Background

The Salvador–Warts–Hippo pathway (known as Hippo pathway) was first discovered to be involved in controlling tissue growth in Drosophila melanogaster in 2002, and it has recently emerged as a critical tumor-suppressor network (1). The Hippo pathway is a highly evolutionarily conserved pathway that controls multiple functions that are crucial to several carcinogenesis processes such as proliferation, apoptosis, and stem cell maintenance.

The core of the mammalian Hippo pathway consists of a protein complex that includes kinases MST1 and MST2 (also known as STK4 and STK3), large tumor suppressors 1 and 2 (LATS1 and LATS2), and adaptor proteins SAV1 (Salvador homolog 1) and MOB kinase activator 1A and 1B (MOB1A and MOB1B). MST1 and MST2 facilitate LATS1 and LATS2 phosphorylation, which in turn facilitates LATS-dependent phosphorylation of the homologous oncoproteins YAP (Yes-associated protein; encoded by YAP1) and TAZ (PDZ-binding motif, also known as WWTR1). When the Hippo pathway is active, its main effectors, YAP and TAZ, are phosphorylated by the core Hippo complex and retained in the cytoplasm where their activity is inactive or suppressed, YAP and TAZ translocate to the nucleus in response to various upstream inputs. These upstream inputs can be divided into those controlling the pathway by regulating YAP/TAZ in the cytoplasm by physical interaction, and those that activate the core kinase complex MST/LATS leading to YAP/TAZ phosphorylation (10).

Hippo controls cell proliferation and survival mainly by sensing the physical state of cells within a tissue through several mechanisms. Unlike other pathways, Hippo does not have dedicated extracellular ligand–receptor complexes. Instead, the upstream signaling of Hippo involves many mechanisms and other signaling pathways. These upstream inputs can be divided into those controlling the pathway by retaining YAP/TAZ in the cytoplasm by physical interaction, and those that activate the core kinase complex MST/LATS leading to YAP/TAZ phosphorylation. Some of the most relevant upstream regulators of Hippo include the following: (i) FERM domain–containing proteins NF2 and KIBRA and WILLIN (5), (ii) polarization and adhesion proteins, including those controlling basolateral polarity like the CRUMBS complex (7), and planar cell polarity like the FAT and Dachsous family of cadherins (8). Cell adhesion proteins, such as α-catenin and E-cadherin (9), (iii) extracellular factors, G protein–coupled receptors (GPCR) and tyrosine kinase inhibitor (TKI) receptors, and (iv) changes in mechanical forces regulated by Rho and F–actin polymerization that can also regulate YAP/TAZ nuclear localization (10).

Other proteins can also directly affect TAZ and YAP. These include WBP2, MASK proteins, HIPK2, and TAZ. Moreover, other proteins can interact with the upstream kinase complex. Of particular interest is Rassf1, a tumor-suppressor frequently methylated in several tumors, which can act as a Hippo regulator. Rassf1a can bind MST regulating LATS1/2 phosphorylation and promoting proapoptotic signals through p73.

Abstract

The Salvador–Warts–Hippo pathway controls cell fate and tissue growth. The main function of the Hippo pathway is to prevent YAP and TAZ translocation to the nucleus where they induce the transcription of genes involved in cell proliferation, survival, and stem cell maintenance. Hippo signaling is, thus, a complex tumor suppressor, and its deregulation is a key feature in many cancers. Recent mounting evidence suggests that the overexpression of Hippo components can be useful prognostic biomarkers. Moreover, Hippo signaling appears to be intimately linked to some of the most important signaling pathways involved in cancer development and progression. A better understanding of the Hippo pathway is thus essential to untangle tumor biology and to develop novel anticancer therapies. Here, we comment on the progress made in understanding Hippo signaling and its connections, and also on how new drugs modulating this pathway, such as Verteporfin and C19, are highly promising cancer therapeutics.
For more detailed information on Hippo upstream regulators and downstream effectors, we refer the reader to some of the excellent reviews previously published (8, 11).

**Clinical–Translational Advances**

Disruptions in the correct function of this pathway have been found to take part in several tumorigenesis mechanisms. However, in human cancer, mutations in the Hippo components are infrequent (12). The most established mutation is located in the tumor-suppressor NF2, an upstream Hippo regulator, causing the autosomal dominant syndrome type 2 neurofibromatosis that entails, among others the development of meningiomas and schwannomas (13). In addition, mutations and deletions in LATS2 can be frequently found in malignant mesothelioma (14). In mice, mutations in Hippo components lead to developmental deficiencies within the intestinal epithelium, liver, or skin keratinocytes (15–17). Although YAP/TAZ–activating mutations have not been described, high YAP/TAZ nuclear levels are present in several cancer types (18). High YAP/TAZ nuclear levels favor cell proliferation and survival as well as the acquisition of a cancer-promoting phenotype. Stem cell maintenance is intimately linked to Hippo signaling in tumor cells. In breast tumors, in vitro studies show how TAZ acts as a stem cell promoter, providing stem cells with self-renewal and tumor-initiating capacity. This property is acquired in part by forming a complex with the polarity complex...
SCRIBBLE that leads to induction of the epithelium–mesenchymal transition (EMT; ref. 6). In neuroblastoma cell lines, studies have shown that TAZ upregulates connective tissue growth factor (CTGF) known to induce EMT (19). Moreover, in oral cancer cells, TAZ has also been found to be involved in TGFβ1-induced EMT (20).

Cancer stem cells are believed to be resistant to chemotherapeutic agents. Recently, several works have linked Hippo effectors YAP and TAZ to chemoresistance in various cancer types. In breast cancer cell lines, the overexpression of TAZ correlated with taxol resistance. In this work, oncogenes Cyr61 and CTGF were identified as TAZ transcriptional targets. By knocking down both Cyr61 and CTGF through shRNAs, TAZ-induced resistance to taxol was reversed (21). Moreover, in metastatic breast cancer cells compared with non-metastatic cells, TAZ was identified as a mediator of this metastatic ability, conferring chemoresistance and migratory activity (22).

In colon cancer, chemoresistance to 5-fluorouracil (5-Fu) has been linked to a quiescent status favored by the selection of colon cancer stem cells resistant to cytotoxic drugs. In colorectal cancer cell lines resistant to 5-Fu, it has been shown that in 5-Fu-free conditions, YAP silencing and subsequent reduction of YAP nuclear activity lead to induced cellular quiescence (23).

YAP/TAZ activity has also been implicated in chemoresistance in other tumor types. In hepatocarcinoma, the expression of SIRT1, a protein involved in tumorigenesis, metastasis, and cell survival is upregulated, which correlates with CTGF mRNA levels. SIRT1 deacetylates YAP2, which in turn increases the YAP2/TEAD complex and inhibits cell growth in hepatocellular carcinoma cells (24). In non–small lung cancer, it has been suggested that TAZ expression is an intrinsic mechanism of T790M-induced resistance to EGFR–TKIs (25).

As TAZ/YAP mutations are uncommon other mechanisms are likely responsible for Hippo’s relevance in cancer. Increasing evidence is suggesting that YAP/TAZ regulation derives from a complex network of interactions with other critical pathways that modulate YAP/TAZ activity such as TGFβ, Notch, Wnt, EGFR, and angiogenesis:

- TGFβ signaling in cancer is complex, suppressing oncogenic events at an early stage and promoting an aggressive metastatic phenotype at later cancer stages. YAP and TAZ possess domains that facilitate the interaction with TGFβ-controlled SMADs (26).
- In response to TGFβ stimulation, TAZ binds SMADs 2, 3, and 4, thus regulating and promoting SMAD-mediated transcription. Nonetheless, YAP is also able to bind SMAD7, increasing the repressing role of SMAD7 over TGFβ signaling (27).
- Notch signaling, essential in stem-cell renewal and differentiation, is also partially controlled by Hippo. The expression of the Notch ligand Jagged-1 is upregulated by nuclear YAP in colorectal and hepatocarcinoma tissue samples and correlates with the patient survival (28).
- Wnt signaling is essential in embryonic development, and aberrant Wnt/β-catenin signaling contributes to cancer development and progression. Wnt activity is in part regulated by the Hippo pathway. Phosphorylated YAP/TAZ interacts with DVL in the cytoplasm, thus inhibiting nuclear β-catenin translocation and Wnt target gene expression (29). In addition, TAZ and YAP can directly bind to β-catenin, leading to the cytoplasmic sequestration of the Hippo effectors suppressing their nuclear activity. In colon cancer cell lines with intact Wnt/β-catenin signaling, down-regulation of Hippo signaling results in increased β-catenin activity (30). Interestingly, in colon cancer cell lines harboring mutations within Wnt signaling components, the Wnt pathway has been found to promote YAP expression through a β-catenin–TCF4 complex that directly binds a DNA enhancer element located in the first intron of the YAP gene (31).

The EGFR pathway has a wide map of molecular interactions that includes the Hippo pathway. The EGFR downstream branch Ras–MAPK regulates YAP and TAZ promoting their nuclear translocation acting upstream or at LATS level (32). Other Hippo upstream factors like Rassfl1a, intimately linked to EGFR signaling, can inhibit LATS activity by disrupting the apoptosis inhibitory complex formed by Raf and MIST2 allowing YAP/TAZ nuclear translocation and association with the proapoptotic protein p73. Rassfl1a also regulates the expression of the EGFR ligand amphiregulin (AREG) through Hippo activation (33). In colon cancer, AREG expression is associated with the prognosis of KRAS wild-type patients treated with anti-EGFR therapies. In KRAS mutant patients, Rassfl1a activity through Hippo signaling might also be of critical importance as mutant KRAS binds directly to Rassfl1 to activate Hippo signaling and promotes apoptosis through p53 (34). In esophageal cancer, YAP1 has been shown to induce EGFR overexpression leading to chemotherapy resistance (35). Moreover, in pancreatic KRAS-mutant mice models, YAP was found to be an essential oncogenic KRAS effector (36). Hippo also regulates the other EGFR downstream branch PI3K–Akt–mTOR (37).

Hippo signaling is also involved in one of the key processes that favor tumor progression, angiogenesis. It is believed that intra-tumor hypoxia increases the percentage of breast cancer stem cells. This molecular mechanism is not well understood but could be explained, in part, by the fact that hypoxic conditions regulate TAZ and YAP in cancer cells (38). The hypoxia hallmark HIF1α binds directly to WWTR1 gene (that codifies for TAZ), activating the TAZ mRNA transcription that helps maintain a stem cell phenotype (39). In bone metastasis samples from breast cancer, HIF1α has been described to colocalize with TAZ in the nucleus. Under hypoxic conditions, nuclear HIF1α and TAZ favor tumor genesis by leading to increased transactivation by HIF1α DNA binding (40). This increased rate of gene expression likely affects several target genes. Angiopoetin-2, an important angiogenesis regulator, has recently been found to be one of the YAP transcriptional targets in vitro and in vivo (41).

- Many other pathways interact and regulate Hippo signaling. Of interest is the GPCR pathway that can either stimulate or inhibit Hippo tumor-suppression activity depending on the ligand (42).

The Hippo pathway is the common link of multiple critical pathways involved in the development and progression of cancer. This fact makes it an exciting and important pathway for the discovery of new biomarkers like the expression of YAP and/or TAZ. Most studies correlate nuclear or nuclear and cytoplasmic YAP/TAZ overexpression with a worse outcome (43–46). In addition, a gene-expression signature reflecting the activation of YAP1 has been associated with poor prognosis and cetuximab resistance in KRAS wild-type patients (47). On the other hand, YAP/TAZ cytoplasmic expression is correlated with a more favorable prognosis (48). The expression of other Hippo components such as LATS has also been associated with a better outcome. In non–small cell cancer patients, LATS overexpression and the consequent negative regulation of YAP correlate with longer overall survival (OS; ref. 49).

Besides YAP/TAZ expression, pharmacogenomic studies have evaluated several genetic variants within Hippo components as
potential biomarkers. In localized prostate cancer, a polymorphism that affects STK3 (MST2) expression has been reported to correlate with biochemical recurrence (50). In patients with cutaneous melanoma, SNPs in YAP and TEAD4 have been associated with the survival of these patients (51). In colorectal cancer polymorphisms in the Hippo pathway also have been found to affect the recurrence rate in high-risk stage II and stage III colon cancer treated with 5-Fu–based chemotherapy (52). Moreover, some of these polymorphisms have also been found to influence progression-free survival and OS in metastatic colorectal cancer patients treated with cetuximab (53).

The clinical significance of Hippo signaling makes it a highly attractive targetable pathway. Currently, there are no approved cancer therapies targeting the Hippo pathway, but several molecules and pathway modulators are in early stages of clinical development (Table 1; Fig. 1). The Hippo pathway plays an essential role in tissue growth, regeneration, and repair, raising the concern of potential side effects with inhibitors of Hippo signaling.

The goal of targeting Hippo for cancer treatment is to increase its function as a tumor suppressor. For example, C19, a small molecule, can induce phosphorylation of MST/LATS, leading to increased TAZ cytoplasmic levels and TAZ degradation by the GSK3β–associated destruction complex involved in Wnt signaling (54).

The broad-spectrum TKI dasatinib inhibits YES1, which is required for the YAP–β-catenin complex and might affect Hippo signaling in β-catenin–dependent tumors. Dasatinib is currently being investigated in colorectal cancer with promising results (55).

Conclusions

The importance of Hippo signaling deregulation in several mechanisms involved in cancer development, progression, and resistance to cancer treatment has underlined the critical role of the Hippo pathway as a tumor suppressor. Increasing evidence demonstrates that Hippo activity affects the patients’ prognosis.
As a result, new therapeutics targeting Hippo are currently under development and, although in initial stages, studies suggest that some new and old molecules and drugs can modulate Hippo signaling and reduce cancer progression. The Hippo pathway is, however, involved in multiple physiologic processes maintaining tissue homeostasis, thus, potential side effects should be closely monitored.

Overall, the Hippo pathway is the newest and probably the most complex tumor suppressor. Better understanding Hippo signaling and modulation will surely lead to new therapeutic approaches against cancer.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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References

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Hippo as a Tumor Suppressor

Molecular Pathways: Hippo Signaling, a Critical Tumor Suppressor

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