

Study on the Response of Yeast MCC Microdomain against High Salt Concentration Stress

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Summary

Plasma membrane is the forefront of sensing environmental changes and has an important role for induction of proper stress responses. It has many kinds of proteins and lipids, which do not distribute randomly. Some kinds of proteins and lipids assemble and form lateral membrane compartments called as “rafts” or “microdomains”. It was reported that these domains were rich in sterols and sphingolipids. MCC (membrane compartment of Can1p)/eisosome is known as a plasma membrane microdomain in budding yeast *Saccharomyces cerevisiae*, and it includes 22 proteins such as Can1, Tat2, Fur4, and Pil1. Since its functions and stress responses remain to be clarified, we investigated the stress response of the MCC under high-salt hyperosmotic conditions that are commonly found during the process of brewing and bread-making. High-salt stress caused the accumulation of Can1 and sterols following the formation of their large foci on the plasma membrane. Additionally, such a stress response was inhibited by pre-treatment with filipin and myriocin, a sterol-binding reagent and a sphingolipid biosynthesis inhibitor, respectively. These results indicate that plasma membrane sterols and sphingolipids are presumably required for the formation of MCC large foci. Analysis using transmission electron microscopy (TEM) clarified that deep invagination of the plasma membrane was induced under hyperosmotic conditions. Our findings suggest that making deep invagination of the plasma membrane causes the formation of MCC large foci under high-salt hyperosmotic conditions. In contrast, a salt-tolerant yeast *Zygosaccharomyces cerevisiae* did not form large foci of sterols under conditions of high-concentration salt stress. This finding clearly indicates the difference in the physiological characteristics of membrane microdomains between *S. cerevisiae* (baker’s yeast) and *Z. rouxii* (soy sauce yeast).