ABSTRACT

THE EFFECT OF CARPEL AND STAMEN PRIMORDIA-TARGETED ETHYLENE PRODUCTION AND PERCEPTION ON SEX EXPRESSION IN MELON (CUCUMIS MELO L.)

By

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Commercial melons (Cucumis melo L.) are typically andromonoecious, first producing vegetative nodes followed by a male flower-only phase, then a male and bisexual flower phase. Unisexuality arises from differential suppression of sex organ primordia, and ethylene is a key factor modulating sex expression. Thus, a comprehensive model of melon sex determination must include sex organ suppression developmental stages, known sex genes and phenotypes, and ethylene effects. Previous work in our lab using transgenic melons expressing the ethylene receptor mutant etr1-1 under floral primordia-targeted promoters indicated stamen primordia, not carpel primordia, need to perceive ethylene for carpel development. Previous research reported that the G locus, responsible for carpel suppression, encodes a WIP1 transcription factor, and the A locus, responsible for stamen suppression in bisexual flowers, encodes an ethylene biosynthetic enzyme gene, 1-aminocyclopropane-1-carboxylic acid synthase (ACS). However, it is unknown how molecular ethylene production influences carpel development promotion.

To further examine the roles of floral organ primordia in promoting carpel development, transgenic melons were produced targeting ACS expression to either stamen and petal primordia (AP3::ACS), or carpel and nectary primordia (CRC::ACS). AP3::ACS melons showed increased A gene expression, and decreased G expression. Increased femaleness was observed, manifested as increased carpel-bearing buds, decreased male buds, male-only phase loss, and gain of a

bisexual-only phase not seen in wild type. Microscopic analysis of apices showed reduced progression of floral buds into sex determination stages. In contrast, CRC::ACS melons showed no difference in sex expression patterns or sex gene expression. These results, coupled with knowledge of sex gene identities and sex phenotypes, led to an integrated model of melon floral sex determination.

Increased femaleness was also observed in transgenic melons targeting etr1-1 to carpel and nectary primordia (CRC::etr1-1). To investigate if this phenotype is useful for increased and earlier fruit set, CRC::etr1-1 melons were examined in the field. Transgenic plants had earlier and increased number of carpel-bearing flowers and fruit set. However, CRC::etr1-1 fruit were smaller, resulting in equivalent kg/plot, and showed either earlier ripening (line M5), or no obvious external ripening (line M15). Externally green M15 fruit had extensive internal ripening with elevated internal ethylene levels, equivalent to wild type orange fruit. Expression of etr1-1 was higher in M15 exocarp compared to mesocarp, likely leading to external ripening inhibition.

It has been proposed that, in addition to the two major sex loci, one or more modifiers act to stabilize gynoecious and hermaphrodite genotypes. Other members of the ACS or ACC oxidase (ACO; ethylene biosynthetic enzyme) families may modulate sex determination. To evaluate gene expression within different sex genotypes, hermaphrodite (ggaa) and monoecious (G-A-) lines were produced from a gynoecious (ggAA) and andromonoecious (GGaa) cross. F1 progeny were monoecious as predicted and F2 sex phenotype segregation ratios were consistent with a four gene model. Three new ACS gene members were identified using the melon genome; expression of the 7 ACS and 3 ACO genes was analyzed in apices of different genotypes. All ACS and ACO members showed higher expression in gynoecious and hermaphrodite apices compared to andromonoecious and monoecious. Together, these studies provide further insight

into ethylene perception and production influences in sex expression in melon.