



Main Research Activities

In recent years Dr. Raggi research activity has been mainly focused on the study of genetic diversity and its evolution in barley (*Hordeum vulgare*) [1,2], common bean (*Phaseolus vulgaris*) [3,4], myrtle (*Myrtus communis*) [5] and in two different species of the Brassica genus [6–8]. He was also involved in the development of cultivars for sustainable agriculture in barley [9] and common bean [4-10]. Flowering time control in beans, and the genes involved in the process, were also target of his research activity by means of association studies on candidate genes [11] and genome wide [12]. Other researches concerned the study of the microbiome of the seeds of different common bean varieties [13], the usefulness of molecular markers in analyzing artworks [14,15] and classify different truffle species [16-18].

References

- [1] L. Raggi, V. Negri, S. Ceccarelli, Morphological diversity in a barley composite cross-derived population evolved under low-input conditions and its relationship with molecular diversity: indications for breeding, *J. Agric. Sci.* 154 (2016) 943–959.
- [2] L. Raggi, S. Ceccarelli, V. Negri, Evolution of a barley composite cross-derived population: an insight gained by molecular markers, *J. Agric. Sci.* 154 (2016) 23–39.
- [3] S.M. Klaedtke, L. Caproni, J. Klauk, P. De Grandville, M. Dutartre, P.M. Stassart, et al., Short-Term Local Adaptation of Historical Common Bean (*Phaseolus vulgaris* L.) Varieties and Implications for In Situ Management of Bean Diversity, *Int. J. Mol. Sci.* 18 (2017) 1–19.
- [4] L. Caproni, L. Raggi, C. Tissi, S. Howlett, R. Torricelli, V. Negri, Multi-Environment Evaluation and Genetic Characterisation of Common Bean Breeding Lines for Organic Farming Systems, *Sustainability*. 10 (2018) 1–17.
- [5] C. Mele, L. Corona, S. Melito, L. Raggi, M. Mulas, Industrial Crops & Products The genetic diversity of selections and wild populations of myrtle revealed by molecular geographic contexts, *Ind. Crop. Prod.* 132 (2019) 168–176.
- [6] S. Ciancaleoni, L. Raggi, V. Negri, Assessment of spatial–temporal variation in natural populations of Brassica incana in south Italy: implications for conservation, *Plant Syst. Evol.* 304 (2018) 1–15.
- [7] S. Ciancaleoni, G.L. Chiarenza, L. Raggi, F. Branca, V. Negri, Diversity characterisation of broccoli (*Brassica oleracea* L. var. *italica* Plenck) landraces for their on-farm (in situ) safeguard and use in breeding programs, *Genet. Resour. Crop Evol.* 61 (2013) 451–464.
- [8] S. Ciancaleoni, L. Raggi, V. Negri, Genetic outcomes from a farmer-assisted landrace selection programme to develop a



- synthetic variety of broccoli, *Plant Genet. Resour.* 12 (2014) 349–352.
- [9] L. Raggi, S. Ciancaleoni, R. Torricelli, V. Terzi, S. Ceccarelli, V. Negri, Evolutionary breeding for sustainable agriculture : Selection and multi-environmental evaluation of barley populations and lines, *F. Crop. Res.* 204 (2017) 76–88.
- [10] L. Caproni, L. Raggi, S. Ceccarelli, V. Negri, A. Carboni, In-Depth Characterisation of Common Bean Diversity Discloses Its Breeding Potential for Sustainable Agriculture, *Sustain.* 11 (2019) 1–20.
- [11] L. Raggi, C. Tissi, A. Mazzucato, V. Negri, Molecular polymorphism related to flowering trait variation in a *Phaseolus vulgaris* L. collection., *Plant Sci.* 215–216 (2014) 180–9.
- [12] L. Raggi, L. Caproni, A. Carboni, V. Negri, M.N. Nelson, Genome-Wide Association Study Reveals Candidate Genes for Flowering Time Variation in Common Bean (*Phaseolus vulgaris* L .), *Front. Plant Sci.* 10 (2019) 1–14.
- [13] S. Klaedtke, M.-A.A. Jacques, L. Raggi, A. Prévieux, S. Bonneau, V. Negri, et al., Terroir is a key driver of seed-associated microbial assemblages, *Environ. Microbiol.* 18 (2016) 1792–1804.
- [14] E. Albertini, L. Raggi, M. Vagnini, A. Sassolini, A. Achilli, G. Marconi, et al., Tracing the biological origin of animal glues used in paintings through mitochondrial DNA analysis., *Anal. Bioanal. Chem.* 399 (2011) 2987–95.
- [15] A. Sassolini, A. Lazio, M. Vagnini, D. Aiello, M. Bocchini, MOLECULAR TRACING OF THE BIOLOGICAL ORIGIN OF DRYING OILS USED IN WORKS OF ART, *Int. J. Conserv. Sci.* 11 (2020) 381–3992.
- [16] G. Marozzi, G. Maria, E. Suriano, N. Sitta, L. Raggi, H. Lancioni, et al., diversity *Tuber mesentericum* and *Tuber aestivum* Tru ffl es : New Insights Based on Morphological and Phylogenetic Analyses, (n.d.).
- [17] G.M.N. Benucci, L. Raggi, E. Albertini, T. Grebenc, M. Bencivenga, M. Falcinelli, et al., Ectomycorrhizal communities in a productive *Tuber aestivum* Vittad. orchard: composition, host influence and species replacement., *FEMS Microbiol. Ecol.* 76 (2011) 170–84.
- [18] G.M.N. Benucci, L. Raggi, G. Di Massimo, L. Baciarelli-Falini, M. Bencivenga, M. Falcinelli, et al., Species-specific primers for the identification of the ectomycorrhizal fungus *Tuber macrosporium* Vittad., *Mol. Ecol. Resour.* 11 (2011) 378–81.