RESEARCH HIGHLIGHTS

Figure 1. The 90% C.L. upper limit as a function DM mass for spin-independent isoscalar WIMP-nucleon cross-section for several DM search experiments. Reprinted with permission from [1]. Copyright Science China Press and Springer-Verlag Berlin Heidelberg 2014.

at the Gran Sasso laboratory in Italy, is commissioned to begin in late 2015. The global race to detect DM is becoming tighter than ever.

Xiao-Gang He
Department of Physics and Astronomy, Shanghai
Jiao Tong University, China
E-mail: hexg@sjtu.edu.cn

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PLANT & ANIMAL SCIENCE

Bitter but tasty cucumber

Xiao-Ya Chen

Plant natural products consisting mainly of phenolic compounds, alkaloids and terpenoids, are valuable for both plants and humans. Recently a breakthrough has been made in elucidation of biosynthesis of cucurbitacins [1], a class of highly oxygenated tetracyclic triterpenoids present in the family Cucurbitaceae, which confer unpleasant bitter taste to help the plant to wade off herbivores and are exploited by humans in form of traditional herbal medicines for their anti-inflammatory, hepatoprotective and potential antitumor properties [2,3]. Widely consumed as vegetables and fruits, the cultivated non-bitter cucurbits, e.g. cucumber, melon and watermelon, are domesticated from their extremely bitter ancestors thousands of years ago. However, some of domesticated cultivars would turn bitter when they were grown under stress, e.g., drought or low temperature, seriously affecting their quality and marketability. The underlying mechanism remains largely unknown. Recently, several studies have shown that plant secondary metabolites are biosynthesized by clustering of functionally related enzymes [4]. However, whether similar triterpenoid biosynthetic cluster also exists in cucurbits and more importantly, how to regulate the gene clusters in plants are unknown.

After the initiation of cucumber genome project, Sanwen Huang and colleagues have de novo sequenced the genome of cucumber and draw the first cucumber variation map [5,6]. By integrating these big genomic data and multiple research tools, they cloned the cucumber bitterness gene (Bi), which participates the first committed step of cucurbitacin C (Cuc C) biosynthesis. Identification of two non-bitter mutants and analysis of cucumber variation map lead to the discovery of Bl (bitter leaf) and Bt (bitter fruit), two bHLH

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**Figure 1.** Accurate manipulation of the bitterness biosynthesis in different cucumber tissues by activation of \( Bl \)'s expression in leaves and downregulation of \( Bt \)'s expression in fruits. The whole plant is bitter to wade off herbivores and potential drug reservoir, while its fruit is non-bitter, promising high commodity trait as vegetables.

transcription factors that directly regulate the expression of \( Bi \) in cucumber leaf and fruit, respectively. Through co-expression and co-regulation studies, a 9-gene module responsible for Cuc C biosynthesis in cucumber was uncovered and functions of four enzymes, including \( Bi \), two \( P450 \)s and one \( ACT \), have been characterized. \( Bl \) and \( Bt \) are two master regulators, directly controlling the expressions of the 9-gene module in leaf and fruit, respectively, which is the first example of how the gene cluster is regulated in plant. Mutations occurred within \( Bt \) promoter region decreased its expression in the fruit tissue, and may be selected and fixed during the cucumber domestication. Among these mutations, a single-nucleotide polymorphism (SNP, G/A) is essential for cucumber to response to cold stress. Once mutated from ‘G’ to ‘A’, non-bitter cucumber would not turn bitter even grown under cold stress while otherwise would.

The discovery of bitterness biosynthesis, regulation and domestication in cucumber provides possibility to develop a new non-bitter cucumber by accurately tuning the bitterness biosynthesis in different plant tissues, which protect plants from herbivores with their own weapon systems but avoid the unpleasant bitter taste in the fruit (Fig. 1). And this study also opens a door to metabolic engineering cucurbitacins as potential anti-tumor drugs. However, we must notice that there are five enzymes whose biochemical functions are still unclear. It’s a big challenge to elucidate the whole pathway of cucurbitacin biosynthesis in future.

Xiao-Ya Chen
Institute of Plant Physiology and Ecology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, China
E-mail: xychen@sibs.ac.cn

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