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Abstract

Bitter gourd (Momordica charantia L.) is both medicinally and economically highly valued

cucurbit. Hybrid vigor has been well exploited for early maturity, higher yields and other genetic and agronomic traits. However, hybrid seed production in bitter gourd is labor-intensive requiring manual bagging and hand pollination. Use of gynoecious lines as female parent that produce only female flowers have not only reduced the labor requirement, but also have increased yields in hybrids and have good combining ability. However, early phenotypic detection of gynoecy in breeding lines is difficult as gynoecy is highly influenced by environment. To identify the candidate genes governing gynoecy, differentially expressing gene between a gynoecious (Gy323) and a monoecious line (DRAR-1) were explored. 7865 genes were differentially regulated between two lines and 4131 genes were up regulated in gynoecious lines. Up regulated genes in gynoecious line; BTB/POZ domain-containing protein that regulate floral development and previously reported ethylene biosynthesis and regulation genes in cucumber and melon; 1-aminocyclopropane-1-carboxylate oxidases and 1-aminocyclopropane-1-carboxylate synthase and ethylene receptor and ethylene responsive proteins were identified as putative candidate genes for gynoecy in bitter gourd.

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Index Terms

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