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TOWARDS AN EVALUATION OF LEVELS OF MICROSYNTENY BETWEEN *PHASEOLUS VULGARIS* AND *MEDICAGO TRUNCATULA*

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Currently, high density meiotic maps are lacking for several important crop legume species, limiting the resolution with which agronomically and nutritionally important traits can be mapped and ultimately cloned. It has been proposed that the high level of observed synteny between legume species can be exploited to translate gene (and therefore marker) content from soon to be fully sequenced model legume genomes - *Lotus japonicus* and *Medicago truncatula* to less well resourced species such as *Phaseolus vulgaris*[1]. However, good overall macrosynteny is not always mirrored by high levels of local conservation in gene content and order. Thus, we have set out to obtain a semi-quantitative estimate of levels of microsynteny between the model legume *M. truncatula* and *P. vulgaris*. The approach used is to utilise conserved legume family markers distributed across the *Phaseolus* genome developed by University of Aarhus to identify *Phaseolus* BAC contigs orthologous to sequenced regions of the *Medicago* genome. The *P.vulgaris* ('BAT93') BAC contigs are analysed for their gene content with respect to the established gene content of the orthologous region of the *Medicago* genome. We will present an up to date report on the status of this ongoing work.