Genetic control of nodulation specificity in *Medicago truncatula*

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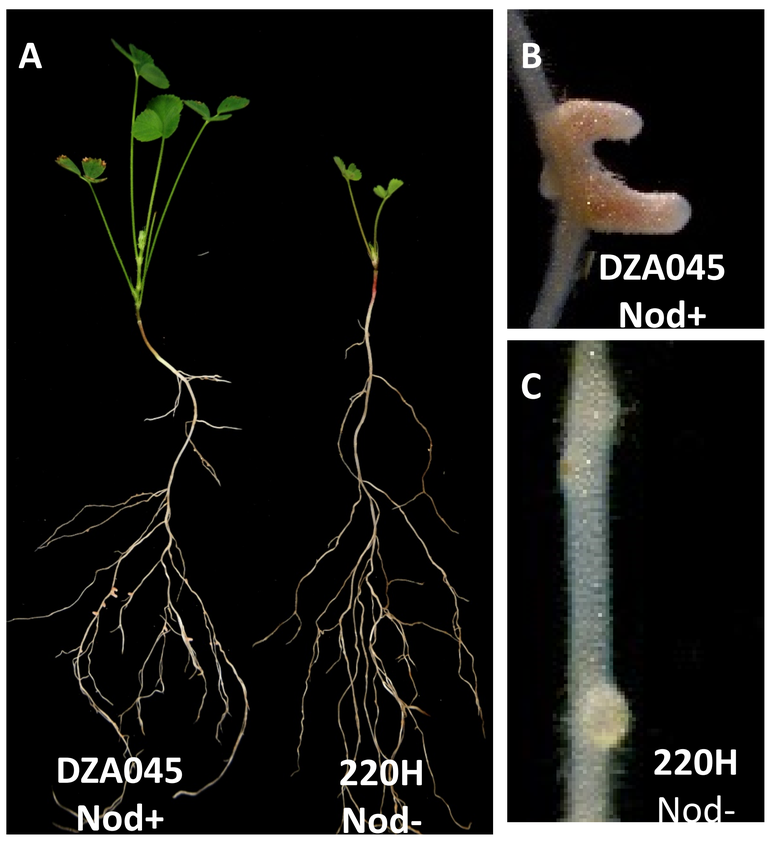
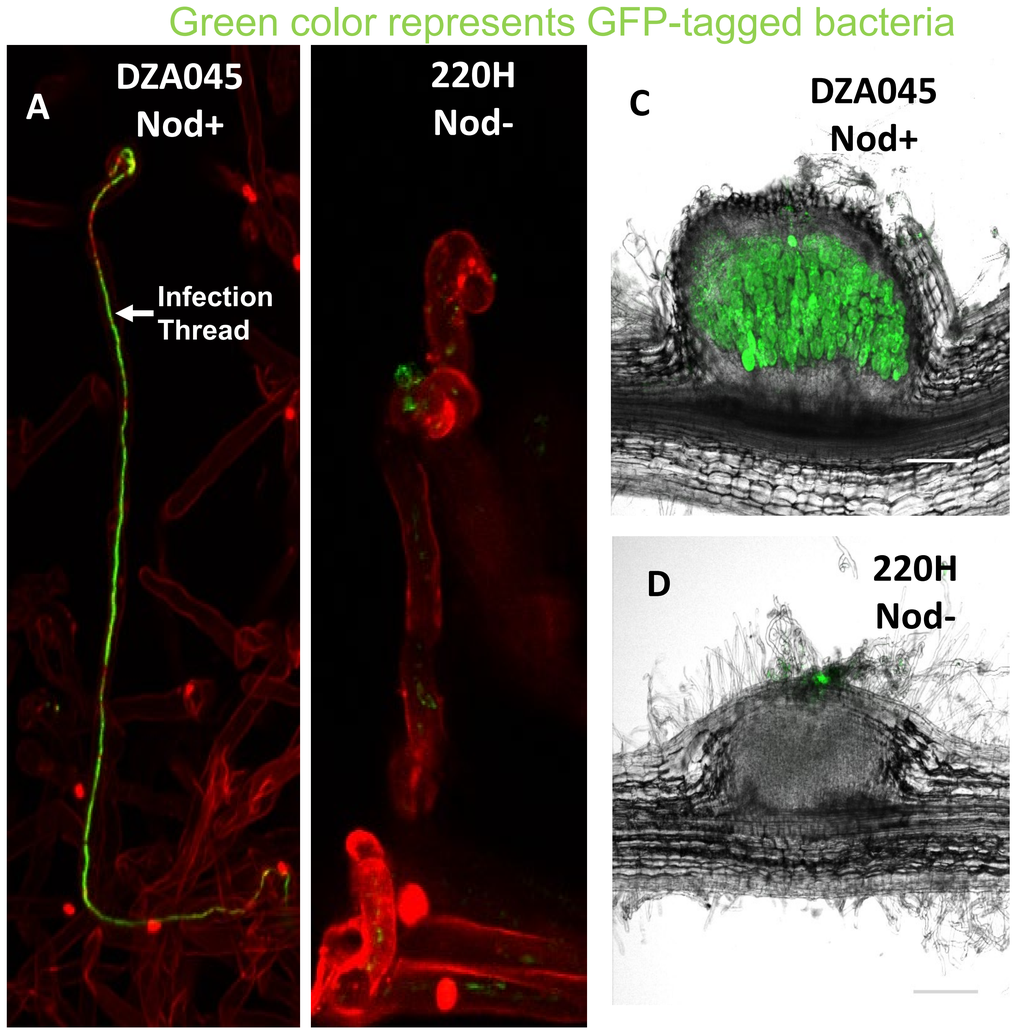
Abstract Legumes can form root nodules through interaction with soil bacteria known as rhizobia. Within the root nodules, bacteria can convert atmospheric nitrogen into ammonia that can be used by the plant. Development of this symbiotic relationship is highly specific, depending on host and bacterial genotypes. Incompatibility occurring at early phases of the interaction can prevent bacterial infection and nodulation. Genetic control of symbiosis specificity is complex, involving various genetic and molecular mechanisms. The objective of this project is to identify and characterize host genes that control nodulation specificity in *Medicago truncatula*.

1. Identification of plant genotypes with differential nodulation phenotypes with the bacterial strain ABS7



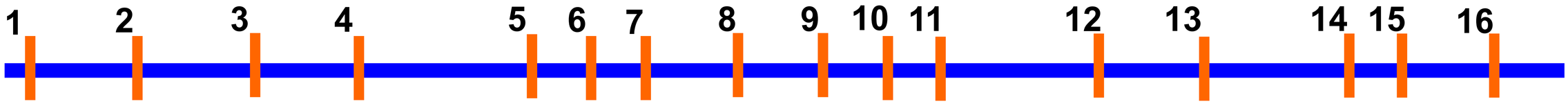
2. Nod- phenotype is caused by host resistance to infection

Green color represents GFP-tagged bacteria



3. Mapping the underlying genetic locus in an F2 population

- ~1,500 F2 plants were screened and the Nod-/Nod+ fits the 3:1 ratio.
- A single dominant locus restricts nodulation by *S. medicae* ABS7 and this locus was mapped within 260-kb on chromosome 8.



Number	Gene ID	Gene description
1	Medtr8g014930	LRR receptor-like kinase
2	Medtr8g014970	LRR receptor-like kinase
3	Medtr8g015010	LRR receptor-like kinase
4	Medtr8g015040	LRR receptor-like kinase
5	Medtr8g015100	LRR receptor-like kinase
6	Medtr8g015120	LRR receptor-like kinase
7	Medtr8g015150	LRR receptor-like kinase
8	Medtr8g015170	LRR receptor-like kinase
9	Medtr8g015190	LRR receptor-like kinase
10	Medtr8g015200	LRR receptor-like kinase
11	Medtr8g015290	LRR kinase family protein
12	Medtr8g015340	LRR receptor-like kinase
13	Medtr8g015370	GRF zinc finger protein
14	Medtr8g015420	cytochrome P450 family protein
15	Medtr8g015430	vacuolar protein sorting-associated protein 26A
16	Medtr8g015450	transcription factor

4. Future work:

- Fine mapping of the locus to narrow down the number of candidate genes.
- Validate the candidate genes.
- Study the mechanism controlling nodulation specificity.