

# Profile of Michael N. Hall, 2017 Albert Lasker Basic Medical Research Awardee: Target of rapamycin, cell growth, and translational control

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Michael N. Hall (Fig. 1) is the winner of the 2017 Lasker Award “for discoveries concerning the nutrient-activated TOR proteins and their central role in the metabolic control of cell growth.” His seminal and paradigm-shifting discoveries were attained using the yeast *Saccharomyces cerevisiae*. More recently, he made a number of breakthrough discoveries in mammalian systems wherein he showed that the target of rapamycin (TOR) plays a major role in regulating whole-body metabolism in multicellular organisms.

The TOR story began more than 50 years ago, when an expedition was sent by Ayerst Research Laboratories (now Pfizer, located 6 miles from my house) to isolate

novel compounds from soil microorganisms. Their quest took them to Easter Island, and ultimately resulted in the isolation of *Streptomyces hygroscopicus*. In 1975, it was reported that this bacterium produces a compound with antifungal activity (1). The compound rapamycin was named after the indigenous name of the island, Rapa Nui. In the same year, an unrelated important finding was reported by several research groups, the discovery that eukaryotic messenger RNAs (mRNAs) contain the structure m<sup>7</sup>GpppN (where N is any nucleotide) at their 5′ termini. The structure was termed “cap” (e.g., refs. 2 and 3). Hall was the first to mechanistically link these two discoveries, inferring that TOR controlled growth by effecting the initiation of translation (discussed below).

Over 25 years ago, Hall screened for yeast cells that become resistant to rapamycin. This monumental experiment led to the discovery of TOR, and transformed our understanding of cell growth control. TOR, which is a large, atypical serine/threonine kinase, is an evolutionarily conserved key regulator of eukaryotic cell growth. To reach this conclusion, Hall provided the first evidence that akin to stimulating cell division (i.e., increase in cell number by cyclin-dependent kinase), nutrients also stimulate cell growth (i.e., increase in cell mass), and this is chiefly achieved via TOR. He recently reflected on his journey leading to these pivotal discoveries (4). Briefly, Hall discovered two TOR genes in yeast (5) that, when mutated, conferred resistance to rapamycin. Hall and co-workers (6) went on to clone the yeast TOR1 and TOR2 genes, and deciphered their functions through painstaking and scrupulous work that led to the discovery and characterization of two multisubunit complexes, TORC1 and TORC2 (7). A single gene encoding the mammalian ortholog, which is referred to as mammalian/mechanistic TOR (mTOR) was cloned a year after the cloning of the yeast genes by several groups (8–11). Yeast and mammalian TOR complexes contain multiple subunits, and are strikingly similar in subunit composition, demonstrating their evolutionarily conserved role in regulating cell growth. For instance, TORC1 is sensitive to rapamycin and contains the core subunits of TOR, LST8, and raptor (Lst8 and Kog1 in yeast, respectively), while TORC2 is resistant to acute rapamycin treatment and contains LST8, rictor, and mSin1 (AVO3 and AVO1 in yeast, respectively), in addition to TOR (7, 12–14).

Notably, there was a long lag between TOR’s discovery and cloning, and establishment that TOR is indeed a protein kinase. Even as late as 1995, in a review by Hunter (15) on the lipid/phosphatidylinositol 3-kinase-related kinase family, it was rightfully questioned whether TOR is, in fact, a protein kinase, despite having some of the conserved protein kinase catalytic motifs. Several papers suggested that TOR might also be a



**Fig. 1. Michael N. Hall, winner of the 2017 Albert Lasker Basic Medical Research Award, pictured in 2015 for the Gairdner National Program Lecture in Montreal. Image courtesy of University of Basel/Gairdner Foundation.**

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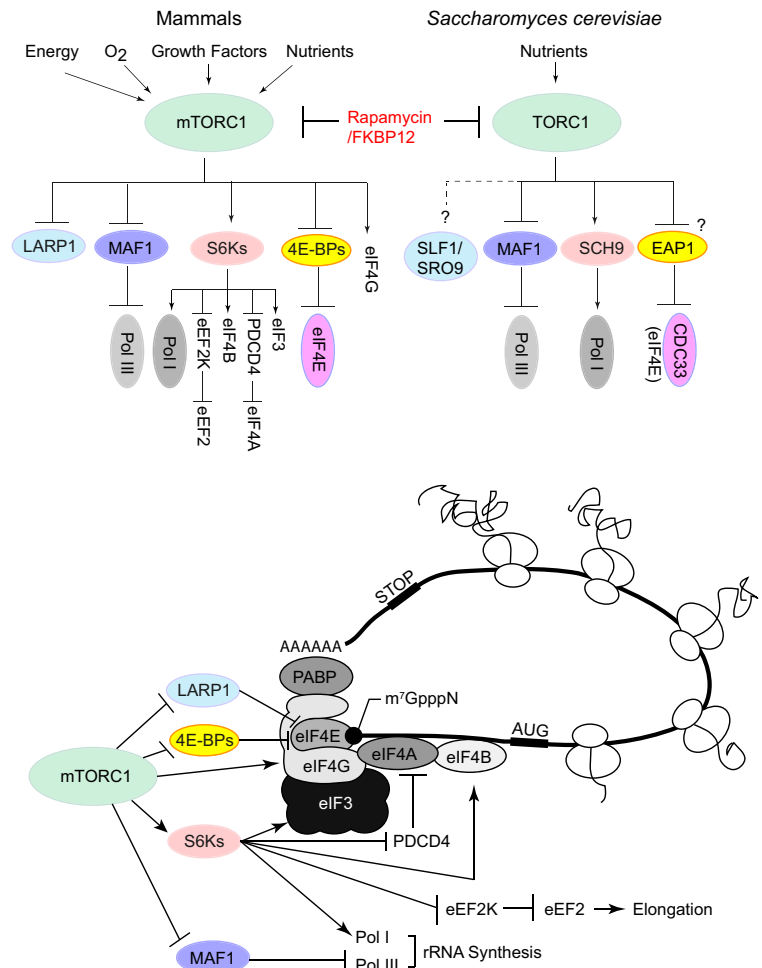
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lipid kinase because of its similarity to the authentic phosphatidylinositide (PI) kinases. It was not until biochemical work in 1997/1998 that the first compelling evidence emerged that mTOR is a protein kinase that can phosphorylate two of its major targets 4E-BP1 and S6 kinase (S6K) (16–18) (discussed below).

Although the regulation of TORC1 by nutrients is remarkably complex in mammalian cells, strikingly, many of the critical regulators are conserved from yeast to humans (19, 20). In the last two decades, Hall and others contributed seminal discoveries pertinent to the role of TOR in cell homeostasis and pathological conditions across all eukaryotic kingdoms. TOR plays a pivotal role in aging, and it is frequently dysregulated in many human disorders, including cancer, diabetes, and autoimmune diseases. In the mammalian brain, TOR complexes are critical for synaptic plasticity and memory formation, and their importance is underscored by a large number of neurological disorders in which TOR activity is perturbed (21).

It was established that mTORC1 is activated by extracellular stimuli, including growth factors and hormones, via the PI3K-AKT pathway (22–24), which is one of the most frequently hyperactivated pathways in cancer. Akt acts on tuberous sclerosis complex, for which there is no counterpart in budding yeast, upstream of Rheb and mTORC1. The activity of mTORC2 is also controlled by insulin, growth factors, and serum, and it phosphorylates AKT, thereby increasing its activity (25). These findings positioned mTOR as a prime target for the development of anticancer drugs. Indeed, rapamycin and its analogs (rapalogs) exhibit an optimal therapeutic window and are already in clinical use for a variety of cancers, including breast and kidney cancers. In addition, new drugs that directly target the kinase site of mTOR and thus inhibit both TORC1 and TORC2 (second-generation mTOR inhibitors), as well as those where targeting of the kinase site and allosteric inhibition are combined (third-generation mTOR inhibitors) (26), have recently been developed. Many of these drugs are currently being tested in a large number of clinical trials.

The identification of TOR's downstream effectors represented a turning point in our understanding of the molecular basis of TOR's function in the cell. I have been fortunate to collaborate with Hall throughout the years. Before our collaboration, regulation of cell growth and translation were studied as two separate processes. However, Hall first showed that rapamycin inhibits protein synthesis in yeast, and our seemingly independent lines of research then started to converge to ultimately position TOR as a major regulator of mRNA translation. Key to the understanding of the mechanism by which TOR regulate protein synthesis was the discovery of the 4E-binding protein (4E-BP) (27, 28). Cap-dependent mRNA translation is mediated by the eukaryotic initiation factor 4F (eIF4F) complex that binds to the mRNA 5'-cap structure to facilitate the recruitment of the ribosome to the mRNA. The eIF4F complex consists of the cap-binding subunit eIF4E, the RNA helicase eIF4A, and the scaffolding protein eIF4G (29). It is thought that eIF4A unwinds the secondary



**Fig. 2. Regulators of mRNA translation downstream of TORC1/mTORC1.** Rapamycin in a complex with the immunophilin FKBP12 (12-kDa FK506-binding protein) inhibits TORC1/mTORC1 activity. Many targets of *S. cerevisiae* TORC1 and mTORC1 are orthologous translation factors. In mammals, in addition to 4E-BPs, many other components of the translation machinery are regulated by mTORC1 (details are provided in ref. 34). For example, an inhibitor of eIF4A, PDCD4, is phosphorylated by S6 kinase (S6K; an mTORC1 target), which leads to its ubiquitination and degradation by the proteasome. In addition, the synthesis of all of the components of the ribosome, including rRNAs (via regulation of RNA polymerases and phosphorylation of transcription factors) and ribosomal proteins [via phosphorylation of LA-related protein 1 (LARP1)], is controlled by mTOR (35, 36). LARP1 in mammals contains the La-motif, an RNA-binding domain found in all eukaryotes. It controls translation of mRNAs containing a terminal oligopyrimidine sequence at their 5' termini (36). SLF1 (SMC5–SMC6 complex localization factor 1) and SRO9 (suppressor of RHO3 protein 9) are paralogous RNA-binding proteins that contain the highly conserved La-motif and control translation. MAF1 is a repressor of RNA polymerase III. S6Ks (ribosomal protein S6K1 and S6K2) are mammalian AGC (named after protein kinase A, G, and C) family protein kinases, which phosphorylate, in addition to S6, several initiation factors (eIF3 and eIF4B), and eukaryotic elongation factor 2 kinase (eEF2K) (35). SCH9 in *S. cerevisiae* is the functional ortholog of mammalian S6K. The 4E-BPs and EAP1 are described in the main text. CDC33 is the *S. cerevisiae* eIF4E. The sizes of the translation factors are not to scale. Question marks indicate that further work is required to support the data.

structure present in the 5' UTR of the mRNA to promote the binding of the ribosome and scanning of the 5' UTR (29). The 4E-BPs exist in all eukaryotes, ranging from yeast to human (with the exception being *Caenorhabditis elegans*). In mammals, the 4E-BPs constitute a family of small-molecular-weight proteins that bind to eIF4E and



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