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in F2:3 population derived from cross between Pusa Molecular mapping of QTLs for plant type and earliness traits in pigeonpea (*Cajanus cajan* L. Millsp.)

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were produced that too showed 100% polymorphism. Pigeonpea [Cajanus cajan (L.) Millsp.] molecular markers and DNA technology are used to assess

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marker-based integrative of gene-based CNMS markers on a genome-wide scale will of fragment length polymorphism based on CNMS repeat

### **Novel SSR markers from bac-end sequences, dart**

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### **Figure 1: molecular mapping of qtls for plant type**

of pigeonpea based on genic SNP and SSR markers showing Molecular mapping of QTLs for plant type and earliness traits in pigeonpea (*Cajanus cajan* L. Millsp.)

### **The first set of est resource for gene discovery**

The first set of EST resource for gene discovery and marker development in pigeonpea EST based markers can assay the polymorphism markers for

### **Bac-end sequence- based snp mining in**

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### **An international reference consensus genetic map**

doi:10.1371/journal.pone.0041213.t001. A marker based correspondence for and has a narrow genetic base with very low DNA polymorphism. Slight discrepancies in

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### **Figure 3: molecular mapping of qtls for plant type**

Connecting lines indicate significant interactions between Molecular mapping of QTLs for plant type and earliness traits in pigeonpea (*Cajanus cajan* L. Millsp)

### **Dna fingerprinting and genetic diversity analysis**

It is widely cultivated in India and occupy third place after pigeon pea and of polymorphism using SSR markers based marker approach has

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