

or (c) slightly longer (middle stigma only) than lemma as in well developed ones. Only in such cases at least a portion of stigma comes out on opening of floret.

The stigma is usually two in number, the third one is not well developed. The entire stigmatic portion is only 3–4 mm long. Tip of middle stigma of 1.5–2 mm struggles, along with stamens, to come out when lemma and palea widen. Rest of stigma remains inside the closed floret. The receptive stigmatic portion exposed to receive pollen is thus very limited.

The bristle-like hairs of palea (Figure 1 a) are longer than the stigmatic hairs and in an opened floret the exposed but small stigmatic portion is often covered (?) by the hairs on the two keels of palea. Possibly this can act as a barrier preventing stigma from receiving the pollen grains.

Moreover, the reported¹⁰ higher percentage of sterility (70–92%) of pollen may also contribute to the sterility in *B. vulgaris*.

The available evidence points to the imminent danger of extinction of this mysterious species due to (i) the death of clumps after flowering, (ii) the lack of fruit set, (iii) the inherent 'unhealthy'

nature of stigma to receive pollen, (iv) the possible role of bristle-like hairs as barriers preventing pollination, and (v) the high pollen sterility.

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Restriction fragment length polymorphisms of the rRNA genes in some pulses

Recognition and exploitation of variations among genetically divergent groups of germplasm are fundamental in breeding and genetic engineering programmes. Restriction fragment length polymorphisms (RFLPs), random amplified polymorphic DNAs (RAPDs), DNA finger printing, inter simple sequence repeat amplification (ISSR) and amplified fragment length polymorphisms (AFLPs) are powerful tools for studies of plant genetics, evolution, germplasm diagnosis and crop improvement^{1–4}. These techniques allow a direct analysis of the plant genome at the DNA level. RFLP analyses have been used as molecular markers to construct linkage maps of crop plants, to mark quantitative trait loci and to complement phylogenetic relationships in

several plant taxa^{5–7}. rRNA genes, although not with the same impact as chloroplast DNA, have proven to be of tremendous utility in phylogenetic reconstruction⁸. They also provide valuable genetic markers for the analysis of genomic relationships among cultivated species and their wild relatives⁹. The tandem arrays of rDNA repeat units, generally located in the nucleolar organizing regions (NORs) of chromosomes, combine highly conserved gene regions, encoding rRNA, with more variable intergenic spacer regions (IGS). IGS regions, which separate the adjacent transcription units, have been found highly variable in sequence, length and copy number of subrepeats in several plant genera¹⁰. Because rRNA gene

sequences are subjected to relatively rapid rates of concerted evolution¹¹, they produce DNA fragmentation patterns that are highly homogeneous within individuals and among closely related populations or species, yet exhibit characteristic heterogeneity between groups. In comparison, single copy gene markers¹² often tend to exhibit as much within-group as between-group variation in plant species. rRNA polymorphisms can, therefore, constitute useful genetic markers^{9,13}. To achieve a better understanding and to provide molecular evidence for the systematic relationship between and within some populations of *Lablab*, *Dolichos* and *Vigna* species we investigated the polymorphism of the rRNA genes.

Five populations of *Lablab purpureus*,