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This review focuses on trends in genetic improvement of a significant representative forage crop, *Trifolium pratense* (red clover) classified taxonomically into the agronomically outstanding family *Fabaceae*. Red clover breeding is aimed at improving traits like persistency, resistance to biotic and abiotic factors, forage yield and quality characteristics such as protein quality and stability. Isoflavone content in forage is important for cattle reproduction. Interspecific hybridization of red clover with the related wild species *T. medium* was used for the introgression of useful traits into red clover. The breeding strategy for the new variety Pramedi included hybrid plants with different DNA contents, repeated backcrosses with red clover, followed by family selection. New techniques of molecular genetics are becoming available to breeders for

transferring key and complex traits into improved red clover varieties. Techniques such as marker-assisted selection and candidate gene identification can increase the speed and precision with which traits may be selected.

Comparative sequence data analyses helped to identify genes for polyphenol oxidase enzymes and isoflavone synthase in red clover useful for DNA genotyping of individuals and breeding of improved high-quality red clover varieties.

Keywords:

candidate gene; genetic marker; molecular genetics; red clover; wide hybridization

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