**Peer-reviewed international publications:**

1. **Pootakham W**\*, Mhuantong W, Putchim L, Yoocha T, Sonthirod C, Kongkachana W, Sangsrakru D, Naktang C, Jomchai N, Thongtham N, Tangphatsornruang S. (2018) Dynamics of coral-associated microbiomes during a thermal bleaching event. MicrobiologyOpen. In press.
2. Wanlayaporn K, Somyong S, **Pootakham W**, Shearman J, Vanavichit A, Kumur P, Chee PW, Tragoonrung S. (2018) QTL mapping of pericarp thickness in immature and mature stages in Thai tropical sweet corn (Zea mays var. saccharata). Chiang Mai Journal of Science, 45 (1), pp. 177-187.
3. **Pootakham W\***, Mhuantong W, Yoocha T, Putchim L, Sonthirod C, Naktang C, Thongtham N, Tangphatsornruang S. (2017) High resolution profiling of coral-associated bacterial communities using full-length 16S rRNA sequence data from PacBio SMRT sequencing system. Scientific Reports, 7, Article number: 2774. doi10.1038/s41598-017-03139-4.
4. **Pootakham W,** Sonthirod C, Naktang C, Ruang-Areerat P, Yoocha T, Sangsrakru D, Teerawattanasuk K, Rattanawong R, Lekawipat N, Tangphatsornruang S. (2017) *De novo* hybrid assembly of the rubber tree genome reveals evidence of paleotetraploidy in *Hevea* species.Scientific Reports, 7, Article number: 41457. doi10.1038/srep41457.
5. **Pootakham W,** Sonthirod C, Naktang C, Nukoon J, Sangsrakru D, Tangphatsornruang S. (2016) Effects of methylation-sensitive enzymes on the enrichment of genic SNPs and the degree of genome complexity reduction in a two-enzyme genotyping-by-sequencing (GBS) approach: a case study in oil palm (*Elaeis guineensis*).Mol Breeding. 36:154. doi: 10.1007/s11032-016-0572-x.
6. Shearman, JR, Sonthirod, C, Naktang, C, **Pootakham, W**, Yoocha, T, Sangsrakru, D, Jomchai, N, Tragoonrung, S, Tangphatsornruang, S. The two chromosomes of the mitochondrial genome of a sugarcane cultivar: Assembly and recombination analysis using long PacBio reads (2016) Scientific Reports, 6, Article number: 31533. doi:10.1038/srep31533.
7. Surat, W, Mhuantong, W, Sangsrakru, D, Chareonviriyaphap, T, Arunyawat, U, Kubera, A, Sittivicharpinyo, T, Siripan, O, **Pootakham, W**. Gut bacterial diversity in plasmodium-infected and plasmodium-uninfected anopheles minimus (2016) Chiang Mai Journal of Science, 43 (3), pp. 426-439.
8. **Pootakham W,** Ruang Aree-rate P, Jomchai N, Sonthirod C, Sangsrakru D, Yoocha T, Theerawattanasuk K, Nirapathpongporn K, Romruensukharom P, Tragoonrung S, and Tangphatsornruang S. (2015) Construction of a high-density integrated genetic linkage map of rubber tree (Hevea brasiliensis) using genotyping-by-sequencing (GBS). Front. Plant Sci. 6:367. doi: 10.3389/fpls.2015.00367
9. **Pootakham W,** Jomchai N, Ruang Aree-rate P, Shearman J, Sonthirod C, Sangsrakru D, Tragoonrung S and Tangphatsornruang S. (2015) Genome-wide SNP discovery and identification of QTL associated with agronomic traits in oil palm using genotyping-by-sequencing (GBS). Genomics. 105:288-295. doi:10.1016/j.ygeno.2015.02.002
10. **Pootakham W,** Shearman J, Chanprasert J, Sangsrakru D, Jomchai N, Sonthirod C, Tragoonrung S and Tangphatsornruang S. (2014) Large-scale, genome-wide SNP discovery through RNA-seq and SNP genotyping by targeted enrichment sequencing in cassava. PlosOne. 9:e116028. doi: 10.1371/journal.pone.0116028.
11. Aksoy M, **Pootakham W,** and Grossman A. (2014) Critical function of a *Chlamydomonas reinhardtii* putative polyphosphate polymerase subunit during nutrient deprivation. Plant Cell. 26:4214-4229. doi: 10.1105/tpc.114.129270.
12. **Pootakham W**, Uthaipaisanwong P, Sangsrakru D, Yoocha T, Tragoonrung S, and Tangphatsornruang S. (2013) Development and characterization of single-nucleotide polymorphism markers from 454 transcriptome sequences in oil palm (*Elaeis guineensis*). Plant Breeding. 132:711-717.
13. Aksoy M\*, **Pootakham W\***, Pollock SV, Moseley JL, Gonzalez-Ballester D, and Grossman AR. (2013) Tiered regulation of sulfur starvation in *Chlamydomonas reinhardtii* and identification of an associated regulatory factor. Plant Physiol. 162:195-211. \*These authors have equal contributions.
14. **Pootakham W**, Chanprasert J, Jomchai N, Sangsrakru D, Yoocha T, Tragoonrung S, and Tangphatsornruang S. (2012) Development of genomic-derived simple sequence repeat markers in *Hevea brasiliensis* from 454 genome shotgun sequences. Plant Breeding. 131:555-562.
15. **Pootakham W**, Chanprasert J, Jomchai N, Sangsrakru D, Yoocha T, Therawattanasuk K, and Tangphatsornruang S. (2011) Single nucleotide polymorphism marker development in rubber tree, *Hevea brasiliensis* ([Euphorbiaceae](http://en.wikipedia.org/wiki/Euphorbiaceae)). Am J Bot. 98:e337-338.
16. Gonzalez-Ballester D, **Pootakham W**, Mus F, Yang W, Catalanotti C, Magneschi L, Higuera JJ, de Montaigu A, Prior M, Galván A, Fernandez E,and Grossman AR. (2011) Reverse genetics in Chlamydomonas: a platform for isolating insertional mutants. Plant Methods. 7:24-36.
17. **Pootakham W**, Gonzalez-Ballester D, and Grossman AR. (2010) Identification and regulation of plasma membrane sulfate transporters in Chlamydomonas*.* Plant Physiol. 153:1653-1668.
18. Grossman AR, Gonzalez-Ballester D, Shibagaki N, **Pootakham W**, and Moseley JL. (2009) Chapter 15: Responses to macronutrient deprivation. Abiotic adaptation in plants: Physiological, molecular and genomic foundation. Pareek, A.; Sopory, S.K.; Bohnert, H.J.; Govindjee (Eds.)
19. MoseleyJL, **Pootakham W**, Gonzalez-Ballester D, Bailey S, and Grossman AR. (2008) Genetic interactions between regulators of the Chlamydomonas phosphorus and sulfur starvation responses. Genetics. 181:889-905.
20. [Gonzalez-Ballester D, Pollock SV, **Pootakham W**, and Grossman AR.](http://www.ncbi.nlm.nih.gov/pubmed/18326790?ordinalpos=1&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DefaultReportPanel.Pubmed_RVDocSum) (2008) The central role of a SNRK2 kinase in sulfur deprivation responses. Plant Physiol. 147:216-227.
21. [Merchant SS, Prochnik SE, Vallon O, Harris EH, Karpowicz SJ, Witman GB, Terry A, Salamov A, Fritz-Laylin LK, Maréchal-Drouard L, Marshall WF, Qu LH, Nelson DR, Sanderfoot AA, Spalding MH, Kapitonov VV, Ren Q, Ferris P, Lindquist E, Shapiro H, Lucas SM, Grimwood J, Schmutz J, Cardol P, Cerutti H, Chanfreau G, Chen CL, Cognat V, Croft MT, Dent R, Dutcher S, Fernández E, Fukuzawa H, González-Ballester D, González-Halphen D, Hallmann A, Hanikenne M, Hippler M, Inwood W, Jabbari K, Kalanon M, Kuras R, Lefebvre PA, Lemaire SD, Lobanov AV, Lohr M, Manuell A, Meier I, Mets L, Mittag M, Mittelmeier T, Moroney JV, Moseley J, Napoli C, Nedelcu AM, Niyogi K, Novoselov SV, Paulsen IT, Pazour G, Purton S, Ral JP, Riaño-Pachón DM, Riekhof W, Rymarquis L, Schroda M, Stern D, Umen J, Willows R, Wilson N, Zimmer SL, Allmer J, Balk J, Bisova K, Chen CJ, Elias M, Gendler K, Hauser C, Lamb MR, Ledford H, Long JC, Minagawa J, Page MD, Pan J, **Pootakham W**, Roje S, Rose A, Stahlberg E, Terauchi AM, Yang P, Ball S, Bowler C, Dieckmann CL, Gladyshev VN, Green P, Jorgensen R, Mayfield S, Mueller-Roeber B, Rajamani S, Sayre RT, Brokstein P, Dubchak I, Goodstein D, Hornick L, Huang YW, Jhaveri J, Luo Y, Martínez D, Ngau WC, Otillar B, Poliakov A, Porter A, Szajkowski L, Werner G, Zhou K, Grigoriev IV, Rokhsar DS, and Grossman AR.](http://www.ncbi.nlm.nih.gov/pubmed/17932292?ordinalpos=2&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DefaultReportPanel.Pubmed_RVDocSum) (2007) The *Chlamydomonas* genome reveals the evolution of key animal and plant functions. Science. 318:245-250.
22. [Pollock SV, **Pootakham W**, Shibagaki N, Moseley JL, Grossman AR.](http://www.ncbi.nlm.nih.gov/pubmed/16307308?ordinalpos=3&itool=EntrezSystem2.PEntrez.Pubmed.Pubmed_ResultsPanel.Pubmed_DefaultReportPanel.Pubmed_RVDocSum) (2005) Insights into the acclimation of *Chlamydomonas reinhardtii* to sulfur deprivation. Photosyn Res. 86:475-489.