

Exploration of Single Nucleotide Polymorphisms Associated with Salt Intake

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Summary

Chronic excess salt intake induces hypertension and atherosclerosis and increases the risk of developing cardiovascular disease. The salt intake in the Japanese population is among the highest in the industrialized world. Therefore, practical salt reduction guidance is needed to maintain and improve the population's health. Consequently, we conducted four studies to identify genetic regions associated with salt intake and salt-taste preference to find genetically high salt intakes.

In Study 1, a path analysis was conducted to examine the association between salt intake measured, salt-taste preference and salt-taste sensitivity data. The results showed that salt-taste preference was inversely related to salt intake, while salt-taste sensitivity was not significantly associated with salt intake. Study 2 found that a single nucleotide polymorphism (rs671) in the alcohol dehydrogenase (*ALDH2*) gene, which has been strongly associated with food intake behavior in previous studies, may be associated with salt intake. Study 3 developed a photographic dietary assessment utilizing a smartphone application and measured salt intake more accurately than the food frequency method. Finally, study 4 identified gene loci suggesting an association with salt taste preference by genome-wide association study.

These results suggest that it is challenging to utilize salt taste preference data to estimate salt intake and that salt intake and taste preference should be considered separately. Therefore, future genome-wide association analyses of the salt intake should be conducted the photographic dietary assessment, which is more accurate than the food frequency method in estimating salt intake. The results of this study are expected to provide a knowledge base for personalized salt reduction guidance that takes genetic constitution into account.