B8. Metabolism of [^{14}C]Gibberellin A_{12} and Major GA Biosynthetic Pathway in Chinese Yam, *Dioscorea opposita* Thunb. cv. Tsukune, Shoots

Sang-Kuk Kim[1], Sang-Chul Lee[2], Soo-Won Jang[2], Tae-Shik Park[1], and In-Jung Lee[2,*]

[1]Institute of Bioresources, Gyeongbuk Provincial Agricultural Technology Administration, Andong 760-891, Korea

[2]Division of Plant Biosciences, Kyungpook National University, Daegu 702-701, Korea

Objectives

GA biosynthetic pathway in Chinese yam have been identified from extracts of leaves and bulbils. Two non C-13 hydroxylation routes are predominant in Chinese yam shoots, however, and in these GA biosynthetic pathways, origin of active GA_4 in time-course feeding is not determined in this plant.

Materials and Methods

The substrate was dissolved in ethnol:water (1:1, v/v) and ca. 10$\mu\ell$ was dropped to surface of shoots. Shoots of tubers were harvested at 6, 12, 18 and 24 h after feeding, respectively. For feeds, 20 each of shoots of the tubers were subjected to 370 Bq per seedlings. Seedlings were grown under continuous light condition until final harvesting. [^{14}C]GA_{12} was obtained from Professor Lewis N. Mander (Australian National University, Canberra, Australia). Analysis of GAs were followed the reference (Lee et al., 1998).

Results and Discussion

Eight endogenous gibberellins (GAs) have been identified (Tanno et al., 1992) in non-dormant bulbils of the Chinese yam. Furthermore, eleven GAs including GA_1 have been also identified and quantified (Kim et al., 2002) in Chinese yam leaves during tuber enlargement. However, it is not clear that which GA biosynthetic pathway is dominated in the Chinese yam, although two GA biosynthetic pathways are present. In determining of feeding of [^{14}C]GA_{12} in shoots of the Chinese yam (*Dioscorea opposita* cv. Tsukune), we found that major GA biosynthetic pathway was non C-13 hydroxylation route like previous reports. In time-course of feeding results, however, predominant GA biosynthetic pathway in the Chinese yam shoots was non C-13 hydroxylation following as $GA_{12}\rightarrow GA_{15}\rightarrow GA_{24}\rightarrow GA_{36}\rightarrow GA_4$. Hereby, we suggest that bioactive GA_4 could be involved in controlling GA-induced dormancy in the Chinese yam.

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*Corresponding author: TEL: 053-950-5708, E-mail: ijlee@knu.ac.kr