

María Muñoz-Amatriáin – Research Statement

As my academic career has developed, my research interests have focused on two main areas: (1) the identification of existing genetic variation that can be introduced into crops, and (2) the development of new tools and resources that will allow us to improve our ability to characterize and exploit this variation. It is now more than any other time in history that research in crop genetics is needed to meet a major challenge that the world faces: increasing food production under rapidly changing environmental and socio-economic conditions. Although this is big challenge, I am confident that we can succeed by efficiently integrating research in genetics/genomics and soil science with plant breeding programs.

Most of my career has been dedicated to the study of barley, a versatile cereal crop that adapts well to different environments. I have been actively involved in two large Coordinated Agricultural Projects (CAPs) called the Barley CAP and the Triticeae CAP. Under their umbrellas I have helped characterize important breeding materials from the University of Minnesota malting breeding program and the Oregon State University winter barley program. These studies have facilitated the selection of targets for the improvement of malting quality and cold tolerance. I developed one of the most widely used barley consensus genetic maps, which has assisted marker-assisted selection, association mapping studies and map-based cloning. Given my deep appreciation for the value of biodiversity for crop improvement, one of the most satisfying projects I have been involved in is the genetic characterization of the USDA barley core collection. With 2,419 locally adapted landraces and breeding materials, this is one of the most important barley genetic resources in the world. It is rewarding to see how this study is impacting the barley breeding communities, which have used its outcomes to identify beneficial alleles for many abiotic and biotic stresses.



Variation in grain (A) and spike (B) morphology existing in the USDA barley core collection. Image from Muñoz-Amatriáin et al., *Brief Funct Genom* 2014)

The availability of reference genomes is crucial to associate trait variations with sequence features in a high resolution manner. I have been an active follower of progress made by the International Barley Sequencing Consortium (IBSC), attending and participating in their meetings, and utilizing their latest resources. I have also been involved in projects leading to improved genome resources for the research community. In collaboration with members of the IBSC, I conducted experiments that determined the extent of copy number variation (CNV) in the barley genome. Using a panel of fourteen accessions chosen to represent barley diversity, I identified an extensive catalogue of CNVs affecting almost 15% of the genome and 9.5% of the coding regions that were surveyed, with a noticeable enrichment for disease-resistance genes. More recently, I was involved in the U.S. completion of efforts to sequence 15,622 gene-rich barley BACs. I am a very collaborative person and I had an important role in the decision of sharing these sequences with members of the IBSC. Today they are part of the complete sequence of the barley genome.

I have used my expertise in barley to develop genome resources for cowpea. Cowpea is a warm-season legume closely related to common bean. Since cowpea is most important in developing countries, it has lacked the genomic resources available for other major crops.

I have participated in the development of a 60K SNP genotyping assay for cowpea, which is being extensively used for genotyping breeding materials from the U.S. and West African breeding programs and it is producing an outpouring of new marker-trait associations. By developing first a draft genome sequence and now a fully annotated reference genome sequence (available from Phytozome), breeders and other cowpea scientists can now access sequences and genes surrounding their SNPs of interest. Given the notable sequence variation observed between individuals of the same species, which implies that a single genome sequence might not represent the genome of a species, current work includes the sequencing and *de novo* assembly of a diverse set of cowpea genomes for pan-genome analysis. This would help define the portion of the genome present in all individuals ("core genome") and the portion that is present in only one or a subset of individuals ("dispensable genome"). The dispensable genome can play a crucial role in the species' ability to adapt to local environments. In addition, my passion for accessing and exploiting germplasm diversity has motivated me to assemble a cowpea minicore collection of 384 worldwide accessions (the "UCR minicore"). I've led the genotyping and the production of pure seeds from each accession, and I have distributed some of those seeds to several collaborators in the U.S., Nigeria, and Uganda. Phenotyping for a variety of traits has been/is being conducted at different locations in California and Africa, and I have no doubt this UCR minicore will become a great resource for exploiting cowpea germplasm diversity for gene discovery, germplasm enhancement and variety development.

One of the most rewarding parts of my job is that projects are very linked to breeding applications. I interact with barley breeders in the U.S. and I provide support to access new genome resources. I also communicate frequently with West African breeders and I am involved not only in helping them analyze the genetic data to make breeding decisions but also in training the next generation of cowpea breeders. My hope is that all these efforts will have a real impact on the lives of smallholder farmers in those regions and will also boost cowpea production here in the U.S.

At Colorado State University I would anticipate continuing and building on this track record of accomplishment within the context of crops that are (or may be) relevant to Colorado and surrounding regions. I would communicate with researchers, breeders and farmers to get an understanding of the challenges and opportunities for improving local food production in Colorado. My strategy would be to ensure that the most current and appropriate genetics/genomics tools as well as the most suitable germplasm are used to address those challenges and opportunities. At the same time, I would ensure that my research findings contribute to a fundamental knowledge of crop plant genetics and genomics. The great challenges of climate change, land degradation and food security require the application of innovative technologies and strategies to agricultural systems to increase productivity and profit while reducing environmental damage. I believe that my research pursuits and interests would greatly complement those of the Department of Soil and Crop Sciences at Colorado State University.