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Development of codominant SCAR markers linked to powdery mildew resistance in melon (*Cucumis melo* L.)[†]

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Powdery mildew in melon (*Cucumis melo* L.) is significant disease caused by the fungus *Sphaerotheca fuliginea*. This disease is a major limiting factor for the production of melon throughout the world. The most effective strategy to control powdery mildew is to introduce the resistance into new commercial cultivars during melon breeding. But, breeding resistant cultivars is very difficult and time consuming because *S. fuliginea* is obligate parasite. In order to reduce breeding time and costs, we adapted marker assisted breeding system to breed powdery mildew resistant cultivars. A segregating F2 population was obtained by crossing resistant inbred line "RA1", derived from European melon cultivar, with susceptible inbred line "RA2" to elucidate the genetic nature of the resistance and to develop DNA markers linked to the resistance locus. This F2 population was evaluated for response to the pathogen *S. fuliginea* in natural field condition. Distribution of powdery mildew incidence in 277 F2 plants did not agree with the segregation pattern of monogenic or digenic inheritance indicating that the resistance to powdery mildew is controlled by more than two genes or quantitatively. We identified two markers linked to the resistance locus using DNA fingerprinting technique combined with bulked segregant analysis. These two markers associated with powdery mildew resistance were converted to SCAR marker, and named PMR1 and PMR2. PMR1 is co-dominant marker, while PMR2 is dominant marker. PMR1 and PMR2 was tested in individual F2 plant and seemed to be closely linked to powdery mildew resistance locus with major effect. These SCAR markers would be used as reliable selection marker that was able to detect powdery mildew resistance in melon breeding.

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