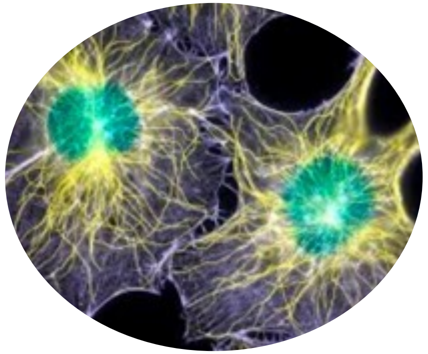


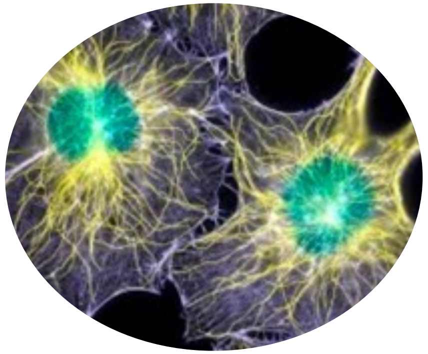
Fisiologia Celular e Molecular

Mestrado em Biologia Molecular e Genética

2º Semestre

6 ECTS

Aula T3 – 23 Fev 2023



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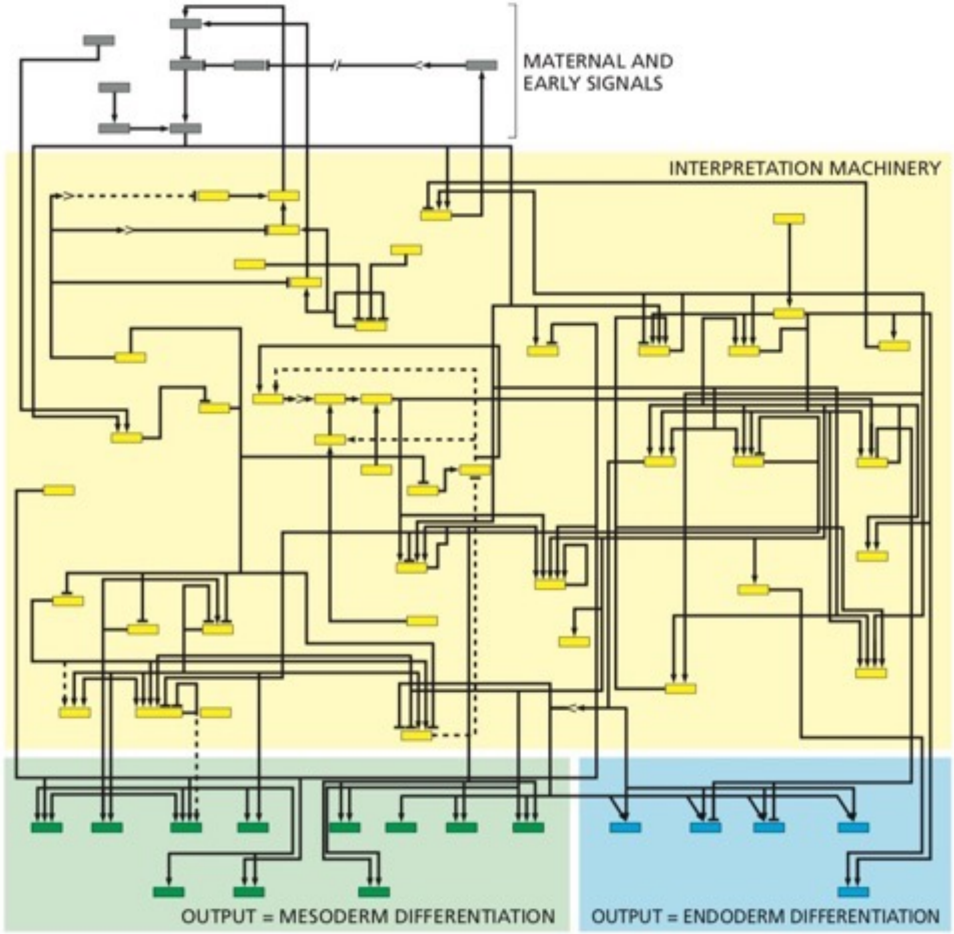
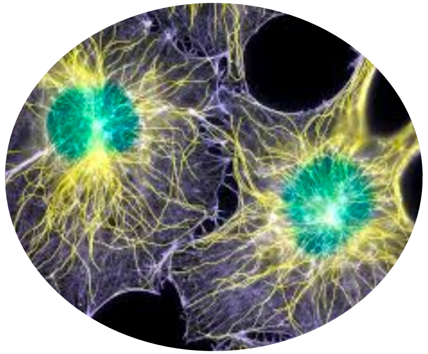


Figure 7–42 The exceedingly complex gene circuit that specifies a portion of the developing sea urchin embryo. Each *colored small box* represents a different gene. Those in *yellow* code for transcription regulators and those in *green* and *blue* code for proteins that give cells of the mesoderm and endoderm, respectively, their specialized characteristics. Genes depicted in *gray* are largely active in the mother and provide the egg with cues needed for proper development. As in Figure 7–40, arrows depict instances in which a transcription regulator activates the transcription of another gene. Lines ending in bars indicate examples of gene repression. (From I.S. Peter and E.H. Davidson, *Nature* 474:635–639, 2011. With permission from Macmillan Publishers Ltd.)



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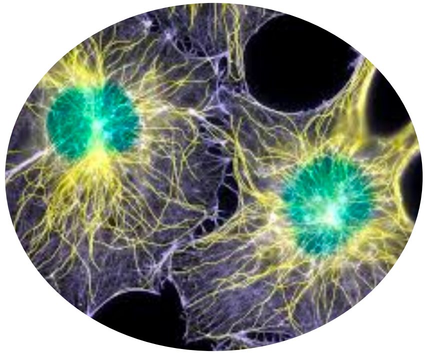
The enigma of environmental pH sensing in plants

Huei-Hsuan Tsai[1] and Wolfgang Schmidt[1,2,3] ✉

Environmental pH is a critical parameter for innumerable chemical reactions, myriad biological processes and all forms of life. The mechanisms that underlie the perception of external pH (pH_e) have been elucidated in detail for bacteria, fungi and mammalian cells; however, little information is available on whether and, if so, how pH_e is perceived by plants. This is particularly surprising since hydrogen ion activity of the substrate is of paramount significance for plants, governing the availability of mineral nutrients, the structure of the soil microbiome and the composition of natural plant communities. Rapid changes in soil pH require constant readjustment of nutrient acquisition strategies, which is associated with dynamic alterations in gene expression. Referring to observations made in diverse experimental set-ups that unambiguously show that pH_e per se affects gene expression, we hypothesize that sensing of pH_e in plants is mandatory to prioritize responses to various simultaneously received environmental cues.



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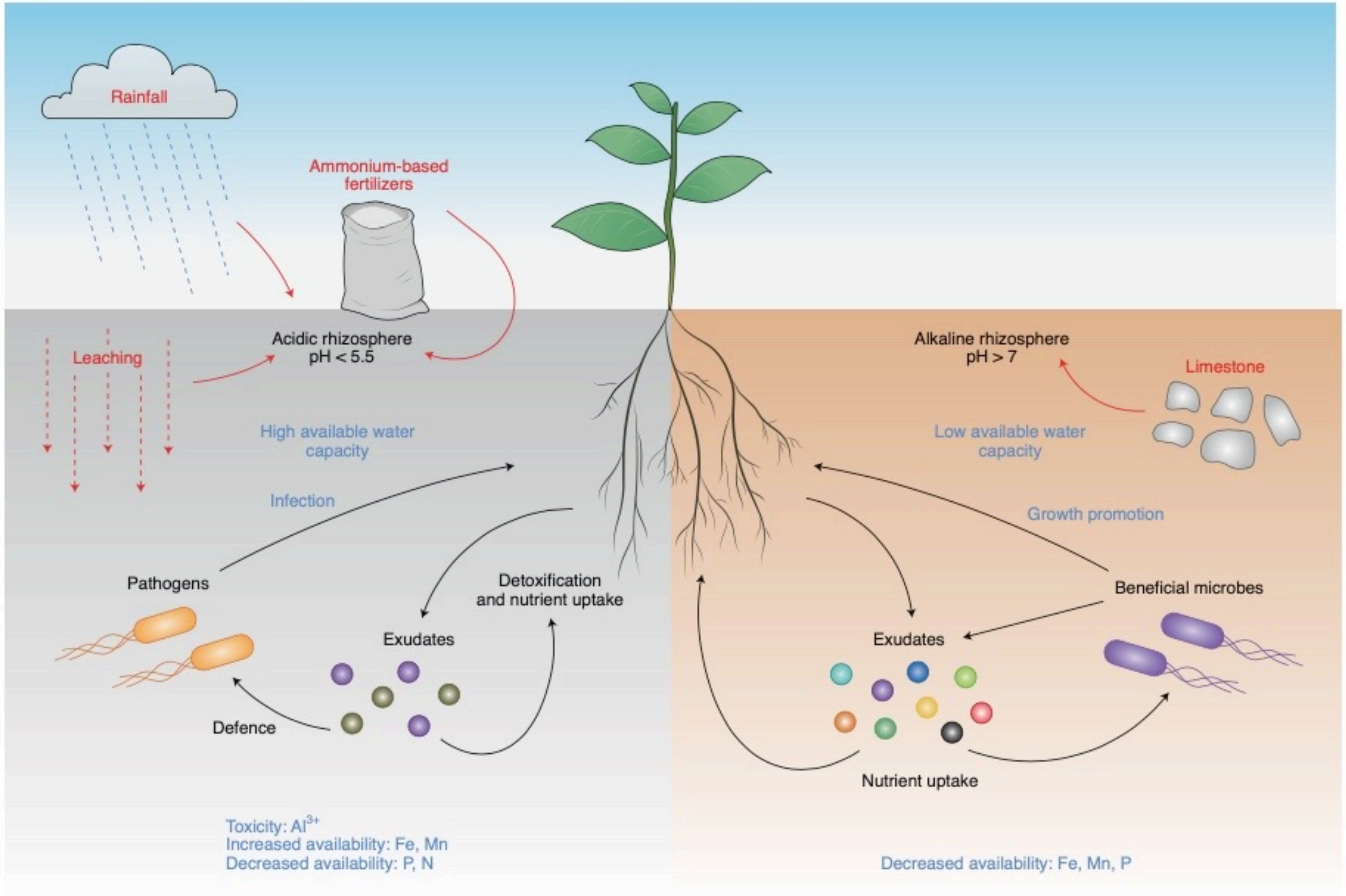
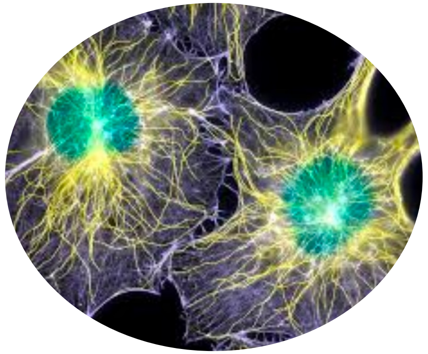


Fig. 1 | Factors that determine soil pH and effects of soil pH on plants. Soil pH-determining factors are indicated in red text, while effects of soil pH on plants are denoted in blue text. The main factors that cause soil acidity are leaching of alkaline elements by excessive rainfall and ammonium-based fertilizers. Major limitations of plant growth in acid soils are caused by pathogen infection, aluminium (Al^{3+}) toxicity, potentially toxic levels of Mn and Fe and decreased availability of P and N. Alkaline soils are mostly caused by limestone sediments and affect plant growth by low available water capacity and decreased availability of Fe, Mn and P. Changes in soil pH are accompanied by shifts in microbiome structure; beneficial soil microbes prefer neutral or mildly alkaline pH conditions, while lower soil pH alters the microbiome population to a more pathogen-dominated population. To cope with constraints associated with different soil pH environments, plants alter the compositions of root exudates to improve, tune or prioritize detoxification processes, and adapt nutrient-acquisition strategies and pathogen-defence responses.

External pH sensing

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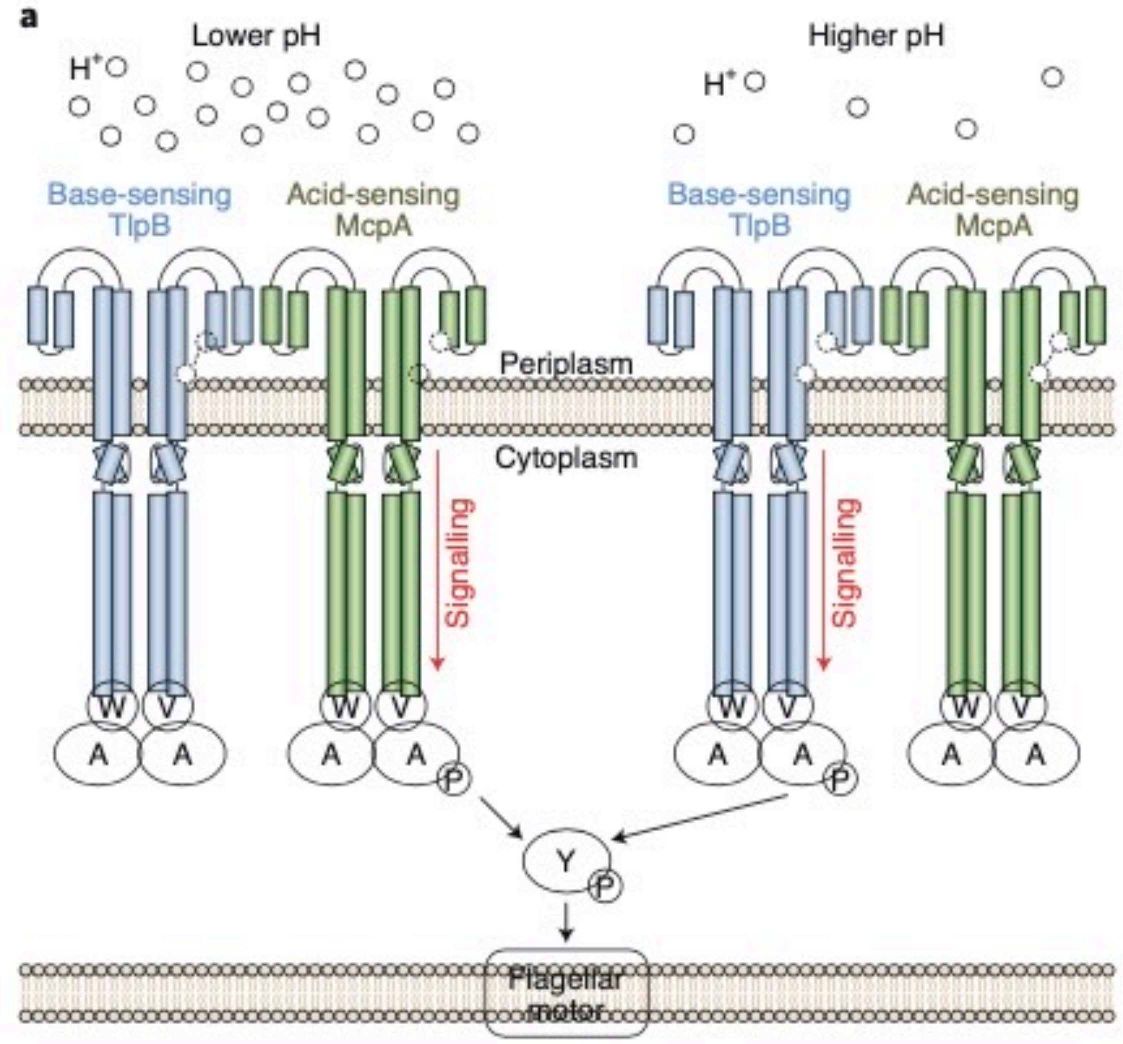
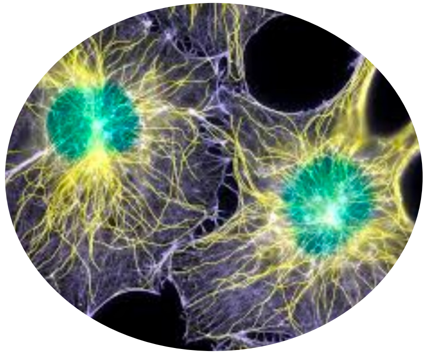


Bacillus subtilis



External pH sensing in bacteria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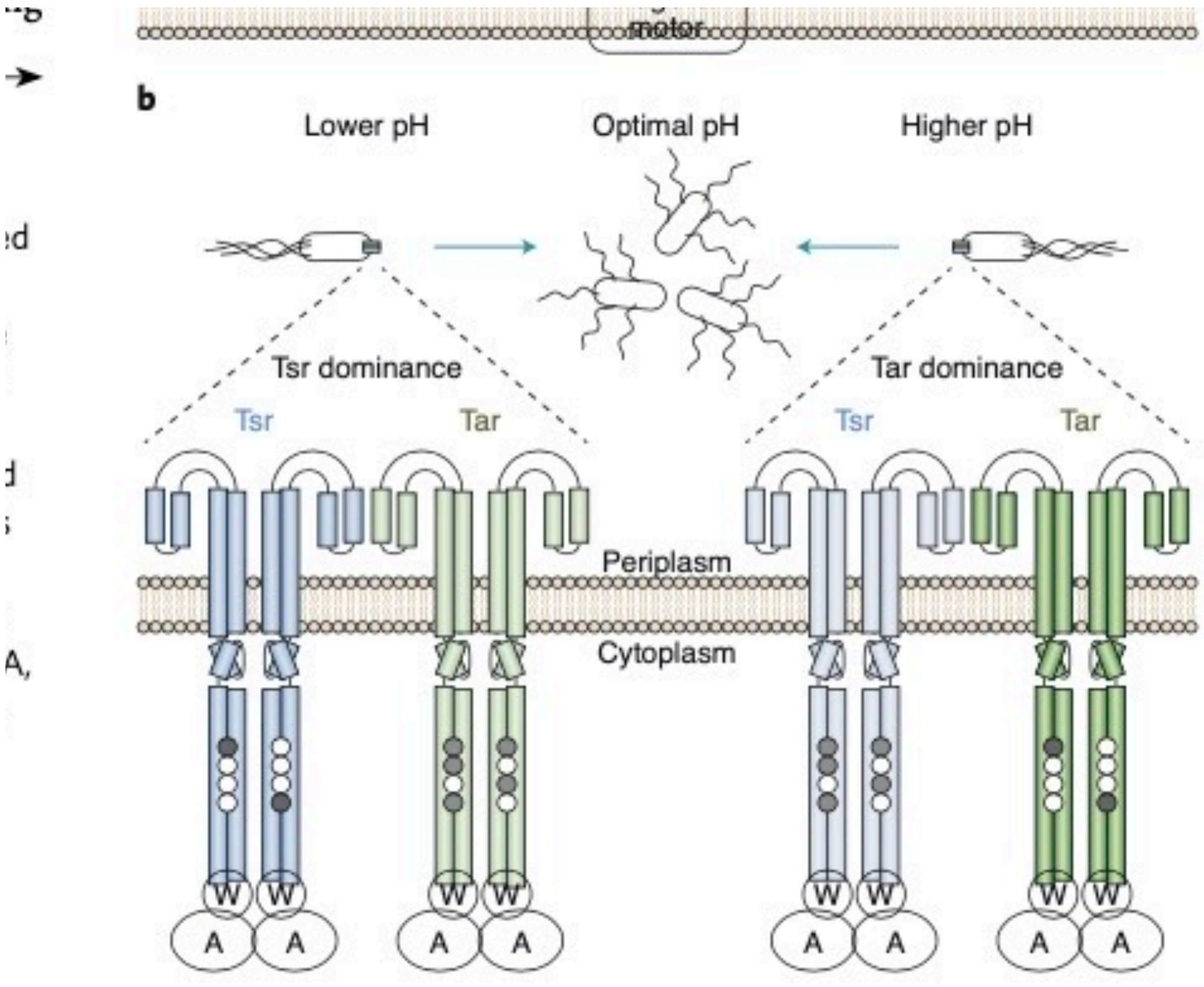
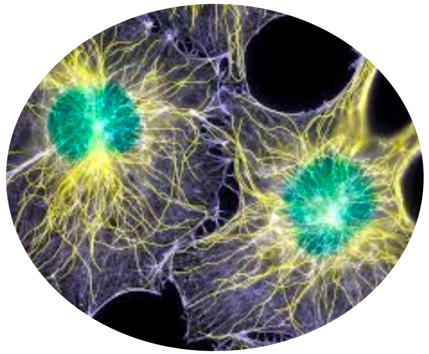


Escherichia coli



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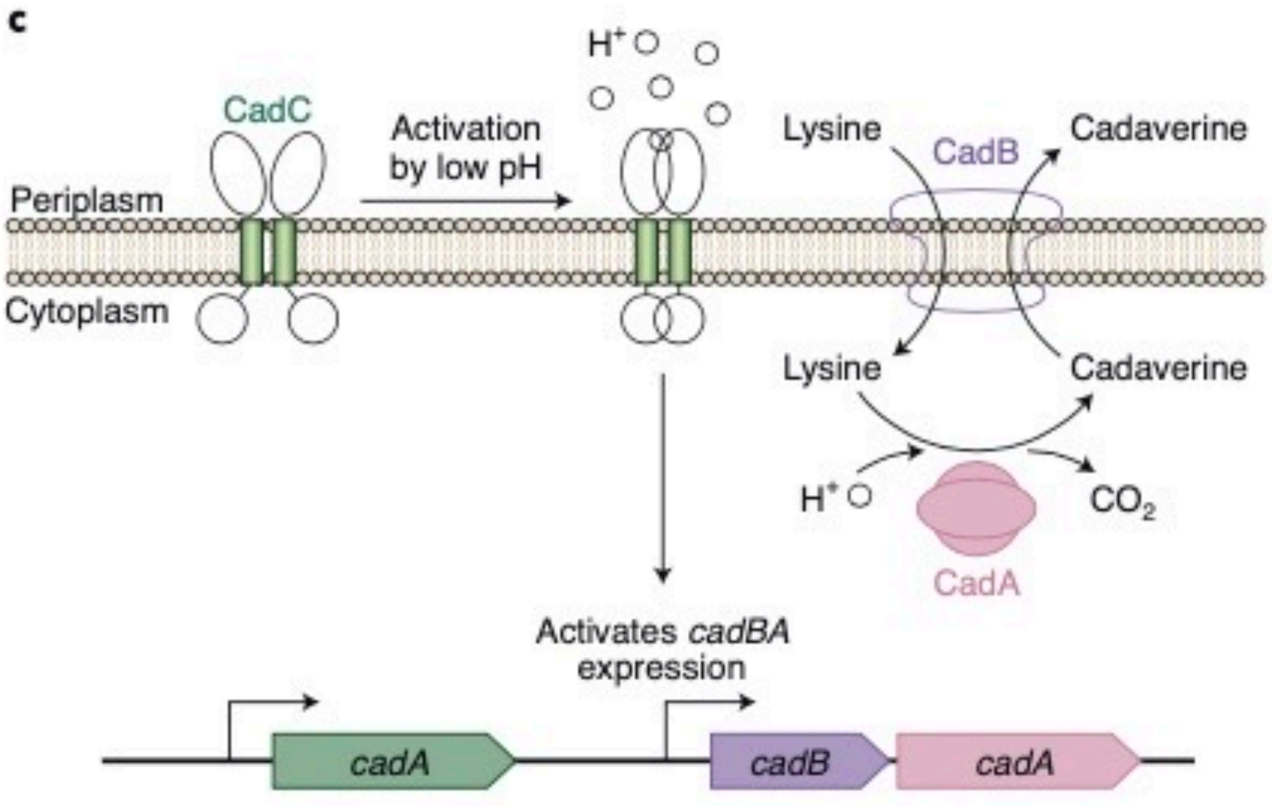
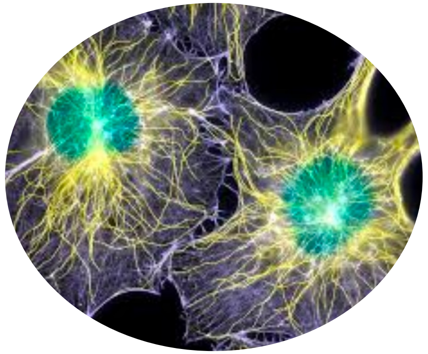


Cadaverine

The CadC-mediated signalling system of *E. coli* for sensing low external pH.

External pH sensing in bacteria



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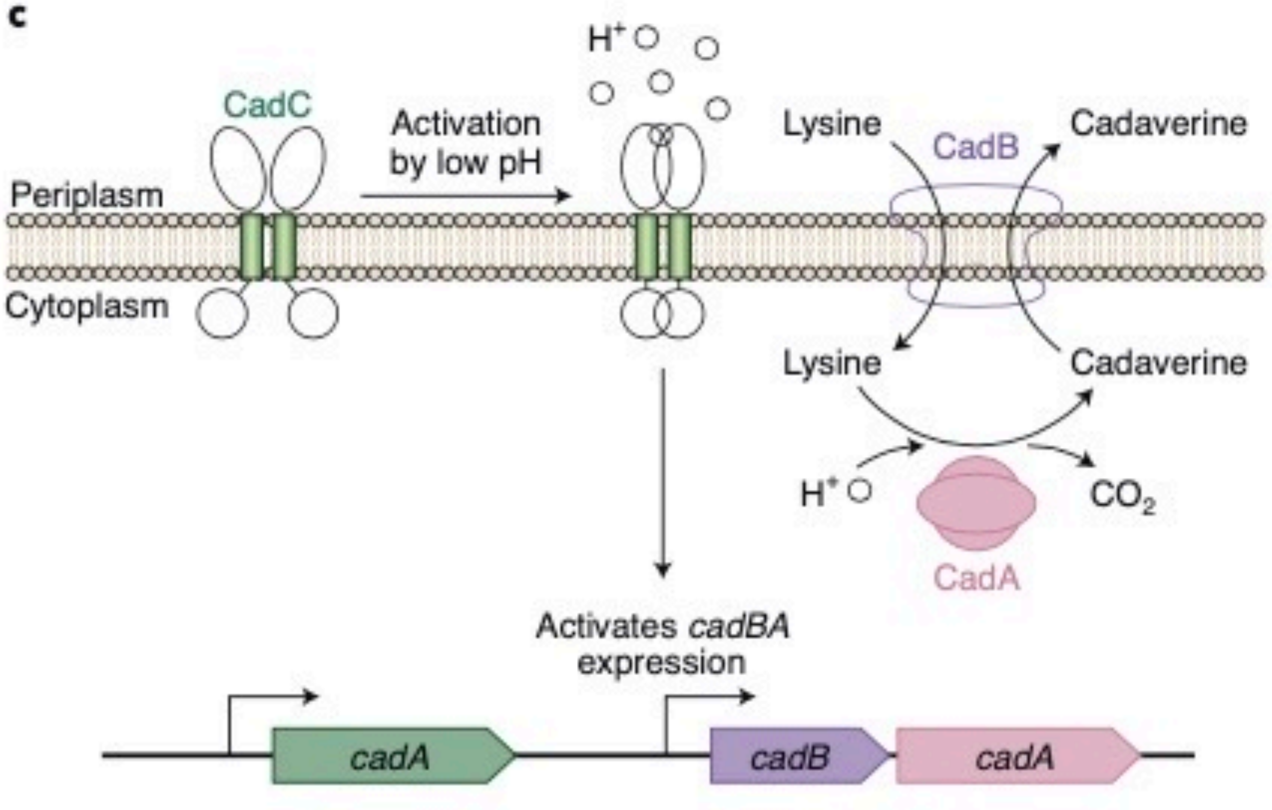

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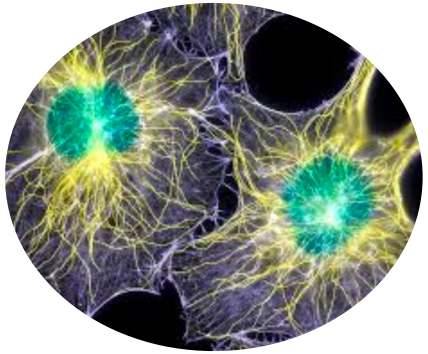

External pH sensing in Eukaryotes – acid sensing ion channels

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Huei-Hsuan Tsai[1] and Wolfgang Schmidt[1,2,3] ✉

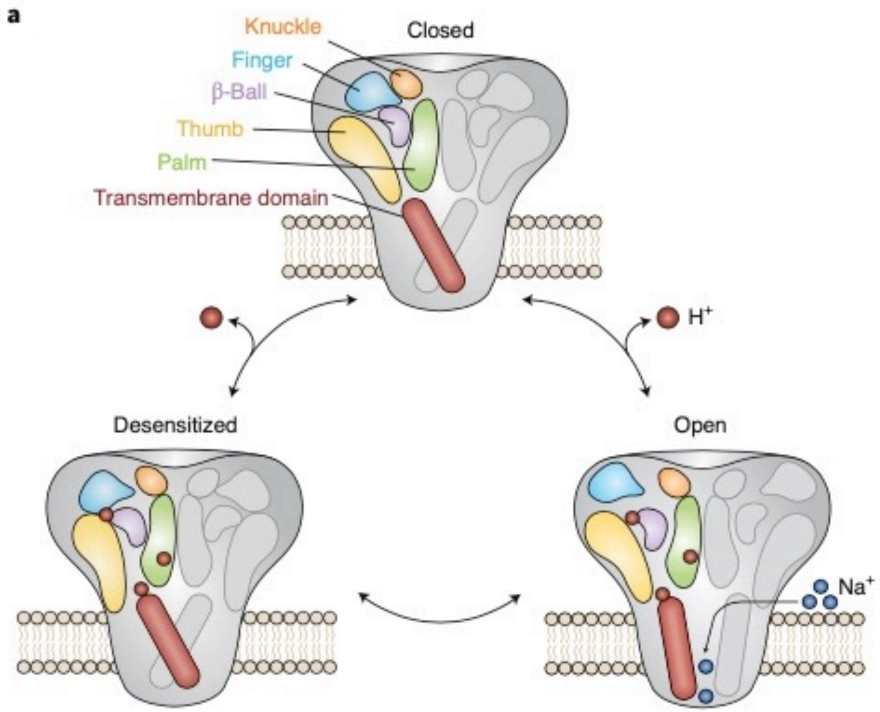
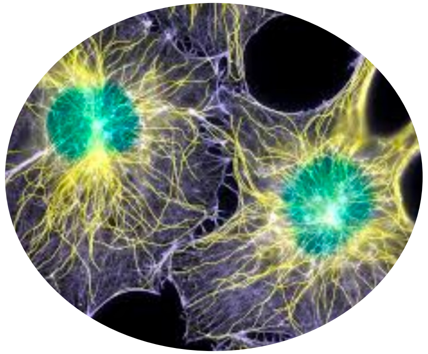


Fig. 3 | pH sensing in eukaryotes. a, ASIC gating in mammalian cells. Schematic view of an ASIC trimer showing the domains of one of the three subunits in the closed, open and desensitized states. In the closed state, the thumb is pushed away from the β-ball and finger domains, keeping the transmembrane domain in a constricted conformation that closes the pore. Following extracellular acidification, several domains become protonated (red circles), leading to structural rearrangements that open the pore to allow transient permeation of sodium ions (Na^+; blue circles). Desensitization of the channel occurs after continued exposure to protons, leading to a constricted conformation of the transmembrane domain that resembles the closed state. **b**, Rim-pathway-mediated pH sensing and signalling in *S. cerevisiae*. External pH is sensed by a PM complex consisting of the sensing components Rim21 and Dfg16, the chaperone Rim9 and the α-arrestin Rim8. In response to a neutral or alkaline pH signal, Rim8 binds to the cytoplasmic tail of Rim21 and Dfg16, which promotes the recruitment and assembly of ESCRTs to form a scaffolding platform for the Rim proteolysis complex (Rim23, Rim20 and the protease Rim13). Rim13 catalyses the pH-dependent cleavage and activation of the transcription factor Rim101. Once activated, cleaved Rim101 localizes to the nucleus to regulate gene expression required for the adaptation to alkaline pH. Panel **a** adapted with permission from ref. [35], Elsevier.



External pH sensing in Eukaryotes

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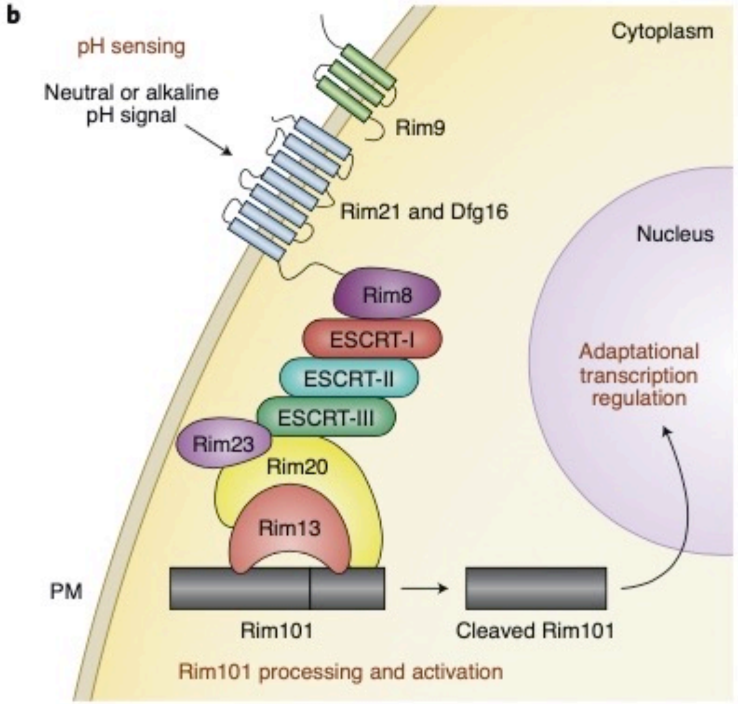

Saccharomyces cerevisiae

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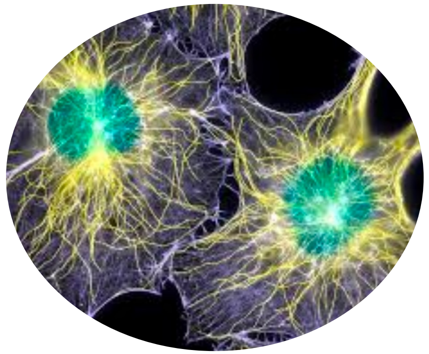

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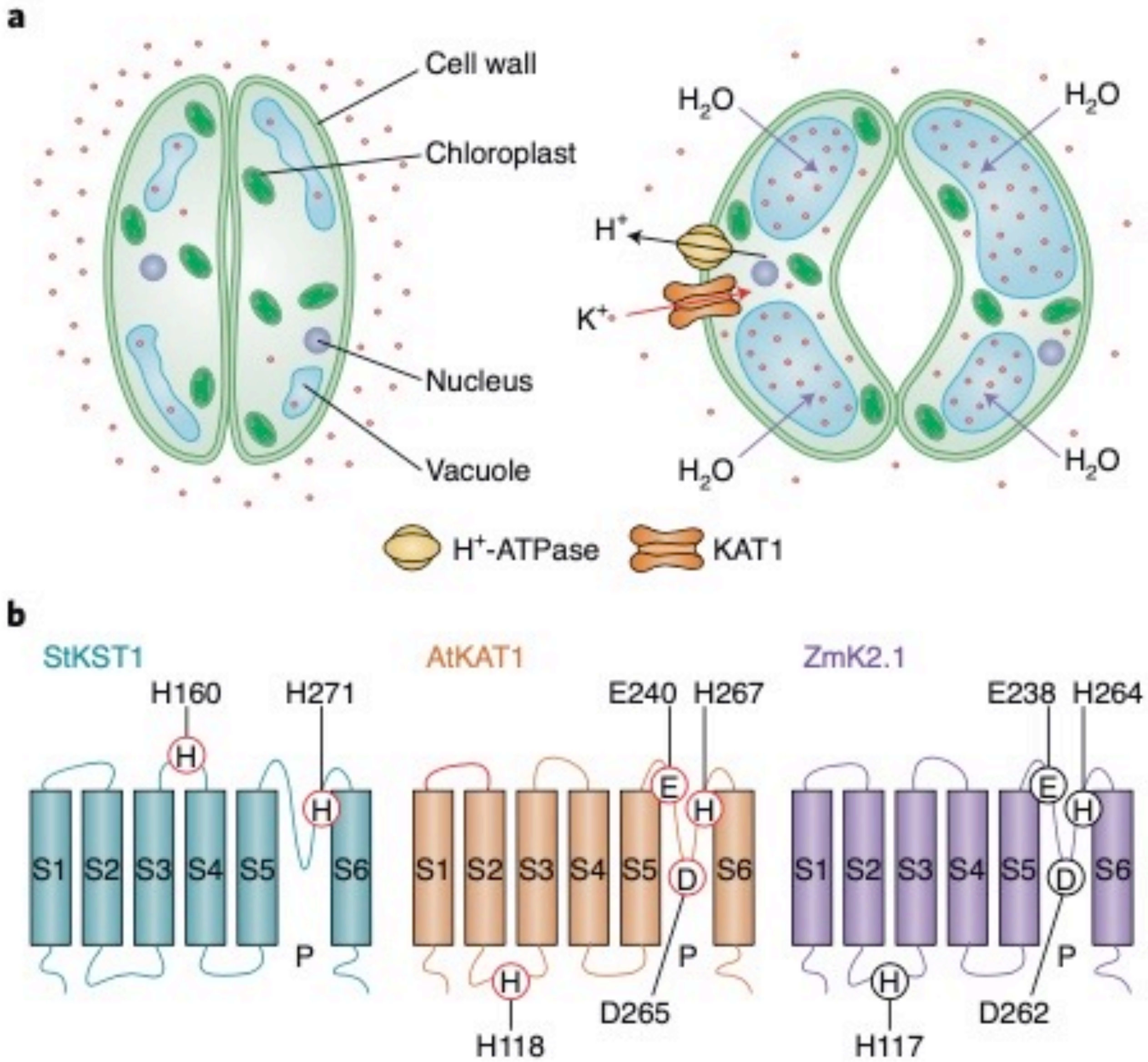
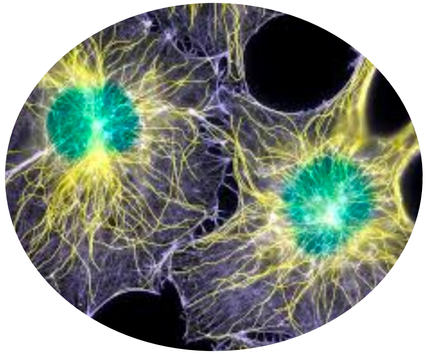


Fig. 4 | Acid-activated K_{IR} channels in plants. a, Role of K_{IR} channels in stomatal guard cells. Stomatal opening is facilitated by H^+-ATPase-mediated extracellular acidification and the subsequent activation of pH sensors on KAT-type K^+ channels that leads to K^+ influx, increase in turgor pressure and opening of the stomatal pore. KAT1 is shown as an example. **b**, General structure of the voltage-dependent K^+ channels StKST1, AtKAT1 and ZmK2.1. Transmembrane segments are denoted as S1–S6, P indicates the pore region. Amino acid residues and linkers that contribute to pH sensitivity are indicated by red circles/line for StKST1 and AtKAT1. Important residues in AtKAT1 are conserved in the maize homologue ZmK2.1, but despite sequence and structural homologies, ZmK2.1 is not activated by acidification. Instead, the S1–S2 linker appears to be the determining factor that distinguishes pH sensitivity between AtKAT1 and ZmK2.1.



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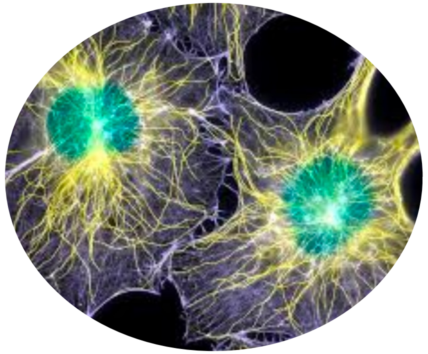

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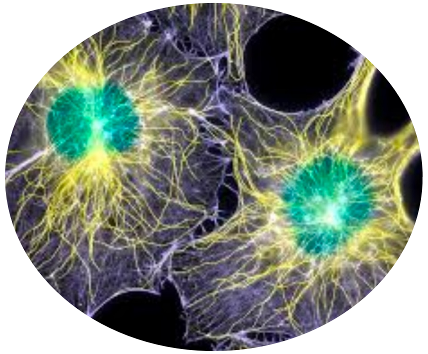

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Isto é o objectivo de todos os trabalhos que vamos desenvolver em FCM