Colloquium

Auxin Signalling: Deconstructing a Long-Standing Paradigm in Plant Biology & A Huge Molecular Proton Pump - How Complex I Works?

Jiri Friml & Leonid Sazanov
ISTA

Host: Carl-Philipp Heisenberg

Auxin Signalling: Deconstructing a Long-Standing Paradigm in Plant BiologyAuxin is a major endogenous regulator of plant growth and development and one of the longest-studied plant hormones. The discovery that auxin induces the transcription of hundreds of genes enabled the identification of key transcriptional regulators: Auxin Response Factors (ARFs) and their repressors, the Aux/IAA (Auxin/Indole-3-acetic acid) proteins. In parallel, genetic screens for auxin-insensitive mutants uncovered components of the ubiquitin ligase machinery responsible for targeted protein degradation, most notably TIR1 (Transport Inhibitor Response 1), an F-box component of the ubiquitin ligase complex.The resulting model is remarkably simple: auxin promotes the interaction between TIR1-type auxin receptors and Aux/IAA co-receptors. This leads to Aux/IAA ubiquitination and degradation, releasing ARFs from repression and enabling transcriptional responses. The model elegantly explained existing observations, inspired the discovery of analogous repressor-degradation mechanisms in other pathways, and withstood the test of time for more than two decades.Nevertheless, live imaging using a vertical-stage microscope developed at ISTA revealed that auxin-induced root growth inhibition occurs within 30 seconds—far too rapidly to involve transcription. This finding led to the discovery that TIR1-type receptors also function as adenylyl cyclases (ACs), enzymes that produce cyclic AMP (cAMP), a prominent second messenger in animal cells. Subsequent studies demonstrated that cAMP is an indispensable component of auxin signal transduction, fundamentally challenging the canonical model of auxin action.Here, I will trace the history of auxin signalling, from its discovery to the unexpected revisions that have recently reshaped the field._____A Huge Molecular Proton Pump - How Complex I Works?Mitochondria are the “powerhouses” of eukaryotes. Mitochondrial (and often bacterial) respiratory chains comprise several large, inner-membrane-embedded protein assemblies. Complexes I, III, and IV create a proton gradient across the membrane, which then drives the rotary ATP synthase. This system powers life by continuously providing ATP—humans turn over roughly their body weight of this energy-rich molecule every day. We study the structure and mechanism of these enzymes and their supercomplexes using cryogenic electron microscopy (cryo-EM) and functional assays.Complex I is the first and largest enzyme in the chain, consisting of up to 45 different subunits with a total molecular mass of about 1 MDa. It

couples the transfer of two electrons from NADH to ubiquinone to the translocation of four protons across the membrane by a mechanism that is still hotly debated. Complex I has three antiporter-like subunits plus one additional similar domain, which were previously thought to be responsible for pumping one proton each per catalytic cycle.We have solved high-resolution cryo-EM structures of complex I from several mammalian, yeast, and bacterial species under various conditions, including catalytic turnover. Unexpectedly, we demonstrated that only one distal antiporter-like subunit is capable of ejecting protons into mitochondrial intermembrane space (or bacterial periplasm). Dramatic conformational changes around the quinone-binding cavity couple the redox reaction to proton translocation during “open-to-closed” state transitions of the enzyme. In the “open” state, the Q-cavity is widely open, allowing quinone to enter and exit. In the “closed” state, the cavity is tightly enclosed around the bound quinone, meaning the protons needed to complete quinone reduction must originate from the central axis of the membrane domain. This initiates a “domino-effect” cascade of electrostatic interactions within the antiporter-like subunits, ultimately resulting in the ejection of four protons per catalytic cycle from the distal subunit.Our proposed mechanism for complex I is an unexpected combination of conformational changes and electrostatic interactions. It challenges the paradigm held over the last decade, yet it is robust and explains all the unique features of complex I resolved in recent structural studies.

Monday, June 22, 2026 11:30am - 12:30pm

Raifeisen Lecture Hall

This invitation is valid as a ticket for the ISTA Shuttle from and to Heiligenstadt Station.
Please find a schedule of the ISTA Shuttle on our webpage:
https://ista.ac.at/en/campus/how-to-get-here/ The ISTA Shuttle bus is marked ISTA Shuttle (#142) and has the Institute Logo printed on the side.