

Bioinformatics Workgroup Co-Chair Candidate

Dorrie Main, Ph.D.

Associate Professor of Bioinformatics
Dept of Horticulture and Landscape Architecture
Washington State University

I am an Associate Professor of Bioinformatics at Washington State University, with a Ph.D. in Bioscience and Biotechnology and a M.S. in Information Management for the University of Strathclyde in Scotland. I combined these disciplines in 2000 and began working at a postdoctoral researcher in bioinformatics at Clemson University Genomics Institute in South Carolina and became the Director of Bioinformatics a couple of years later. My first project as an independent investigator was the Cotton Microsatellite Database, funded by Cotton Incorporated. When I moved to WSU in 2005, the database remained at Clemson and was expanded very nicely by Dr. Anna Blenda into the Cotton Marker Database (www.cottonmarker.org, Blenda *et al.*, 2006) that I am sure many of you use or have used. While at Clemson I also worked on Cotton EST and BAC end sequence analysis, as reported in the papers by Arpat *et al.*, 2004 and Frelichowski *et al.*, 2006. My main research areas of interest involves comparative genomics, genome evolution and developing useful online tools and resources for biologists. I am the lead investigator of several genomics, genetics and breeding databases including the Genome Database for Rosaceae (www.rosaceae.org), the Citrus Genome Database (www.citrusgenomedb.org), the Cool Season Food legume Database (www.coolseasonfoodlegume.org) and developed the Cacao Genome Database (www.cacaogenomedb.org). In the last year my group began converting CottonDB (www.cottondb.org) into a Tripal (Ficklin *et al.* 2011) type database, CottonGen (www.cottongen.org), supported by funding from industry and USDA-ARS. We are very fortunate to have Dr. Jing Yu, the CottonDB guru join our group to work on CottonGen. If elected to serve as ICGI Bioinformatics Working Group co-chair, I will work to ensure bioinformatics is well represented in the community, provide advice and guidance on bioinformatics analysis and data sharing and encourage the use of standardized ontologies to describe cotton data.