

# Index

## A

- ABA. *See* Abscisic acid (ABA)
- Abaxial layer, 127
- ABC transporter, 366
- Abiotic stress, 71
- ABNORMAL LEAF SHAPE 2 (ALE2), 129
- Aboveground, 328, 332, 343
- Abscisic acid (ABA), 184–187, 200, 203
- Accessions, 327, 342, 343
- Accuracy, negative, 13, 16
- Acetabularia, 23
- Actin
- cytoplasmic, 27
  - filamentous, 27, 29
  - structured, 25, 27, 29
- Actinorhizal plants
- CCaMK, 268
  - DMI1, 268
  - DMI2, 268
  - Frankia, 268
  - Glomus intraradices*, 268
  - LCOs, 268
  - Myc factor, 268
  - Nod factors, 268
  - short chitin oligosaccharides; COS, 268
- Adaxial cell layer, 127
- Aequorin, 29
- AGAMOUS (AG), 124, 126
- AGO9, 127
- Airborne signals, 94, 97
- Aleurone, 20, 21, 172, 174, 183, 185–188
- Alkaloids, 200, 201
- Amides, 258, 271
- Amino acids
- shoot-to-root, 100, 101
  - systemic, 100
- Ammonia, 337, 341
- Amoeba, synthetic, 24
- Amylase, lateral, 20
- Amyloplast(s), 53–59, 61, 62
- Antagonism, 200, 206
- Anther(s), 130, 177
- Anthocyanin, 21
- Antipodal, 172, 174, 176–177
- Antirrhinum*, 125, 126
- APETALA 1 (AP1), 124, 125
- APETALA 2 (AP2), 124
- APETALA 3 (AP3), 124, 126
- Aphid, 198, 200
- abiotic stresses, 97
  - biotic, 97
  - local, 98
  - systemic signals, 98
- Apoplast, 215, 217, 218, 220–223
- Apoptosis, 173, 177, 181
- Apospory, 127
- Applications, 246–247
- ARABIDOPSIS CRINKLY 4 (ACR4), 129, 130
- Arabidopsis thaliana*, 123, 327, 331–343
- Arbuscular mycorrhizal fungi, 362–364, 370
- ARF3, 127
- ARF4, 127
- Aromatics, 204
- Associations, 143
- Autophagosomes, 184

Auxin(s), 39, 42, 46, 53, 59–62, 200, 204  
 plasmodesmatal, 32  
 positive, 21  
 Azelaic acid, 45

## B

*Bacillus subtilis*, 332, 333, 338, 341  
 Bacteria, 327–344  
 BAM receptors, 129  
 (E)- $\beta$ -Caryophyllene, 205  
 Behaviour, 16, 17, 20, 22, 24, 26, 28, 32  
 Below-ground, 205, 328, 332  
 Benzenoids, 202, 204  
 Benzylcyanide, 198  
 Betaproteobacteria  
 AHLs, 258, 262  
 BraI/R, 262  
 Burkholderia, 256, 262  
 Cupriavidus, 256  
 LuxI, 258, 262  
 LuxR, 258, 262  
 3-oxo-C12-HSL, 262  
 Beta-rhizobia, 255, 256, 259, 261, 266, 274  
*Burkholderia*, 256, 257, 266  
 Bet hedging, electrical, 16  
 $\beta$ -glucosidase, 199  
 Biocommunication, 1–8  
 Biofilm(s), 353, 354  
*Burkholderia*, 257, 265, 266  
 core nod factor, 265, 266  
 flavonoid, 266  
 Nod factor, 265, 266  
 Biotrophs, 37, 44, 46, 76  
 Bistable, 14, 15  
 BRASSINOSTEROID INSENSITIVE 1  
 (BRI1), 129  
 Brassinosteroid receptor, 129  
 Brassinosteroids, 39, 43, 46, 203  
 BRI-associated kinase 1, 352  
 Bruchnins, 198  
*Burkholderia cepacia*, 350  
 2,3-butanediol, 338, 339

## C

Ca<sup>2+</sup>  
 actin, 29, 31  
 cytoplasmic, 29–30  
 Caeliferin, 199  
 Callose, 43, 128, 175  
 Camalexin, 76  
 Carpel(s), 124  
 Catalase, 187

C2-domain, 129  
 Cell-autonomous, 94, 108  
 Cell-non-autonomous, systemic response, 94  
 Cells, 51–61  
 Cellularization, 176, 183  
 Cellulase, 215, 224  
 Cellulose biosynthesis  
 CesA, 149  
 CSL genes, 149  
 Cell wall, 124, 125, 129, 131  
 Cell wall-degrading enzymes  
 arabinogalactan endo-1,4-beta-galactosidase, 146  
 1,4- $\beta$ -glucanase, 146  
 endoxylanase, 146  
 pectate lyase, 146, 147  
 polygalacturonase, 146  
 Cell wall-modifying enzymes  
 expansin, 142, 147  
 expansin-like protein, 147  
 pectin acetyltransferase, 149  
 pectin methyltransferase, 148  
 Central cell, 172, 176, 179  
 Central zone (CZ), 124  
 CENTRORADIALIS (CEN), 125  
 Cereals, 172, 183–186  
 Chalaza, 128  
 Charcoal, 330, 331, 336  
 Chitin  
*burkholderia*, 265  
 chitin receptor, 269  
 COS, 268, 269  
 LCO structure from the mycorrhizal symbiont, 265  
 LysM domains, 269  
 LysM-RLK/NFP, 264, 269  
 Myc, 268, 269  
 NFR1/NFR5, 264, 269  
 nod factor, 264, 265, 268, 269  
 Chitin molecules  
 lipochitooligosaccharide (LCO), 264  
 LysM domain, 264, 269  
 LysM-RLK/NFP, 264, 269  
 mycorrhizal symbiosis, 264, 268, 269  
 NFR1/NFR5, 264, 269  
 nod boxes, 264  
 NodD, 264, 265, 268  
 nod factor, 264, 265, 268, 269  
 Chloroplast, 68, 69, 71  
 Chorismate mutase, 224–225  
 CLAVATA3 (CLV3), 128, 129  
 Clotho, 176  
 CLV1, 128–130  
 CLV2, 128, 129

CO<sub>2</sub>, 338, 340–342  
 Coadaptatory interaction, 367, 369, 371  
 Cocultivation, 327, 332, 336–338,  
 342, 343  
 Cofilin, 29  
 Collagen, 24–26  
 Columella cell(s), 54, 55, 57–61  
 Communication, 1–8  
 Communication highway, 344  
 Communicative competence, 5  
 Conformational spread, 27–29  
 CONSTANS (CO), 125  
 Context, 4  
 Conventional farming, 367, 371  
 Cooperativity, 27–29  
 Coordination, 2  
 Copy numbers, intrinsic, 14  
 Coronatine, 39  
 Corpus, 124  
 CORYNE (CRN), 129  
 CRINKLY4 (CR4), 129  
 Cyst nematodes  
*Globodera rostochiensis*, 146  
*Globodera spp.*, 144  
*Globodera tabacum*, 149  
*Heterodera schachtii*, 146–149  
*Heterodera spp.*, 144  
 Cytochalasin D, 31  
 Cytokinins, 39, 43  
 Cytoplasm  
 micro-domains, 32  
 structured, 22–27

**D**  
 Decision, 2  
 Defence(s), 3–6, 8, 92–97  
 plant, 197–207  
 Defensive proteins  
 arginases, 316  
 cysteine protease, 316  
 protease inhibitors, 316  
 threonine deaminases, 316  
 DEFICIENS (DEF), 126  
 DETORQEO (DOQ), 129  
 Dimethyl disulfide (DMDS), 337  
 Direct defense, 197, 198, 200, 201, 204,  
 205, 207  
 Division, 19, 29  
 DMDS. *See* Dimethyl disulfide (DMDS)  
 DNA  
 fragmentation, 178, 184, 187, 188  
 methylation, 127

Dormancy, stochastic, 19, 21  
 Dose response, 19  
 Double fertilization, 172, 179

**E**

Effector, 214–216, 219–220, 224–225  
 Effector proteins, 351–352, 357  
 Egg cell, 124, 127, 172, 176, 179  
 Electrical, 93, 94, 108  
 Electric potential waves (EPWs), 93–94  
 Electron cloud, structured, 28  
 Elicitors, 75  
 β-glucosidase, 310  
 bruchins, 310  
 caeliferins, 306, 309, 312  
 fatty acid-amino acid conjugates (FAC),  
 305, 306, 308, 309, 312, 315, 321  
 glucose oxidase, 310  
 inceptin, 306, 308, 309, 312, 321  
 volicitin, 306  
 Elicitors(eliciting), 199  
 Embryo, 17, 171, 172, 175–177, 179–186, 188  
 Embryo sac, 172, 174–177  
 Embryo surrounding region (ESR), 183, 184  
 Emission, 327, 328, 330, 331, 334, 338,  
 340, 342  
 Endodermis, 54–56, 60  
 Endosperm, 172, 174, 179, 181–186, 188  
 Endothecium, 130  
 Entropy, structured, 27, 28, 30  
 Epidermis, 124–127, 129, 130  
 EPWs. *See* Electric potential waves (EPWs)  
 ERECTA (ER), 129  
*Erwinia spp.*, 350  
*Escherichia coli* O157:H7, 350  
 ESR. *See* Embryo surrounding region (ESR)  
 Ethylene (ET), 39, 41, 43, 45, 46, 77, 184,  
 199, 355–356  
 Euglena, 23  
 Evolution, 124, 130, 218, 222, 223, 227  
 Extrafloral nectar, 303, 304, 318, 320, 321  
 EXTRA MICROSPOROXYTES1 (EMS1), 130  
 EXTRA SPOROGENOUS CELLS (EXS), 130

**F**  
 F-actin, 56–58  
 Fatty acid, 67, 68, 75  
 Fatty acid conjugates(FACs), 199  
 F-box protein, coronatine, 71–72  
 Feedback, 13–21, 32  
 FEI1, 130

- FEI2, PERK4, 143  
 Female gametophyte, 171–176, 179, 183  
 Feronia, 179, 180  
 Fertilization, 124, 172–175, 178–184  
 Flagellin insensitive 2 (FLS2), 351, 352, 355  
 Flavonoid, 362  
 Floral development, 123–131  
 Floral induction, 123, 125  
 Floral meristem (FM), 123–126, 129  
 Floral organs, 123, 124, 127, 129  
*FLORICAULA (FLO)*, 126  
 Florigen, 102–104, 125, 131  
 Flower, 124, 126  
 Flowering, 90, 102–108  
 FLOWERING LOCUS T (FT), 102–103, 125  
 FLS2. *See* Flagellin insensitive 2 (FLS2)  
 Food-borne bacterial poisonings, 349  
 Forisomes  
   heating, 97  
   wounding, 97  
 FT. *See* FLOWERING LOCUS T (FT)  
 Fungi, 71, 78
- G**
- GA. *See* Gibberellic acid (GA)  
 Gametes, 172, 176, 182  
 Gametophyte(s), 124, 127, 128, 172, 173  
 Gas chromatography/mass spectrometry (GC/MS), 330, 331  
 Gel(s)  
   cytoplasmic, 24, 27, 29  
   intelligent polymer, 24  
   microdomains, 24  
   phase transition(s), 27–32  
   structured, 24, 28–32  
   synthetic polymer, 28  
 Gelatin  
   phase change, 28  
   vicinal, 25  
 Gelsolin, 29  
 Gene activation, 13  
 Genetic circuitry, 14, 17–21  
 Germination, 172, 174, 178, 179, 182, 184–188  
 Gfa2, 179, 180  
 Giant cells, 146, 149  
 Gibberellin(s), 19, 20, 39, 43, 46, 203  
 Gibberellic acid (GA), 185–188  
 Glandular, 202, 203  
 GLOBOSA (GLO), 126  
 Glucose oxidase (GOX), 206  
 Glucosinolates, 74, 200, 201  
 GLVs. *See* Green leaf volatiles (GLVs)  
 Glycerol-3-phosphate, 45  
 GOX. *See* Glucose oxidase (GOX)  
 Grafting, 91, 99, 102, 103  
 Gravimorphogenesis, 52, 61  
 Gravitropism, 51–61  
 Green fluorescent protein (GFP), 126, 129  
 Green leaf volatiles (GLVs), 45, 202, 203  
 Guard cell, 22  
 Gynoecium, 124
- H**
- H-bonds, 24  
 HCN, 337  
 Hemibiotrophs, 37  
 Herbivore induced plant volatiles (HIPVs), 198, 199, 202, 204–207, 317–319  
 Herbivores, 197–207  
   aphid, 283, 294  
   attract and kill, 295  
   attractants, 287, 295  
   disruption of host finding, 295  
   *Euschistus heros*, 294  
   feeding mechanisms, 304, 305, 318  
   generalists, 304  
   mass trapping, 295  
   *Nezara viridula*, 294  
   Plant-based volatiles, 295  
   push-pull, 295  
   secondary metabolites, 303, 304, 314, 316  
   specialists, 304  
 Heterodimers, 129  
 HIPVs. *See* Herbivore-induced plant volatiles (HIPVs)  
 Histogenic layers, 124–126, 129  
 Homeotic genes, 124  
 Homodimers, 129, 130  
 Hormonal, 19, 21  
 Hormone(s)  
   airborne signals, 97  
   auxin, 225  
   clavata-like element, 219–221  
   c-terminally encoded, 222  
   cytokinin, 225, 227  
   ethylene, 227  
   phytohormones, 199, 203  
 Host plants, *Brassica oleracea*, 282, 290, 293  
 HPL. *See* Hydroperoxide lyase (HPL)  
 HR. *See* Hypersensitive response (HR)

Hydroperoxide lyase (HPL), 318, 320  
 Hypersensitive response (HR), 41, 173, 182,  
 198, 200, 206, 354, 357

## I

Immune system, 351, 356  
 Immunity, 214, 215  
 Inceptin, 199  
 Indirect defense, 197–207  
 Indole-3-acetic acid, 42  
 Induced systemic resistance (ISR), 40, 41,  
 44, 96  
 Inflorescence meristem (IM), 124–126  
 Information, 11–32  
 Information loss(es), 16, 17  
 Inorganic volatiles, 328  
 Insectoral secretions, 75  
 Integrated pest management  
   natural enemies, 281, 295  
   optimization of lures, 295  
 Integuments, 129, 182, 183  
 Interactions, 1–3, 5, 6, 8  
 Inter-cell layer communication, 129  
 Intercellular communication  
   infection spread, 240–241  
   intercellular virus communication:  
     macromolecular signals, 242–244  
   intercellular virus communication: small  
     molecule signals, 241–242  
   RNA silencing, 242–243  
   silencing suppression, 243–244  
 Intercellular signaling, 123–131  
 Interorganismal signaling  
   cross protection, 244, 245  
   synergy, 244, 245  
   vectors, 244  
 Interorganismic, 1, 5–6  
 Interpretation, 4  
 Interspecies hybridization, 184  
 Intracellular viral communication  
   encapsidation, 236  
   mRNA Production, 232–235  
   protein processing, 235  
   replication, 232–236  
   translation, 232–236  
   uncoating, 236, 237  
 Intracellular virus-host communication  
   movement and coat proteins, 237, 238  
   replication complexes and inclusion bodies,  
   237–238  
 Intracellular virus-host interactions  
   DsRNA-dependent kinase, 238–239  
   hypersensitive response, 239–240

Intraorganismic, 1, 2, 5–8  
*In vitro*, 130  
 Isoprene/isoprenoids, 203

## J

Jasmonate-Isoleucine(JA-Ileu), 200, 207  
 Jasmonates/Jasmonic acid (JA), 39–41, 43–46,  
 92, 199, 200, 355–356  
   methyl jasmonate (MeJA), 68, 70, 72,  
   74, 79  
 JA-isoleucine, 312, 313  
 OPDA, 68, 70, 71, 79  
 transport phloem, 93

## K

K<sup>+</sup>, structured, 30  
 Kinase, 128–130  
 Kinase assay, 130  
 Kin recognition, 158, 162–164  
 Kiss of death (KOD), 181  
 KNOTTED1, 125

## L

Lachesis, 176  
 Leaf patterning, 127  
 Learning, 16  
 Leucine-rich repeat (LRR), 128–130  
 Ligand, 124, 130, 131  
 Light, 12, 21, 32  
 Linalool, 204  
 Lipid transfer protein, 95  
*Listeria monocytogenes*, 350, 357  
 L1 layer, 124  
 L2 layer, 124, 126  
 L3 layer, 124, 126

## M

MADS-box, 124  
 Maize, 175, 176, 181, 184, 188  
 MAP kinase, 17  
 Mechanoresponses, 79  
 Mechanostimulation, 79  
 Mechanotransduction, 71  
 Medicago, 226  
 Megaspore, 127, 172, 174–175  
 Megaspore mother cell (MMC), 127, 128  
 Meiosis, 127, 130, 174–175  
 Memorized information, 2  
 Memory, molecular, 16  
 Meristem, 219–221, 226, 227

- MeSA. *See* Methyl salicylate (MeSA)
- Mesophyll, 22
- Message(s), 11–13
- Messenger substances, 3, 5, 6
- Metabolons, 23
- Metacaspases, 174, 181
- Methods, 245–246
- Methyl jasmonate, 39, 41, 45
- Methyl salicylate (MeSA), 38, 45, 204, 206
- Microbial evenness, 368, 370, 371
- Microbiome, 274
- microRNA (miRNA), 3, 7, 8, 14, 15, 42, 99, 106, 125
- Microsporocytes, 130
- miRNA165/166, 125, 127
- Mites
  - Neoseiulus californicus*, 287
  - Neoseiulus womersleyi*, 287
  - Phytoseiulus persimilis*, 287
  - Tetranychus*, 287
  - Tetranychus kanzawai*, 287
  - Tetranychus urticae*, 287
- Mitogen-activated protein kinase, 352, 355–356
- Monoterpenes, 203
- Myc factor, 364
- Mycorrhizal, 164–165
- N**
- Natural enemies
  - parasitoids, 282, 288–295
  - predators, 282–288, 295
- Necrotrophs, 37, 43, 44, 46, 71, 72, 76–77
- Nematode, 361, 364, 365, 369
  - globodera, 214, 217, 219
  - heterodera, 214, 217, 218
  - meloidogyne, 214, 216
  - pratylenchus, 216, 218
- Nematode effectors
  - cellulose binding protein, 147
  - Hs19C07, 148
- Network, cytoplasmic, 22–24
- Neurospora, 23
- Nitrate
  - local response, 100
  - root-to-shoot signalling, 100
  - shoot-to root signal, 100, 101
  - systemic, 100
  - systemic N signalling, 100
- Nitric oxide (NO), 176, 178, 185–187
  - root-to-shoot signalling, 96
  - wound response, 96
- Nitrogen fixation
  - bacteroids, 262, 271–274
  - determinate nodules, 271, 273
  - indeterminate, 271–273
  - NifA, 270, 271
  - nif gene regulation, 270
  - NifL, 270
  - nitrogenase, 270, 272
  - terminal differentiation, 271
- NO. *See* Nitric oxide (NO)
- Nod factor, 362, 364
- Nodulation, 255, 256, 262, 266, 268, 270, 273, 274
- Noise
  - extrinsic, 14, 17, 18, 20
  - intrinsic, 14, 18
  - positive, 14, 15, 17–21, 25, 32
  - probabilistic, 13, 19, 21, 22
  - suppression, 17
- Noncell-autonomous, 109, 125–127, 129
- Nonselself, 2, 5
- Nortia, 179, 180
- Norway spruce, 181
- Nucellus, 127, 128, 172, 175–177
- Nucleases, 178, 182, 187, 188
- Nutrient starvation, long-distance signalling, 98–101
- O**
- Olfactometer, 204
- Oligogalacturonide (OG), 143, 147
- Ontogenesis, 130
- Organic, volatiles, 328, 338
- Organic farming, 367, 369, 371
- Organization, 2, 7
- Organogenesis, 125, 128, 130
- Orthostichies, systemic signal, 91
- Oscillations, 24, 28
- Ovule, 124, 125, 127, 129
- Ovule integuments, 129
- Oxylipin, 67, 68, 78
- P**
- Parasite, 213–215, 217–220, 223–225
- Parasitic weed, 363
- Parasitoid(s), 197–199, 201, 204, 206
  - Cotesia glomerata*, 288, 289, 293

- Cotesia* spp, 288  
 homoterpene (E)-4,8-dimethyl-1,3,7-nonatriene, 293  
 Parasponia, 269  
 Pathogen(s), 90, 92, 94–97, 214, 215, 219–220, 224, 225  
 Pathogen-associated molecular patterns, 351  
 Pathogenesis-related genes, 355  
 Pattern recognition receptors (PRRs), 351, 353  
 PCD. *See* Programmed cell death (PCD)  
 Peripheral zone (PZ), 124  
 Peroxisomes, 68, 69  
 Petal, 124, 125  
 PGPR. *See* Plant growth promoting rhizobacteria (PGPR)  
 Phalloidin, actin, 31  
 Phaseolus, 181  
 Phloem, 89–109, 125  
 Phosphatase, 128  
 Phosphate, long-range signalling, 98–99  
 Photoperiod, 125  
 Phytoalexin, 364  
 Phytoanticipins, 37, 38  
 Phytohormones, 38, 39, 43, 47, 124  
*Picea abies*, 181  
 PIN, 60, 61  
 PIN1, 59, 60  
 PIN2, 59  
 PIN3, 59–61  
 PIN4, 59  
 PIs. *See* Proteinase(protease)inhibitors (PIs)  
*PISTILLATA (PI)*, 124, 126  
 Placental habit, 173  
 Placental tissue, 124  
 Plant defense, 67–79  
 Plant growth promoting rhizobacteria (PGPR), 338, 366  
 Plasma membrane, 128  
     cooperative, 28  
 Plasmodesmata (PD), 31–32, 124–128  
 Polarity, positive, 15  
 Pollen, 17, 172, 174, 177, 178, 180, 181  
 Pollen mother cells (PMCs), 130  
 Pollen-pistil interactions, 174, 178  
 Pollen tube, 176–180  
 Pollination, 178, 179  
 POLTERGEIST (POL), 128  
 Polyhydroxybutyrate (PHB)  
     bacteroids, 271–273  
     infection thread, 271  
     nitrogenase, 272  
 Polyploidization, 184  
 Polyribosomes, 23  
 Postembryonically, 123  
 Predaceous insects  
     *Coccinella septempunctata*, 283  
     *Cycloneda sanguinea*, 283  
     *Eriopis connexa*, 283  
     *Hippodamia variegata*, 283  
     *Podisus maculiventris*, 283  
 Predatory mite, 204, 207  
 Priming, extrafloral nectar, 320  
 Probabilistic, 13, 19, 21, 22  
 Profilin, 31  
 Programmed cell death (PCD), 171–188, 356, 357  
 Prokaryotes, 327, 330  
 Promoter, 324–327, 336  
 Proteases, 174, 182, 184, 187, 188  
 Proteinase inhibitors, 44, 74  
 Proteinase(protease)inhibitors (PIs), 200, 201, 207  
 Protein storage vacuoles (PSVs), 185–187  
 Proton transfer reaction/mass spectrometry (PTR/MS), 331  
 PRRs. *See* Pattern recognition receptors (PRRs)  
*Pseudomonas aeruginosa*, 350, 357  
 PSVs. *See* Protein storage vacuoles (PSVs)  
 PTR/MS. *See* Proton transfer reaction/mass spectrometry (PTR/MS)  
 Pyrosequencing, 366–368
- Q**  
*QUIRKY (QKY)*, 129  
 Quorum sensing  
     *N*-acyl-homoserine lactone (AHL), 258  
     autoinducer, 258, 263  
     Burkholderia, 261, 262, 266  
     lux boxes, 258  
     LuxI, 253, 262  
     LuxR, 258, 262
- R**  
 Reactive oxygen species (ROS), 43, 176, 178, 186, 187  
     heat, 94  
     response to wounding, 94  
 Receptor, 215, 219, 220  
     CrRLKL-81, 141  
     FEI1, 141  
     Lec-RLK, 141  
     LRR-RLK, 141  
     LRX, 141

- Receptor (*cont.*)  
 Mid2, 140  
 PERK, 141  
 THESEUS-81, 143  
 WAK1, 143  
 WAK2, 141, 143  
 wall associated kinase (WAKs), 143  
 Wsc1, 140  
 Wsc2, 140  
 Wsc3, 140
- Receptor-like kinases (RLKs), 128–131
- Receptor-like protein kinase2 (RPK2), 129, 130
- Recognition  
*Aeschynomene indica*, 267  
*Arachis hypogea*, 267  
 CCaMK, 267, 269  
 crack entry, 267  
 cytokinin, 267  
 infection threads, 257, 267  
 NodD, 268  
 root hair invasion, 267  
 symbiosome, 267
- Repeats, 8
- Reproduction, male sterile, 71, 72
- Reproductive organs, 126
- Resource allocation, 198, 200
- Response(s), 13–17  
 behavior, 2, 4, 7  
 heat response, 97  
 hypersensitive response, 94  
 immune response, 94  
 local response, 94, 98, 100  
 stochastic, 13  
 systemic response, 92, 94–97  
 probabilistic, 13  
 wound response, 92, 93, 96
- Retroelements, 8
- R-genes  
 Bph14, 309  
 Mi-1, 309  
 Vat, 309
- Rhizobacteria, 332–338, 342
- Rhizobia, 220, 226–227, 362–365, 370
- Rhizosphere, 332, 340, 362, 363, 365, 370  
 endorhizosphere, 257  
 exorhizosphere, 257
- Rib meristem, 124
- RNAi, 3
- RNA silencing, 8
- Root(s), 157–166, 214, 216–218, 220–224, 226  
 hairs, 17, 21  
 lateral, 17, 20, 21  
 reliable, 17
- Root exudate, 361–367, 370, 371
- Root-knot nematodes  
*Meloidogyne incognita*, 149  
*Meloidogyne spp.*, 144
- ROS. *See* Reactive oxygen species (ROS)
- S**
- SA. *See* Salicylate/Salicylic acid (SA)
- Saccharomyces cerevisiae*, 140, 146
- Salicylate/Salicylic acid (SA), 38–46, 76, 199, 355, 356
- Saliva, 199, 206
- Salmonella*, 349–357  
*S. enterica*, 350–354, 356
- Salmonella* effectors, 352, 356–357
- SAMPs. *See* Symbiotic-associated molecular patterns (SAMPs)
- Sap, 90–92, 94, 96, 99, 101, 103–107, 109
- SCRAMBLED (SCM), 129
- Secondary electron spray ionization/mass spectrometry (SESI/MS), 331
- Secondary metabolites, 74, 75  
 alkaloids, 314, 315, 317  
 anthocyanins, 314  
 cyanogenic glycosides, 315  
 DIBOA, 316  
 glucosinolates, 314, 315  
 isoprenoids, 314  
 phenylpropanoids, 314  
 terpenes, 314, 315, 317
- Sedentary plant-parasitic nematodes, 144, 145, 150
- Seed(s), 17–21, 29, 171–174, 179–186, 188  
 coat, 172, 174, 182–183  
 development, 174, 179–185  
 dormancy, 185
- Selected ion flow tube/mass spectrometry (SIFT/MS), 331
- Self, 2, 5
- Self incompatibility (SI), 172, 173, 178
- Self *versus* non-self, 159–162
- Semiophoric aspects, 246
- Sepal(s), 124, 129
- Serratia odorifera* 4Rx13, 330, 332, 333, 336, 337, 341
- SESI/MS. *See* Secondary electron spray ionization/mass spectrometry (SESI/MS)
- Sesquiterpenes, 203
- Sexual reproduction, 171, 173
- Shannon and Weaver, 38–41
- Shoot apical meristem (SAM), 123, 128, 129
- SHORTROOT, 125



- SI. *See* Self incompatibility (SI)
- SIFT/MS. *See* Selected ion flow tube/massspectrometry (SIFT/MS)
- Signal, 2–7  
 microdomains, 24  
 transduction, 23, 26
- Signaling  
 calcium, 311  
 calmodulin, 311  
 mitogen-activated protein kinases, 312  
 NADPH oxidase, 311  
 Reactive oxygen species (ROS), 311, 312, 321
- Signal transduction  
 GTPase activating protein (GAP), 140  
 guanine nucleotide exchange factor (GEF), 140  
 MAPK3, 143, 144  
 MAP kinase, 140, 147  
 Mpk1, 140, 143  
 Rho1, 140
- Sign-mediated interactions, 2, 5
- S-locus, 178
- Small RNA (sRNAs), 127–128
- Sodorifen, 330
- Soil microbial community, 370
- Solid phase micro extraction (SPME), 330, 331, 339, 341
- SOMATIC EMBRYOGENESIS RECEPTOR KINASE1 (SERK1)**, 130
- Sperm cells, 172, 179, 180
- Spidermite, 204, 206, 207
- SPME. *See* Solid phase micro extraction (SPME)
- Sporophytes, 172, 173, 175
- Spotted knapweed, 367
- Stamen(s), 124
- Staphylococcus aureus*, 350
- Statolith(s), 53–54, 57, 58, 61
- Stem cell(s), 124, 128
- Stigma, 178
- Stochastic, 13–16, 18–22
- Stochastic resonance, negative, 16
- Stress, 7, 8  
 abiotic stress, 92, 96, 97  
 biotic stress, 92–98
- Strigolactone, 363, 364
- STRUBBELIG (SUB)**, 129, 130
- Subepidermal layers, 126
- Sucrose, 96, 98–99, 102, 105–106
- Superoxide dismutase, 187
- SuperQ, 330
- SuperScent database, 330
- Suppression of, 197–207
- Suspensor, 172, 174, 180–181
- Symbiosomes  
 AHLs, 260, 262  
 bacteroids, 262  
 ExpR, 260  
 flavonoids, 267  
 furanones, 263
- Symbiotic-associated molecular patterns (SAMPs)  
 CYCLOPs, 269  
 Devonian age, 269  
 DMI1, 269
- Symbiotic auxotrophy, senescence, 273
- Symplasmic channels, 125
- Symplasmic trafficking, 125
- Synchronisation, 19
- Syncytium, 145, 148
- Synergid Cell, 172, 174, 179–180
- Synergids, 127
- Systemic acquired resistance (SAR), 40, 44–46  
 locally, 95  
 systemic response, 95
- Systemic resistance, 40, 44, 45, 78
- Systemic wound responses, 44
- Systemin, 39, 44, 92–94
- T**
- Tapetum, 130, 172, 177–178
- TAPETUM DETERMINANT1 (TPD1)**, 130
- Tenax, 330, 331
- TERMINALFLOWER1 (TFL1)**, 125, 126
- Terpenes/Terpenoids, 199, 202, 203
- Thigmomorphogenesis, 79
- Threshold (s), 11–32  
 extrinsic, 14, 17, 18, 20  
 red, 21, 32
- TOADSTOOL2 (TOAD2)**, 129
- Touch, 79
- Tracheary element, 173
- Tragedy of the commons, 161, 162
- Transacting* siRNAs (*tasiRNAs*), 127
- Transcription  
 factors, 124  
 noise, 13–16  
 positive, 14, 15, 17, 18
- Translation, 13–16
- Translational fusions, 126
- Transmission, 12–17, 32
- Transorganismic, 1, 5

- Transport  
 collection phloem, 90  
 release phloem, 90  
 systemic signals, 92  
 transport phloem, 90, 93, 96, 97,  
 107, 109
- Transposable elements (TEs), 8, 127
- Trichome, 202, 203
- Tuber formation, 106
- Tunica, 124
- Type III secretion systems (T3SSs), 351, 354,  
 356  
 bacteroid, 270  
 flavonoids, 270
- Tyrosine phosphatase, 356
- V**
- Vacuolar processing enzymes (VPEs), 174,  
 182, 183
- Vacuole(s), 54–57, 60
- Viroids, 8
- Viruses, 6, 8  
 cytoplasmic, 31
- VOC. *See* Volatile organic compounds (VOC)
- Volatile compounds, 73
- Volatile organic compounds (VOC), 304, 306,  
 317, 318
- Volatiles, 327–344  
 plant, 197–199, 201–205, 207
- Volicitin, 199
- VPEs. *See* Vacuolar processing enzymes  
 (VPEs)
- W**
- Water  
 cytoplasmic, 26  
 filamentous, 27  
 structured, 24–30
- Whitefly, 206
- Wounding  
 root-to-shoot, 92  
 shoot-to-root, 92  
 systemic signalling, 95
- WUSCHEL (WUS), 128
- X**
- Xylem, root-to-shoot, 97
- Z**
- ZERZAUST (ZET), 129
- ZHOUP//RETARDED GROWTH OF  
 EMBRYO1 ZOU/RGE1, 183, 184