Mapping Genes Governing Flower and Seedcoat Color in Asparagus Bean (Vigna unguiculata ssp. sesquipedalis) Based on Single Nucleotide Polymorphism and Simple Sequence Repeat Markers

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Abstract. Colors of flower and seedcoat are interesting traits of asparagus bean, a cultivated subspecies of cowpea grown throughout Asia for its tender long green pods. Little is known about the inheritance of these traits including their genome location. We report here the genetic analysis and mapping of the genes governing flower and seedcoat color in asparagus bean based on single nucleotide polymorphism (SNP) and simple sequence repeat (SSR) markers. Analysis of the F1 and F7:8 generation of recombinant inbred lines (RILs) population showed a monogenic inheritance of both traits. Purple flower and brown seedcoat are dominant over white flower and cream seedcoat, respectively. We further show that genes governing flower color and seedcoat color are tightly linked on LG8, ≈0.4 cM apart. Synteny analysis showed that the gene controlling seedcoat color in our study is syntenic to the soybean T locus. The use of the mapping information in asparagus bean breeding is discussed.

Cowpea (Vigna unguiculata L. Walp.) (2n = 2x = 22), a self-pollinating diploid species belonging to the genus Vigna of the Phaseoleae tribe, is an important food legume worldwide. Two main cultivated divisions of cowpea are the ssp. unguiculata and ssp. sesquipedalis. Subspecies unguiculata is the largest cowpea group grown primarily for dry grain and fodder, providing millions of people in Africa, India, the Middle East, and South America with high-protein food stuff (Ehlers and Hall, 1997; Singh, 2002). The ssp. sesquipedalis, also known as asparagus bean or “yard long” bean, is widely grown in east and southern Asia for production of immature pods. Genetic similarity between the two subspecies is high as evidenced by the fact that hybrids are fully fertile and molecular marker systems developed in subspecies unguiculata are effective and readily transferred to subspecies sesquipedalis (Xu et al., 2010).

Flower and seedcoat colors are important agronomic traits of legumes including cowpea. Cowpea seeds with brown or white coat color are preferred in many African regions (Drabo et al., 1987; Langyintuo et al., 2003). Leleji (1972) reported that bumble bees and honeybees show significantly preferred visitation to purple as opposed to white flowers of cowpea. In addition, flower and seedcoat colors are considered useful phenotypic markers in breeding because of their stable expression and convenience for observation. In general, the principal flower color of ssp. unguiculata falls into the classes of white, dark, or purple, pale and tinged (Rachie, 1985). There are lesser variation of flower color in asparagus bean, because an investigation of ≈1000 asparagus bean accessions from various origins of China typically detected only three major types of principal flower color, which are purple, white, and tinged (Wang BG, personal communication). In terms of seedcoat color, a wide range of variations, including black, white or cream, brown, yellow, and red are found in both subspecies.

The inheritance mode of cowpea flower coloring is genotype-dependent. A monogenic inheritance with complete dominance (Padi, 2003; Sangwan and Lodhi, 1998), an interaction of two genes in a complementary manner and an involvement of two genes epistatically interacting were reported in ssp. unguiculata (Mustapha, 2007). A general color factor C is considered responsible for seedcoat color and its absence results in white seeds (Spillman, 1912). In some genotypes, the C factor in combination with other genes conditions certain colors of seedcoat. Spillman and Sando (1930) proposed that six major genes (R, P, B, M, N, U) were involved in different ssp. unguiculata parental lines controlling seedcoat color. What is also worthy to note is that seedcoat color is inherently independent of the seedcoat “eye” pattern, the latter of which usually complicated phenotyping of seedcoat color (Calub, 1968; Kehinde et al., 1997). There has been no report on genetic analysis of flower and seedcoat pigmentation in asparagus bean so far.

Flower and seedcoat coloring is in some cases highly related. Saunders (1960) reported that purple flowers were associated with self-colored or pigmented seedcoats, whereas white flowers were associated with cream/white seedcoat in general. A general flower color factor C has been mapped onto the fourth linkage group of ssp. unguiculata based on amplified fragment length polymorphism (AFLP) markers (Menéndez et al., 1997); however, the location of genes conferring seedcoat color still remains unknown. In this article, we report the inheritance and mapping of the genes controlling flower and seedcoat color in asparagus bean based on our newly constructed asparagus bean reference genetic map (the “ZZ” map), which is enriched with expressed sequence tag (EST)-derived SNPs and SSR markers (Xu et al., 2011).

Materials and Methods

Plant materials included ‘ZN016’, a landrace of asparagus bean originating from southern China, ‘Zhjjiang 28-2’, a commercial cultivar in China, their F1, F2, and the F7:8 generation of RILs population consisting of 209 lines. ‘ZN016’ is white-flowered and cream-seedcoated, whereas ‘Zhjjiang 28-2’ has purple flowers and a brown seedcoat. A completely randomized block design was used having two replicates. For each line, eight to 10 seeds were sown but only four were retained after seedling emergence.

The color of the flower and seedcoat was scored visually. Given that not all the lines flowered at the same day and that color of aged flowers may be confusing, data were...
recorded daily for freshly flowered lines until the latest flowering line had flowered.

Basic statistical analysis, including frequency distribution, chi-square test, and analysis of variance, was conducted with STATISTICA 5.5. The segregation data of each trait was subjected to a 1:1 model, with a chi-squared value of 0.17 and 0.04, respectively. These data were subsequently used in genetic mapping. As a result, the genes controlling flower and seedcoat color were mapped onto the common bean–soybean synteny (McClean, P.E., S. Mamidi, M. McConnell, S. Leleji, O.I. 1972. Apparent preference by bees for different colors in cowpeas. Euphytica 14. UTA, Ibadan, Nigeria.


