Association among aroma volatiles and other traits in near-isogenic lines with firm flesh texture

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Resumen

La calidad en los melones (*Cucumis melo* L.) es un criterio importante para la aceptación del consumidor. Al igual que en cualquier otra fruta, el proceso de desarrollo y maduración involucra una serie de cambios bioquímicos y fisiológicos como la descomposición de la clorofila, la degradación de la pared celular (que resulta desde ablandamiento a cambios en la ultraestructura de la pulpa y del fruto entero), el aumento en el contenido de azúcares y el contenido de sólidos solubles (SSC), la biosíntesis de pigmentos, aromas y la generación de sabor, etc. El objetivo de la tesis doctoral será determinar la calidad global y perfil aromático de al menos una línea casi isogénica (NIL) de melón con diferencias en textura respecto a su parental no climatéricos (PS) para mapear QTLs asociados a la calidad especialmente aromática y textural de la fruta. Utilizando resultados de expresión génica diferencial PS-NIL y el mapa genético de melón y las secuencias previamente almacenada en el GenBank estaremos posicionando genes candidatos y relacionando esta información con el fenotipo.

Palabras clave: Textura, líneas casi isogénicas; comportamiento no climatérico; Mapeo de QTLs; RNA-seq.

Abstract

Quality in melons (*Cucumis melo* L.) is an important criterion for consumer's acceptance. Like any other fruit, melons development and ripening process are linked to a series of biochemical and physiological changes including chlorophyll breakdown, cell wall degradation (leading from flesh to whole fruit softening to changes in ultrastructure), increase in the sugar content and soluble solids content (SSC), pigment biosynthesis, aroma and flavour generation, etc. The goal of the PhD will be to determine global quality and aroma profile at least one near-isogenic lines (NILs) of melon with different texture than its non-climacteric parental PS in order to map QTLs associated with fruit quality and particularly aroma volatiles. Using some results of differential gene expression and the genetic map of melon and the sequences stored in GenBank some candidate genes will be suggested and linking genetic and phenotypic information.

Keywords: Texture, near-isogenic lines; non-climacteric behavior; QTL mapping; RNA-seq.

1. Introduction

The present research will elucidate the quality of melons in their postharvest supply chain as part of our breeding strategies to improve the crop overall quality. This research particularly will gain knowledge based on near-isogenic lines (NILs) of melons and the genetic map of melon [1], a model system where many quantitative trait loci have been identified useful for postharvest purposes, with emphasis on multidisciplinary studies involving quality traits, physiological and biochemical studies, and modelling. The parentals used to generate melon NILs were the cv. T111 of the inodorous group and "*Piel de sapo*" type, and the Korean accession "*Shongwhan Charmi*" (SC) PI 161375 [1]. NILs are almost genetically identical lines differing in small genetic component from its donor parent. This unique feature allows a quick mapping of quantitative trait loci (QTLs) associated with the traits of interest [1], a possibility that is complementing and provides added value to typical postharvest and fruit quality studies [2]. In fact more than 250 QTLs associated with melon fruit quality traits have been mapped so far by the phenotyping work of the UPCT group using the NILs [3, 4] and in other groups [5]. Of particular, our interest are the NILs involved in climacteric behaviour and aroma production, because parental lines of this population showed non-climacteric behaviour

and were non-aromatic in flavour [6]. Other QTLs of interest are fruit weight and shape, texture, colour, fruit composition and nutritional traits, sensitivity to storage disorders and decay, etc. have been previously identified [4] but the knowledge hasn't been explored further using multidisciplinary approaches to study the postharvest quality in melons.

Melon aroma precursors are fatty acids such as the insaturated ones (linolenic, linoleic or oleic acids), and amino acids such as phenylalanine, leucine, isoleucine, valine or methionine. The application of these aminoacids to melon stimulate melon aroma and the catabolism of some of them produce aroma such as methionine [7]. The QTLs associated with aromas derived from aminoacid catabolism are still of interest in melons because only a few of them have been mapped 8]. These QTLs can be transferred to elite cultivars and improve fruit aroma quality and organoleptic properties [9].

2. Materials and methods

The following work actions are proposed to meet the above objectives. Some NILs of melon (NILs) from the collection of Eduardo et al. (2005) [1] and others with fewer introgressions of PI 161375 into the PS genetic background will be used for the studies proposed below such as SC7-2 and SC10-2 [1,10,8].

The methodologies of experimental design, melon crop management, fruit sampling and fruit quality evaluation (including aroma) using univariate and multivariate statistical methodology to discriminate NILs and to map QTLs have been previously published [3,4]. The thesis will be realized following these steps:

1) Sampling and aroma volatile analysis (HS-SPME coupled to RTL GC-MS) [10,4].
2) Data analysis and integration, validation, etc. [8].
3) Characterizing aroma profile in detail of the NIL SC7-2.
4) Identification of some key aroma volatiles of the NIL SC10-2 versus PS.
5) RNA extraction: TRI Reagent RNA isolation protocol.
6) mRNA library preparation and sequencing: TruSeqTM Stranded mRNA Sample Preparation kit protocol (Illumina Inc., Redwood. CA, USA).
7) Transcripomic analysis.
8) Univariate and multivariate statistical analysis (PS vs NIL).
9) QTL mapping and candidate genes location.
10) Association of aroma volatile with other textural traits.
11) Association of aroma volatile with the expression of some genes of interest in SC10-2.
12) Thesis document and presentation.

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4. References

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