Structural dynamics in plant receptor ETR1 after binding of ethylene and 1-methylcyclopropene

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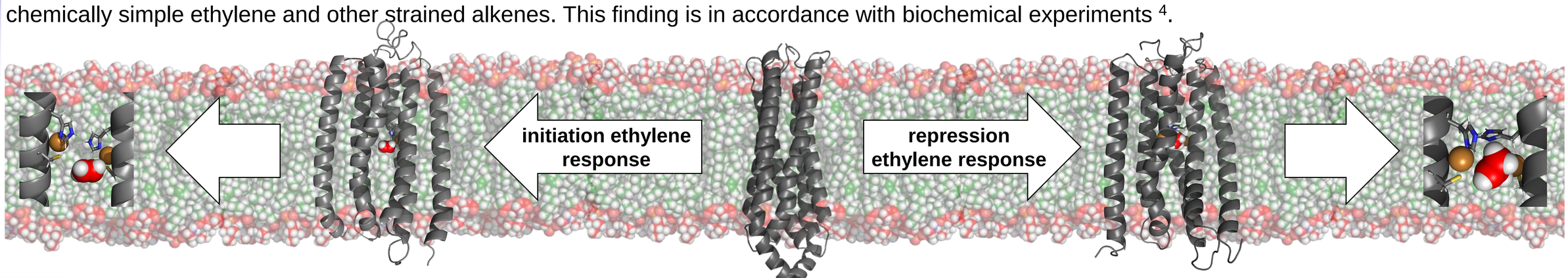
Introduction

The plant hormone ethylene initiates many agronomically relevant reactions, such as fruit ripening, after binding to the transmembrane sensor domain (TMD) of the ethylene receptor ETR1 [1]. To avoid fruit ripening, antagonists such as 1-methylcyclopropene have been characterized [2]. Recent studies proposed the first structural model of the ETR1 TMD by integrating *ab initio* structure prediction and coevolutionary information [3]. However, there is no detailed atomistic knowledge of how the perception of ethylene is transformed into a downstream signal, nor on how antagonists block signal transduction. Here, we show preliminary data suggesting that the TMD undergoes opposite structural dynamics depending on the binding molecule.

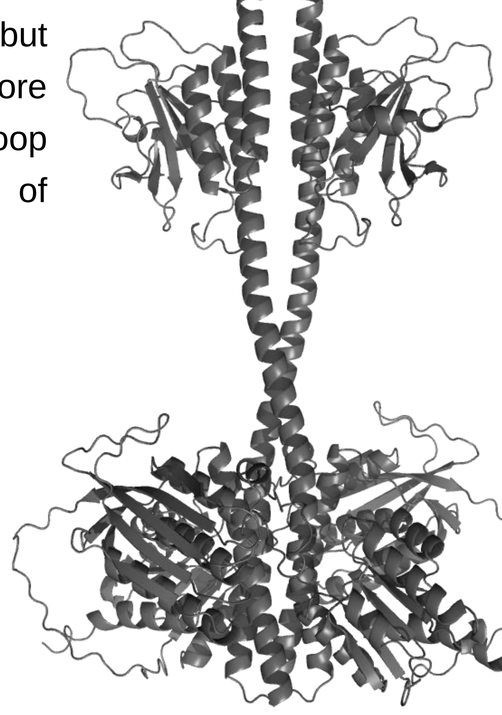
Binding position of ethylene and 1-methylcyclopropene

Using molecular dynamics simulations, we identified binding positions of ethylene and the antagonist 1-methylcyclopropene in the transmembrane sensor domain of ethylene receptor ETR1. Both ligands bind close to a specific cofactor, two copper(I) ions, that ensure a high affinity and specificity for the chemically simple ethylene and other strained alkenes. This finding is in accordance with biochemical experiments [4].



Ethylene binding

After ethylene binding, the whole TMD of ETR1, but especially the bottom part, changes from a curved to a more stretched-out, de-twisted conformation by moving the loop between transmembrane helix 1 and 2 and the end of transmembrane helix 3 more to the center of the TMD.



1-methylcyclopropene binding

In contrast, 1-methylcyclopropene triggers an opposite conformational change than ethylene binding. The TMD changes to an even more curved, more twisted conformation causing transmembrane helix 3 to tilt in the opposite direction compared to the case of ethylene binding.

These opposite shifts but especially the opposite tilt of transmembrane helix 3 may be the key factor in understanding how ethylene perception is transformed into a downstream signal and how antagonists such as 1-methylcyclopropene block this effect.

Summary

Our simulations are the first to investigate structural differences between apo-, ethylene-bound, and 1-methylcyclopropene-bound transmembrane sensor domain in ethylene receptor ETR1. The data indicates that both ethylene and 1-methylcyclopropene bind to the same position in the transmembrane sensor domain. Nevertheless, binding of ethylene leads to a different conformational change than binding of 1-methylcyclopropene. While binding of ethylene causes the two monomers to de-twist, binding of 1-methylcyclopropene causes the opposite effect, ending in a more twisted conformation of the monomers. The de-twist ends in a opposite tilt of the transmembrane helix 3, the linkage to the cytosolic part of ETR1. Therefore, we hypothesize that ethylene binding and specially the following tilt of transmembrane helix 3 may be the key factor in inducing ethylene response in plants. However, further data and experimental validation is needed to prove this hypothesis.

References

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