Phenotyping for BRPF in common bean

Phenotyping for basal root whorl number can be very subjective and time consuming due to ambiguous basal root positions (Please see *Screening of root whorls* under the *General methods and information* page for more information on basal root whorl number). Phenotyping using basal roots per file (BRPF) is an alternative, accurate representation of the basal root positions because basal root occupancy and range are taken into account, and a map of the root can be drawn from the data collected.

Procedure:
Surface sterilize seeds with 10% bleach solution for 1 minute, then rinse seeds for 1 minute with water. Place seeds (micropyle side should be downward) on germination paper or a similar material, roll up the paper, and place in a beaker. Fill the beaker with about 6 centimeters of 0.5 mM calcium sulfate ($CaSO_4$) solution. Place plastic-wrap over the beaker and germination paper rolls to prevent desiccation and contamination. Place the beaker in a germination chamber (at 28 degrees C) for three to four days. The majority of basal roots should be at least 1 centimeter long.

Roots of *Phaseolus vulgaris* all have 4 basal root files that run parallel to the hypocotyl, and can each have a root occupancy (i.e. number of basal roots per file) of 1 to 4 basal roots. For each file, the number of basal roots is recorded (Fig.1). With this data, the average BRPF, maximum BRPF (which is equivalent to the basal root whorl number (BRWN)), minimum BRPF, BRPF range, and total basal root number can be calculated.

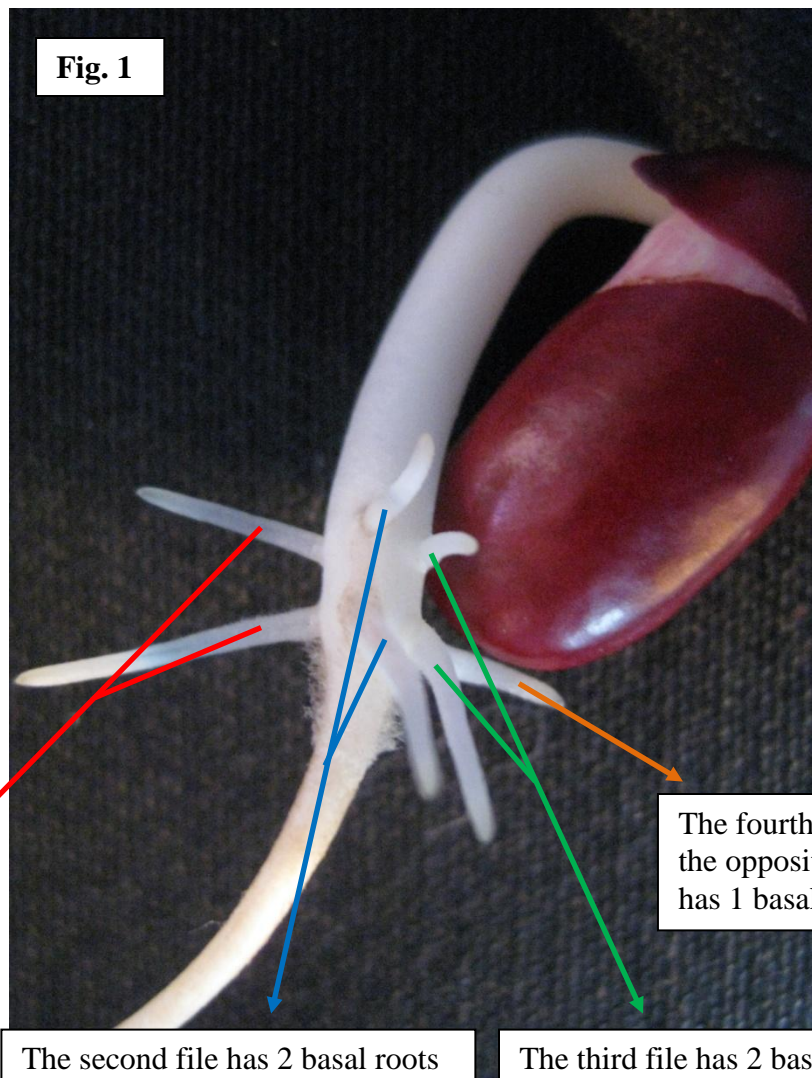Example:

BRPF:
File 1 = 2
File 2 = 2
File 3 = 2
File 4 = 1

Average BRPF = 7/4 = 1.75

Maximum BRPF = 2

Minimum BRPF = 1

Total basal root number = 7

Fig. 1

The fourth file (on the opposite side) has 1 basal root

The first file has 2 basal roots

The second file has 2 basal roots

The third file has 2 basal roots