SCIENTIST PROFILE

1. Name & Designation : Dr. L. Behera
   Senior Scientist
2. Date of Birth : 9th May, 1967
3. Date of joining ICAR : 21st January, 1998
4. Date of joining the present post : 21st January, 2010
5. Qualification (highest degree) : Ph.D (Genetics)
6. Post Doctoral Research Experience/Training:
   - Attended training on "Recent Techniques in Gene Cloning, Sequencing and DNA Profiling" during November 20-29, 2000 conducted by CIMAP, Lucknow
   - Attended training on "Recent Techniques in Plant Genetic Engineering and Molecular Breeding " during November 20-29, 2000 conducted by NRCPB, IARI, New Delhi
   - Attended training on "Bioinformatics" during November 5-25, 2002 conducted by IIT, Bombay.
   - Attended training on "Crop gene Expression Data Analysis and Structural Bioinformatics" during March 1 to 11, 2011 conducted by Crop Bioinformatics Domain Centre of National Agricultural Bioinformatics Grid (NABG), NBPGR, New Delhi
   - Attended training on "Molecular diagnostics for Risk assessment and management of genetically modified crops" during November 8-21, 2011 conducted by NBPGR, New Delhi
   - Attended training on "Computational Genome Analysis Techniques in discovery of agronomically important crop genes" during September24-29, 2012 conducted by National Agricultural Bioinformatic Grid(NABG), Crop and Hort. Domain Centre of NBPGR, New Delhi
7. Area of Specialization/research interest: Molecular Biology and Biotechnology
8. Significant Contribution including products and patents (Five bullets):
   - Developed DNA fingerprints/profiles for 96 local scented cultivars, 48 low land rice genotypes and 48 drought tolerant cultivars, maintainer, 68 CRRI released varieties, restorer, maintainer, CMS lines and pre-release and released hybrids. DNA fingerprints will be useful for future reference and protection of varieties under IPR regime.
   - Developed marker-assisted selection (MAS) kit for gall midge resistance gene, *Gm4* which is presently used to incorporate the gall midge resistance gene, *Gm4* into high yielding cultivars.
   - Major QTL associated with BPH resistance was identified using RIL mapping population developed from TN1/Salakthi. The QTL contributes > 60% to the phenotypic variance (resistance to BPH).
   - The major QTL located on chromosome 3 (closest marker-RM 231) and 11 (closest marker–RM 202) associated with root knot nematode resistance were identified using RIL mapping population developed from Annapurna and Ramakrishna. These QTLs showed phenotypic variance i.e 30.89% and 35.53% which can be used in future for marker-assisted breeding program in incorporating root-knot nematode tolerance, especially to aerobic rice varieties.
   - Molecular analysis of BPH populations of Orissa and Andhra Pradesh indicated the existence of wide genetic variation between BPH populations. The BPH population from Pipili, Odisha was found to be different from others, indicating that Pipili population is genetically differentiated form and there appears to be some kind of reproductive barrier preventing from gene flow.

9. Awards/Honours:

- Received best poster award on 'Host reaction and molecular genotyping to identify pathotype variability in rice root-knot nematode populations in India'. In: National symposium on advances in rice- entomological research in India, 23-24 September, 2004, CRRI, Cuttack.

10. Publications (10 best):

i. **Behera L**, Mohanty S, Pradhan SK, Singh S, Singh ON, Sahu RK, Sahu SC, SK Dash and T Mohapatra (2013). Assessment of genetic diversity of rainfed lowland rice genotypes using microsatellite markers. **Indian Journal of Genetics & Plant Breeding** 73(2): 142-152.

ii. **Behera L**, Patra BC, Sahu RK, Nanda A, Sahu SC, Patnaik A, Rao GJN and Singh ON (2012). Assessment of genetic diversity in medicinal rices using microsatellite markers. **Australian Journal of Crop Science** 6(9): 1369-1376.

iii. **Behera L**, Nanda A, Sahu RK, Jena M, Sahu SC, Patnaik A, Rao GJN and Singh ON (2012). DNA fingerprinting of brown planthopper resistant rice cultivars. **Oryza** 49(2): 80-87.

iv. Jena M, Mohanty SK, Panda RS, Bose LK, **Behera L** and Sahu SC (2012). Two Breeding Lines of rice resistant to the rice root-knot nematode. **Nematologia Mediterranea** 40: 207-208.

v. Nanda A, Kausal L, Jena M, Mohanty SK, Panda RS, **Behera L** and Sahu SC (2011). Host reaction and molecular genotyping to identify pathotype variability in rice root-knot nematode (*Meloidogyne graminicola*) populations. **Oryza** 48(2): 154-159.

vi. Nanda A, Mohanty SK, Panda RS, **Behera L**, Prakash A and Sahu SC (2010).Flanking microsatellite markers for breeding varieties against Asian rice gall midge. **Tropical Tropical Plant Biology** 3: 219-226.

vii. Lima JM, Dass A, Sahu SC**, Behera L** and Chauahan (2007). A RAPD marker identified a susceptible specific locus for gall midge resistance gene in rice cultivar ARC5984. **Crop Protection** 26: 1431-1435.

viii. Joshi RK and **Behera L** (2006). Identification and differentiation of indigenous non-Basmati aromatic rice genotypes of India using microsatellite markers**. African Journal of Biotechnology** 6(4): 348-354.

ix. Sahu SC, Bose L K and **Behera L** (2004). Inheritance of resistance against three biotypes of the Asian rice gall midge, *Orseolia oryzae* (Wood-Mason). **Oryza** 41(1&2): 59-61.

x. **Behera L**, Sahu SC, Rajamani S and Mohan M (2001). Molecular evidence for *Wolbachia* in rice insects. **Current Science** 81(10):1300.