A NOVEL HEXOSE TRANSPORTER IN RICE PUTATIVELY REGULATES THE UPTAKE OF MELATONIN, THE POTENT ABIOTIC STRESS REGULATOR

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The present manuscript represents the identification and predictive structural characterization of novel human GLUT1-orthologue, melatonin transporter (MelT) in plants (especially rice) and its functional ability to transport melatonin. It is reported that melatonin binds to the same residues within GLUT1 as glucose. Homology modelling and docking analyses predicted overall sequence homology of OsMelT with GLUT1. The protein was predicted to contain 12 transmembrane helices and a PF00083.24 sugar transport domain (responsible for melatonin binding and release). The C-terminus was more structured, compared to the N-terminus, and phosphorylation sites were detected throughout the protein. The upstream analysis of MelT showed the presence of cis acting motifs associated with abscisic acid, melatonin regulation and induction to both abiotic and biotic stress. Expression studies validated the up regulation of OsMelT in presence of glucose and higher concentrations of exogenous melatonin. Overall, the study predicted the functional ability of OsMelT to transport melatonin and maintain the uptake and mobilization of the biomolecule at higher concentration.

Key words: *Melatonin, transporter, phylogram, homology modelling, docking analysis, gene expression, bioinformatics.*

НОВИЙ ТРАНСПОРТЕР ГЕКСОЗИ В РИСІ ЙМОВІРНО РЕГУЛЮЄ ПОГЛИНАННЯ МЕЛАТОНІНУ, ПОТУЖНОГО РЕГУЛЯТОРА АБІОТИЧНОГО СТРЕСУ

У цьому рукописі представлено ідентифікацію та прогнозну структурну характеристику нового GLUT1-ортолога людини, транспортера мелатоніну (MelT), в рослинах (особливо в рисі) та його функціональну здатність транспортувати мелатонін. Показано, що мелатонін зв'язується з тими самими залишками в GLUT1, що й глюкоза. Моделювання гомології та докінг-аналіз передбачили загальну гомологію послідовності OsMelT з GLUT1. Було передбачено, що білок містить 12 трансмембранних спіралей та цукротранспортний домен PF00083.24 (відповідальний за зв'язування та вивільнення мелатоніну). С-кінець був більш структурованим порівняно з N-кінцем, і по всьому білку були виявлені сайти фосфорилювання. Висхідний аналіз *MelT* показав наявність цис-активних мотивів, пов'язаних з абсцизовою кислотою, регуляцією мелатоніну та індукцією як до абіотичного, так і до біотичного стресу. Дослідження експресії підтвердили посилення регуляції *OsMelT* у присутності глюкози та підвищених концентрацій екзогенного мелатоніну. В цілому, дослідження передбачило функціональну здатність OsMelT транспортувати мелатонін і підтримувати поглинання та мобілізацію біомолекули за вищих концентрацій.

Ключові слова: мелатонін, транспортер, філограма, моделювання гомології, докінг-аналіз, експресія генів, біоінформатика.

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