,225]. BAK oligomerization triggers OMM permeability, resulting in increased cytochrome C efflux and caspase activation [179,217,223,226–228]. Signaling by ERBB4-EGFR or ERBB4-ERBB2 heterodimers suppresses 4ICD-induced apoptosis by an unknown mechanism.

The cytoplasmic region of ERBB4 also contains a nuclear localization signal [179,212,214,220,229,230] and two LXXLL motifs, which mediate interactions with nuclear (steroid) hormone receptors [179,231,232]. Homotypic 4ICD signaling regulates estrogen receptor alpha signaling and increases the sensitivity of breast cancer cells to tamoxifen [179,217,233–237]. The 4ICD apparently regulates the function of other transcriptional regulatory proteins, including YAP1 [179,199,217,223,234,235,238–240], STAT5a [199,217,229,235], ETO2 [217,221,234,235], TAB2-NCOR [216,217,234,235], and AP-2 [234,235,241].

E. Does Elevated ERBB4 Signaling Create Targets for Therapeutic Intervention in UM?

Given the diversity of ERBB receptor signaling, including non-canonical ERBB4 signaling, we postulate that crosstalk between the CYSLTR2/Gaq/G α 11 and ERBB receptors could be responsible for many of the changes in downstream signaling events implicated in UM, including changes in signaling by pro- and anti-apoptotic proteins [242–244], steroid hormone receptors [245–247], YAP [30,147–149], and STATs [6,11,18,27,46]. Nonetheless, we postulate that the CYSLTR2/Gaq/G α 11 pathway stimulates the RAS-MAPK pathway (and perhaps the PI3K/AKT/mTOR pathway, due to crosstalk with the RAS-MAPK pathway) independent of ERBB receptors. Therefore, we postulate that ERBB receptor signaling cooperates with the RAS-MAPK pathway (and perhaps the PI3K/AKT/mTOR) to drive UM cell proliferation, and that targeting ERBB receptors in combination with the RAS-MAPK pathway is likely to yield greater therapeutic effects than targeting either pathway alone.

This proposed mechanism resembles that for human skin cutaneous melanomas with wild-type *BRAF* alleles (“*BRAF*-WT melanomas”). In such tumors, *ERBB4* transcription or an *ERBB4* gain-of-function mutant allele appears to segregate with a gain-of-function *RAS* allele or a loss-of-function *NF1* allele. Thus, ERBB4 signaling appears to cooperate with the RAS-MAPK pathway to drive *BRAF*-WT melanomas [248,249]. Our lab is working to identify actionable targets within the ERBB4 signaling pathway in *ERBB4*-dependent *BRAF*-WT melanoma cell lines. For example, our preliminary observation that *ERBB2* is both sufficient and necessary for the proliferation of three *ERBB4*-dependent, *BRAF*-WT melanoma cell lines (IPC-298, MEL-JUSO, and MeWo) suggests that targeting signaling by ERBB4-ERBB2 heterodimers may be effective in some *BRAF*-WT melanomas [250].

Finally, four *ERBB4*-dependent *BRAF*-WT melanoma cell lines (IPC-298, MEL-JUSO, MeWo, and SK-MEL-2) harbor apparent driver mutations in *GNA11* or *PLCB4* [251]. These findings suggest

that these cell lines display elevated expression of mature (soluble) ERBB receptor ligands, leading to increased signaling by ERBB4 heterodimers. Moreover, because *GNA11* or *PLCB4* driver mutations are found in many UMs, UMs may also depend on ERBB receptors, and insights into targeting ERBB4-dependent *BRAF*-WT melanomas may apply to UMs. Appropriate cell culture models of UM exist for such experiments [252–254].

5. Conclusions

Uveal melanoma (UM) is the most common primary intraocular malignancy in adults, annually accounting for 4-7 cases per million individuals worldwide. The typical treatment for primary UM includes radiotherapy, photocoagulation, thermotherapy, and surgery. These primary treatment options are, in some respects, quite effective, as the median time to progression to metastatic UM is measured in years. However, metastatic UM is relatively lethal, as the mortality rate at 10-15 years after diagnosis of the primary tumor is approximately 40-50%. This mortality is in part due to the absence of an effective standard treatment for metastatic melanoma.

Thus, there has been much interest in the molecular characterization of UM. As noted elsewhere, mutations in the *CYSLTR2*/ G_{aq}/G_{a11} /*PLCb4* GPCR signaling pathway appear to drive a significant percentage of UM. Hence, canonical effectors of this pathway have been implicated in UM, including PKC, the RAS/MAPK pathway, the PI3K/AKT/mTOR pathway, the Hippo/YAP pathway, and the JAK/STAT pathway. However, therapies targeting this extensive set of pathways are unlikely to be practical in UM treatment, particularly for preventing progression to metastatic UM (mUM).

We propose that ERBB receptor signaling lies upstream of many of these pathways and that targeting ERBB receptor signaling may be effective against UM by simultaneously blocking these pathways. This hypothesis is supported by the fact that the G_{aq}/G_{a11} signaling pathway can stimulate ERBB receptor signaling. Several mechanisms have been proposed for this crosstalk. However, one of the most common mechanisms involves Src-dependent stimulation of MMPs/ADAMs, which cleave the precursor, transmembrane forms of EGF family peptide hormones. The release of soluble, mature forms of EGF family hormones enables them to bind to ERBB receptors and stimulate receptor signaling. Receptor signaling may feature both ERBB receptor homodimerization and heterodimerization. Signaling by receptor heterodimers may be particularly important, as they enable more complex downstream signaling than receptor homodimers. Experimental data support the proposed G_{aq}/G_{a11} -ERBB crosstalk in UM. In human bronchial fibroblasts, the *CYSLTR2* agonist LTC4 potentiates the mitogenic effect of EGF. Four ERBB4-dependent *BRAF*-WT melanoma cell lines possess apparent driver mutations in *GNA11* or *PLCB4*, suggesting that the elevated ERBB4 signaling in these *BRAF*-WT melanoma cell lines is due to increased maturation of soluble EGF family hormones. Human UM cell lines that possess driver mutations in *GNA11* or *GNAQ* could be used to test the hypothesis that these cell lines are ERBB-dependent.

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