hybrids were confirmed using polymorphic SSRs during summer 2014. Single plant progeny method was used for development of F_{1-2} populations during *kharif* 2014 which will be used further for mapping QTLs. SSRs available in the public domain were used in the study. DNA was extracted from young leaves of parents and each F_{1-2} progeny by Cetyl trimethylammonium bromide method (Doyle and Doyle, 1990). Polymerase Chain Reaction (PCR) amplifications were performed in a C1000 thermal cycler (BIO-RAD, USA) under the following conditions: 50ng genomic DNA, 1iM each primer, 100iM dNTPs, 1X Taq buffer with 1.5mM $MgCl_2$, 1.5U *Taq* polymerase. The amplified DNA fragments along with 100bp DNA marker were size separated on 8% polyacrylamide gel stained in silver nitrate.

Hybridization was made between GG-20 and CS-19 under field condition during *kharif* 2013 and 762 pollinations were attempted. At 113 probable cross pods were harvested and these probable cross pods were sown in the field for confirmation of true F_1 hybrids during summer 2014. Four SSRs (PM-179, GM-2032, PM-384, PM-15) highely polymorphic between parents were used for confirmation of true F_1 hybrids. Out of 138 probable F_1 plants, 22 were confirmed as true hybrids. These 22 F_1 plants were harvested plant wise and sown further in single row. Similarly, F_{1-2} plants were harvested in single plant basis and a total of 270 F_{1-2} single plant progenies were harvested. Further, polymorphism survey between parents were done using 1273 SSRs collected from public domain. Two hundred thirty two SSRs out of 1273 screened were found polymorphic between GG-20 and CS-19. Genotyping of 179 $F_{1-2,}$ short listed based on availability of sufficient seed (e" 25 kernels per plant) using 232 polymorphic SSRs are in progress. The QTLs will be associated with resistance to stem rot after phenotyping of 179 F_{2-3} progenies under artifically incoculated conditions. These QTLs would be of help in saturated linkage mapping and pyramiding alleles towards improving resistance to stem rot in groundnut more precisely through MAS. QTLs associated with late leaf spot (LLS) and rust (Khedikar et al. 2010) etc. were identified using SSRs and deployed successfully in MAS in groundnut breeding programme.

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Male sterility in a safflower wild species, *Carthamus palaestinus*

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Natural occurrence of male sterile mutants in a progeny-wise self-pollinated population of safflower wild species, *Carthamus palaestinus* (2*n*=24) and transmission of male sterility to progeny generations have been reported in the present paper. The wild species, *Carthamus palaestinus* (2*n*=24) is a sources of resistance to Fusarium wilt and Alternaria leaf spot which are major diseases of cultivated safflower (Pallavi *et al.,* 2007; Prasad *et al.,* 2008). It produces fertile hybrids when crossed to safflower (*C. tinctorius*, 2*n*=24) (Ashri and Knowles, 1960). The first ever occurrence of natural male sterile mutants in *C. palaestinus* was reported in the present paper.

The progeny-wise self-pollinated population of *C. palaestinus* produced male sterile plants. The pollen of male sterile plants was tested for pollen sterility under trinocular microscope. Pollen grains were stained with 1% acetocarmine. The unstained or lightly stained pollen grains were considered sterile while the well stained grains were considered fertile.

The sterile plants were self-pollinated as well sib crossed with the sister fertile plants. Pair-wise progenies were advanced further and tested for male sterility percent and stability of male sterility. All plants were grown under pollination nets as well the flower heads were covered with butter paper bags to avoid pollen contamination through honeybee.

A few male sterile mutants were observed in a large population of *C. palaestiuns* derived through progeny-wise self-pollination. The initial sterile plants were devoid of pollen and did not produce seed upon self-pollination but produced abundant seed upon sib-crossing with sister fertile plants. The progenies of sib-crosses exhibited complete sterility, partial male sterility and complete male fertility. Complete male sterile plants produced pollen grains; these were unstained and sterile when stained with 1% aceto-carmine as well as of various sizes and sticky. Partially sterile plants had around 70-80% sterile pollen grains, which were smaller than fertile grains and unstained while fertile plants had all uniform sized well stained fertile pollen grains (Fig 1a, b, c). The sterile and partial sterile mutants did not differ from fertile mutants with respect to plant morphology and phenology. Pollen production was abundant in fertile plants as compared to that in partial and complete sterile plants. The male sterile progenies of *C. palaestinus* continued to segregate into complete male sterile, partial male fertile and complete male fertile upon sib-crossing with fertile sister plants in the third consecutive year. The reasons for occurrence of male sterility in *C. palaestiuns* and its stability for possible utilization as a new source of male sterility are being investigated currently.

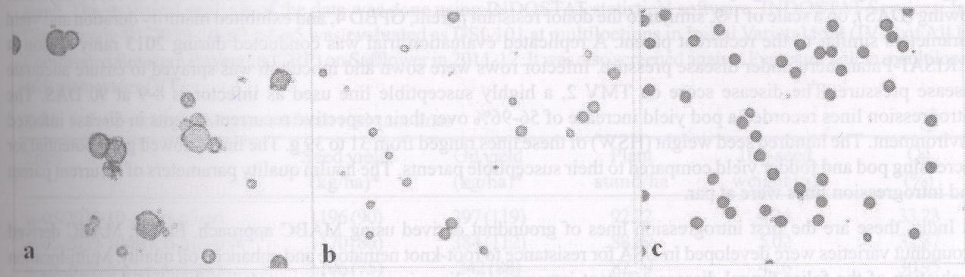

Fig 1. Male sterile mutants in *C. palaestinus*: a) Sterile pollen in complete male sterile mutant; b) Sterile and fertile pollen in partial fertile mutant; c) Fertile pollen in complete fertile mutant

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Evaluation of foliar fungal disease resistant introgression lines of groundnut derived using marker-assisted backcrossing (MABC) approach

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Foliar fungal diseases are important biotic constraints to groundnut production worldwide and account to about 15% of annual pod yield losses in Asia and Africa. Among foliar diseases, late leaf spot caused by *Phaeoisariopsis personata* and rust caused by *Puccinia arachidis* have the greatest impact and they together can reduce pod yield by 50-70% in