

植物ゲノム・遺伝子源解析センター 月例セミナー

とき 平成29年12月20日(水)16時～17時

ところ 農学部 BW106 講義室

題目:

Peanut genomics for improving foliar disease resistance

講師: Department of Biotechnology,
University of Agricultural Sciences, Dharwad India

R. S. Bhat 博士

概略

Peanut, an important food and oilseed crop, succumbs to considerable yield loss due to fungal foliar diseases like late leaf spot (LLS) and rust. In the past, though concentrated efforts were made using conventional breeding, largely they have not been very successful in combining disease resistance, high productivity and desirable pod and kernel features due to various genetic factors. Biotechnological tools, namely markers have the potential to complement the breeding program and address some of the genetic factors. In this regard, considerable efforts have been made by our group to develop genomic resources and to utilize them for breeding for LLS and rust resistance. Some of the achievements include; 1) development of several mapping populations (RILs, ILs/AB-QTL and epi-RILs), mutant resources and heterogeneous inbred family (HIF)-derived near isogenic lines (NILs), 2) development and validation of SNP, AhTE and CAPS markers through genome-wide analysis, 3) construction of genetic/linkage maps, consensus maps and QTL maps, 4) large-scale mutant analysis to identify trait-specific markers, 5) validation of QTL and markers 6) development of backcross breeding lines in TMV 2, JL 24, Dh 86 and ICGS 76 7) development of mutants from the introgression lines. Superior backcross lines with high productivity and resistance to LLS and rust are undergoing second year multi-location trial for variety development and commercial release.

Hake, A. A., Shirasawa, K., Yadawad, A., Nadaf, H. L., Gowda, M. V. C., Nadaf, H. L. and Bhat, R. S., 2017a, Structural mutations among the genetically unstable mutants of peanut (*Arachis hypogaea* L.). *Plant Gene*: (Accepted).

Hake, A. A., Shirasawa, K., Yadawad, A., Sukruth, M., Patil, M., Nayak, S. N., Lingaraju, S., Patil, P. V., Nadaf, H. L., Gowda, M. V. C. and Bhat, R. S., 2017c, Mapping of important taxonomic and productivity traits using genic and non-genic transposable element markers in peanut (*Arachis hypogaea* L.). *PLoS One*, 12(10): e0186113.

Kolekar, R. M., Sukruth, M., Shirasawa, K., Nadaf, H. L., Motagi, B. N., Lingaraju, S., Patil, P. V. and Bhat, R. S., 2017, Marker-assisted backcrossing to develop foliar disease resistant genotypes in TMV 2 variety of peanut (*Arachis hypogaea* L.). *Plant Breed.*: (Accepted).

Nadaf, H. L., Biradar, K. S., Murthy, G. S. S., Krishnaraj, P. U., Bhat, R. S., Pasha, M. A. and Yerimani, A. S., 2017, Novel mutations in oleoyl-PC desaturase (ahFAD2B) identified from new high oleic mutants induced by gamma rays in peanut (*Arachis hypogaea* L.). *Crop Sci.*, 57: 2538-2546.

Pandey, M. K., Khan, A. W., Singh, V. K., Vishwakarma, M. K., Shasidhar, Y., Kumar, V., Garg, V., Bhat, R. S., Chitkineni, A., Janila, P., Guo, B. and Varshney, R. K., 2017, QTL-seq approach identified genomic regions and diagnostic markers for rust and late leaf spot resistance in groundnut (*Arachis hypogaea* L.). *Plant Biotechnol. J.*, 15(8): 927-941.

主催 : 香川大学農学部 植物ゲノム・遺伝子源解析センター

(<http://www.ag.kagawa-u.ac.jp/phytogene/index.html>)