**From Orphan Crop to Cutting-Edge Genomics: a Journey with Lentil**

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At the first ICLGG meeting in 2002 those of us working in pulse crops could only dream of having the genomic resources that Medicago had and the ability to deploy genomic technologies in a breeding program. Fast forward to today where we are now facing down what some days feels like too much genomic data, and we are using genomics to tackle many different breeding targets in a more efficient way. We can now strategically access more diverse cultivate germplasm without compromising adaptation, giving us the ability to make wider crosses. We have moved from assaying single SCAR or SSR markers, often tenuously linked to a trait of interest to genotyping whole genomes. This allows us to look at not just at single nucleotide polymorphisms but also structural variation that can be associated with phenotypic variation. We also have a better picture of what wild lentil genomes look like and can predict how they will interact with the cultivated genome in interspecific crosses. Identifying both beneficial and deleterious regions of wild genomes allows breeders to access useful genetic variability only found in the wild accessions – e.g., disease resistance, while leaving behind the variability that would lead to trouble - shattering or dormancy, for instance. We have gone from being in awe of the Wheat geneticists in the Department to now having them look over our shoulder at some of the tools and approaches we have developed to make the most of technologies in the breeding programs.