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“Genetic diversity and relationship among faba bean (*Vicia faba* L.)
germplasm entries as revealed by TRAP markers”

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Introduction

- Plant of study- Faba bean (*Vicia faba* L.), an ancient food crop for humans and livestock throughout the world.
- Important crop for protein source.
- Needs more cultivation
- Understanding genetic diversity of all the accessions of Faba bean is critical for cultivation programs.
- TRAP technique for determining diversity was used to analyze the various Faba bean populations.
- TRAP- (Target region amplification polymorphism) a PCR technique that uses a fixed primer with known DNA sequence and pairs it with an arbitrary primer that targets an intron or exon region rich in AT or GC areas.

Results

- Found that the TRAP marker system can be used for germplasm fingerprinting.
- Primer combinations determine the efficacy of polymorphisms.
- A dendrogram showed that all of the accessions from all over the world could be divided into five groups. There was a strong correlation between molecular diversity and geographic origin of the accessions. Used pairwise genetic diversity and bootstrap values to analyze tree.
- TRAP was also used to determine the intra-accession genetic variation. It was found that an original accession had a large genetic diversity and an inbred line had very low genetic diversity.
- Used Shannon's index to analyze data- complex way to measure amount of different types (i.e. species) in a data set.

Discussion

- A preliminary screening of primers would make the TRAP method more efficient
- Used Dice's coefficient because it allowed for only counting the pcr fragment that can be seen.
- The high levels of diversity seem to be due to the plants outcrossing capabilities.

Conclusion

- Understanding what lines are very genetically diverse will lead to better breeding programs.
- TRAP is an efficient and affordable way to screen a population for genetic diversity.
- TRAP is a reliable method to determine the amount of intra-accession genetic diversity.