

ADVANCES IN PLANT TROPISMS

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Cover Illustration: In the last few decades, our understanding of the mechanisms of tropistic responses has advanced through the use of insightful strategies and genetic/genomic techniques. Although the most commonly used system is the seedling hypocotyl (phototropism) and root (gravitropism and hydrotropism) of Arabidopsis thaliana (L.) Heyn., the use of novel treatments and other systems have provided unique contributions to the field. Advances have also been made through the availability of microgravity via spaceflight and parabolic flight and the simulated microgravity of clinorotation. Even so, most of the discoveries expanding our knowledge of tropistic mechanisms have come from fundamental, ground based experiments spurred by the imagination and innovation of our research community. Image credits: (top) Arabidopsis seedlings in the background showing root skewing and in the foreground Arabidopsis roots curving in response to gravity (courtesy of Patrick Mason); (bottom, left to right) mutant Arabidopsis inflorescence stem (courtesy of Sarah Acomb and Sarah Wyatt); longitudinal section through a vertical and a horizontally reoriented maize pulivini stained for starch (courtesy of Imara Perera and the NSCORT at North Carolina State); Arabidopsis seedlings from a BRIC 16 space experiment to study the role of the cytoskeleton in tropisms (courtesy of John Kiss); the anticlockwise (left-handed) coiling of the root of the spr1 Arabidopsis mutant. (courtesy of Fernando Migliaccio). Cover design: Adrianna Sutton (http://www.adriannasutton.com).

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Abbreviations

- 153 **Miscellaneous:** AFLP, amplifi ed fragment length polymorphisms; a.s.l., above sea level; bp, base pair; B P, before present; BSA, bovine serum albumin; cpDNA, chloroplast DNA; CTAB, hexadecyltrimethylammonium bromide; cv., cultivar; ddH₂O, double-distilled water; dNTP, deoxyribonucleotide E.C., Enzyme Commission; EDTA, ethylene diamine
- 161 tetra-acetic acid; f. sp., forma specialis; indels, insertions and deletions; ITS, internal transcribed spacer; LM, light microscopy;
- 175 mya, million years ago; PAGE, polyacrylamide gel electrophoresis; PCR, polymerase chain reaction; RAPD, random amplifi ed polymorphic dimorphism; SDS, sodium dodecyl sulfate; SEM, scanning electron
- 183 microscopy; s.l., sensu lato; s.s., sensu stricto; subsp., subspecies; TEM, transmission electron microscopy

Genetics: *A*, mean number of alleles per locus; *D*, mean genetic distance; CI,

- <u>194</u> consistency index; *F*, fi xation index; F_{IT} , total deviation from Hardy-Weinberg expectations; F_{ST} , genetic diversity among populations; F_{IS} , inbreeding within populations; G_{ST} ,
- 203 the proportion of genetic diversity among populations; *H*_e, Hardy–Weinberg expected heterozygosity; *H*_o, observed heterozygosity; M P, most parsimonious tree; *n*, individual chromosome number; Nm, mean number of
- 215 migrants per generation; *P*_p, percentage of polymorphic loci; RI, retention index; *x*, base chromosome number
- Statistics and math: ANOVA, analysis of variance; CV, coeffi cient of variation; df, degrees of freedom; *N*, number of individuals; *p*, probability; *P*, level of signifi cance; PCA, principal components analysis; *r*, coeffi cient of
- 235 correlation; SE, standard error; SD, standard deviation

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