

Curriculum Vitae

Andrea Patocchi



1. Personal information

Researcher IDs

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Date of Birth

19th March 1971

Nationality

Swiss

Civil Status

Married

Contact

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Address Büelenstrasse 8, 8820 Wädenswil

2. Education

1997 - 2000

PhD, Institute of Plant Sciences, ETH Zurich, Switzerland
Thesis “*Map-based cloning of resistance gene homologues in the Vf-region of the apple (Malus sp.)*”

1991 - 1996

Study in Biology at the Swiss Federal Institute of Technology (ETH) Zurich, Switzerland

3. Languages

Italian (mother tongue)
English, German and French (fluently spoken and written)

4. Employment

2019 - current

Deputy Head of Division Plant Breeding, Agroscope

2023 - current

Hear of Fruit Breeding Research Group, Division Plant Breeding, Agroscope Wädenswil

2017 - 2023

Head of Breeding Research Group, Division Plant Breeding, Agroscope Wädenswil

2014 - 2016

Research leader apple genetics and molecular breeding, Plant Protection and Fruit and Vegetable Extension, Phytopathology Group, Agroscope Wädenswil

2006 – 2013

Research leader mycology pome- and stone fruits, Plant Protection and Fruit and Vegetable Extension, Phytopathology Group, Agroscope Wädenswil

2003 - 2006

“**Oberassistent**”, Institute of Integrative Biology (Ecology, Evolution, Infectious diseases) Phytopathology Group (ETHZ)

2000 - 2003

Postdoc, Institute of Plant Sciences, Phytopathology Group (ETHZ)

1996 - 1997

Research assistant at the Institute of Plant Sciences, Phytopathology Group (ETHZ)

5. Institutional responsibilities	Peer of Strategic Research Field “ <i>Breeding and offering efficient and marketable plant varieties</i> ”, Biosafety advisor (Agroscope, Wädenswil)
6. Approved research projects	<p>Principal investigator</p> <p>2004 – 2007 Sustainable Strategies for Fire Blight Control (KTI)</p> <p>2006 - 2010 Identification of candidate genes involved in fire blight resistance in apple (ICG) (COST 864)</p> <p>2009 - 2012 Developing Smart-breeding tools for apricot resistance against the stone fruit pathogen <i>Xanthomonas arboricola</i> pv. <i>pruni</i> (COST 863)</p> <p>2016 - 2019 Development of a pipeline for multi-level assessment of cisgenic apples (SNF grant 31003A_163386)</p> <p>2023-2026 Recombination frequency increase in apple (SNF grant 310030_204549 / 1)</p>
	<p>Research projects (co-Principal Investigator)</p> <p>2000-2003 Cloning of <i>Vf</i>, a disease resistance gene from apple (SNF)</p> <p>2003-2006 Identification of <i>avr</i>-genes in <i>Venturia inaequalis</i> (SNF)</p> <p>2004-2007 Genetic modified apple resistant to apple scab (ETH)</p> <p>2007-2011 Genetically modified apples resistant to scab containing only apple own DNA (NFP59)</p> <p>2008-2011 Züchtung feuerbrandtoleranter Obstsorten (ZUEFOS, FOAG)</p> <p>2012-2013 Züchtung feuerbrandtoleranter Obstsorten (ZUEFOS II, FOAG)</p> <p>2011-2015 Integrated approach for increasing breeding efficiency in fruit tree crops (FruitBreedomics; FP7-265582) (Workpackage leader)</p> <p>2019-2024 Innovations in plant variety testing in Europe (INVITE, H2020)</p> <p>2020-2024 Apfelmukunft dank Züchtung (AZZ, FOAG)</p> <p>2020-2025 Rewiring photorespiration using natural and synthetic pathways to sustainably increase crop yield (Gain4crops, H2020)</p> <p>2023-2027 Tools and methods for extended plant PHENotyping and Enviro-Typing services of European Research Infrastructures (PHENET, HORIZON-INFRA-2022-TECH-01-01)</p>
7. Student supervision	<p>Supervised or co-supervised 17 MSc or BSc-students in apple genomics and genetics as well as phytopathology (ETHZ or Agroscope): Urs Beck, Barbara Bigler, Pierre Coulin, Anna Dalbosco, Nils Erdin, Andreas Gerber, Dafne Gianettoni, Theresa Koller, Doris Herrman, Caterina Matasci, Nicola Sartori, Maja Schaffner Tobias Schmid, Viktor Solenthaler, Simone Schütz-Bühlmann, Giorgia Valsesia, Marcel Walser.</p> <p>Supervised or co-supervised 12 PhD students in apple genomics and genetics (ETHZ or Agroscope): Giovanni Broggini, Paolo Galli, Michael Gygax, Awais Khan, Pierre-Marie Le Roux, Gabriella Parravicini, Sudarsan Padmarasu, Eve Silfverberg-Dilworth, Didier Socquet-Juglard, Michaela Jung, Ayesha Yousaf, Ina Schlathölder.</p> <p>Supervised 4 PostDocs in apple genomics and genetics (Agroscope): Michaela Jung, Beat Keller, Yvonne Möller, Morgane Roth.</p>
8. Teaching	2014 to 2018 (yearly) Horticultural science: Case studies MS ETH Zurich
9. Panels, Boards, Reviewing	Reviewer for Molecular Breeding, Journal of Phytopathology, Tree Genetics & Genomes, Plant Disease, Acta Horticulturae
10. Memberships	Member of EUCARPIA and of the Swiss Phytopathological Society

11. Conference organisation

Annual meeting of the FP7 project 'FruitBreedomics' in Zurich (2014)

12. Hobbies

Fishing, collecting mushrooms, hiking, skiing

13 References

On request

PEER REVIEWED PUBLICATIONS

1999

- Patocchi, A., L. Gianfranceschi and C. Gessler (1999). "Towards the map-based cloning of Vf: fine and physical mapping of the VfRegion." *Theoretical and Applied Genetics* 99(6): 1012-1017.
- Patocchi, A., B. A. Vinatzer, L. Gianfranceschi, S. Tartarini, H. B. Zhang, S. Sansavini and C. Gessler (1999). "Construction of a 550 kb BAC contig spanning the genomic region containing the apple scab resistance gene Vf." *Molecular and General Genetics* 262(4-5): 884-891.

2001

- Vinatzer, B. A., A. Patocchi, L. Gianfranceschi, S. Tartarini, H. B. Zhang, C. Gessler and S. Sansavini (2001). "Apple contains receptor-like genes homologous to the *Cladosporium fulvum* resistance gene family of tomato with a cluster of genes cosegregating with Vf apple scab resistance." *Molecular Plant-Microbe Interactions* 14(4): 508-515.

2002

- Barbieri, M., E. Belfanti, S. Tartarini, B. A. Vinatzer, S. Sansavini, E. Silfverberg-Dilworth, L. Gianfranceschi, D. Hermann, A. Patocchi and C. Gessler (2003). "Progress of map-based cloning of the Vf-resistance gene and functional verification: Preliminary results from expression studies in transformed apple." *Hortscience* 38(3): 329-331.

2003

- Liebhart, R., B. Koller, A. Patocchi, M. Kellerhals, W. Pfammatter, M. Jermini and C. Gessler (2003). "Mapping quantitative field resistance against apple scab in a 'Fiesta' x 'Discovery' progeny." *Phytopathology* 93(4): 493-501.

2004

- Baldi, P., A. Patocchi, E. Zini, C. Toller, R. Velasco and M. Komjanc (2004). "Cloning and linkage mapping of resistance gene homologues in apple." *Theoretical and Applied Genetics* 109(1): 231-239.
- Belfanti, E., E. Silfverberg-Dilworth, S. Tartarini, A. Patocchi, M. Barbieri, J. Zhu, B. A. Vinatzer, L. Gianfranceschi, C. Gessler and S. Sansavini (2004). "The *HcrVf2* gene from a wild apple confers scab resistance to a transgenic cultivated variety." *Proceedings of the National Academy of Sciences of the United States of America* 101(3): 886-890.
- Gygax, M., L. Gianfranceschi, R. Liebhart, M. Kellerhals, C. Gessler and A. Patocchi (2004). "Molecular markers linked to the apple scab resistance gene *Vbj* derived from *Malus baccata jackii*." *Theoretical and Applied Genetics* 109(8): 1702-1709.
- Patocchi, A., B. Bigler, B. Koller, M. Kellerhals and C. Gessler (2004). "*Vr2*: a new apple scab resistance gene." *Theoretical and Applied Genetics* 109(5): 1087-1092.
- Vinatzer, B. A., A. Patocchi, S. Tartarini, L. Gianfranceschi, S. Sansavini and C. Gessler (2004). "Isolation of two microsatellite markers from BAC clones of the Vf scab resistance region and molecular characterization of scab-resistant accessions in *Malus* germplasm." *Plant Breeding* 123(4): 321-326.

2005

- Broggini, G. A. L., B. Duffy, E. Holliger, H. J. Scharer, C. Gessler and A. Patocchi (2005). "Detection of the fire blight biocontrol agent *Bacillus subtilis* BD170 (Biopro (R)) in a Swiss apple orchard." *European Journal of Plant Pathology* 111(2): 93-100.
- Patocchi, A., M. Walser, S. Tartarini, G. A. L. Broggin, F. Gennari, S. Sansavini and C. Gessler (2005). "Identification by genome scanning approach (GSA) of a microsatellite tightly associated with the apple scab resistance gene *Vm*." *Genome* 48(4): 630-636.
- Silfverberg-Dilworth, E., S. Besse, R. Paris, E. Belfanti, S. Tartarini, S. Sansavini, A. Patocchi and C. Gessler (2005). "Identification of functional apple scab resistance gene promoters." *Theoretical and Applied Genetics* 110(6): 1119-1126.
- Valesia, G., D. Gobbin, A. Patocchi, A. Vecchione, I. Pertot and C. Gessler (2005). "Development of a high-throughput method for quantification of *Plasmopara viticola* DNA in grapevine leaves by means of quantitative real-time polymerase chain reaction." *Phytopathology* 95(6): 672-678.
- Zini, E., F. Biasioli, F. Gasperi, D. Mott, E. Aprea, T. D. Mark, A. Patocchi, C. Gessler and M. Komjanc (2005). "QTL mapping of volatile compounds in ripe apples detected by proton transfer reaction-mass spectrometry." *Euphytica* 145(3): 269-279.

2006

- Erdin, N., S. Tartarini, G. A. L. Broggin, F. Gennari, S. Sansavini, C. Gessler and A. Patocchi (2006). "Mapping of the apple scab-resistance gene *Vb*." *Genome* 49(10): 1238-1245.
- Gessler, C., A. Patocchi, S. Sansavini, S. Tartarini and L. Gianfranceschi (2006). "*Venturia inaequalis* resistance in apple." *Critical Reviews in Plant Sciences* 25(6): 473-503.

- Khan, M. A., B. Duffy, C. Gessler and A. Patocchi (2006). "QTL mapping of fire blight resistance in apple." *Molecular Breeding* 17(4): 299-306.
- Silfverberg-Dilworth, E., C. L. Matasci, W. E. Van de Weg, M. P. W. Van Kaauwen, M. Walser, L. P. Kodde, V. Soglio, L. Gianfranceschi, C. E. Durel, F. Costa, T. Yamamoto, B. Koller, C. Gessler and A. Patocchi (2006). "Microsatellite markers spanning the apple (*Malus x domestica* Borkh.) genome." *Tree Genetics & Genomes* 2(4): 202-224.
- Terakami, S., M. Shoda, Y. Adachi, T. Gonai, M. Kasumi, Y. Sawamura, H. Iketani, K. Kotobuki, A. Patocchi, C. Gessler, T. Hayashi and T. Yamamoto (2006). "Genetic mapping of the pear scab resistance gene *Vnk* of Japanese pear cultivar Kinchaku." *Theoretical and Applied Genetics* 113(4): 743-752.

2007

- Antofie, A., M. Lateur, R. Oger, A. Patocchi, C. E. Durel and W. E. Van de Weg (2007). "A new versatile database created for geneticists and breeders to link molecular and phenotypic data in perennial crops: the AppleBreed DataBase." *Bioinformatics* 23(7): 882-891.
- Broggini, G. A. L., B. Le Cam, L. Parisi, C. Wu, H. B. Zhang, C. Gessler and A. Patocchi (2007). "Construction of a contig of BAC clones spanning the region of the apple scab avirulence gene *AvrVg*." *Fungal Genetics and Biology* 44(1): 44-51.
- Gessler, C., and A. Patocchi (2007). Recombinant DNA technology in apple. In *Green Gene Technology* (pp. 113-132). Springer Berlin Heidelberg.
- Iannaccone, M., D. Palumbo, I. Ventimiglia, A. Patocchi, P. Spigno and R. Capparelli (2007). "Use of molecular markers and flow cytometry to preserve ancient Annurca apple germplasm." *Biotechnology Letters* 29(2): 279-284.
- Khan, M. A., C. E. Durel, B. Duffy, D. Drouet, M. Kellerhals, C. Gessler and A. Patocchi (2007). "Development of molecular markers linked to the 'Fiesta' linkage group 7 major QTL for fire blight resistance and their application for marker-assisted selection." *Genome* 50(6): 568-577.

2008

- Bus, V. G. M., D. Chagne, H. C. M. Bassett, D. Bowatte, F. Calenge, J. M. Celton, C. E. Durel, M. T. Malone, A. Patocchi, A. C. Ranatunga, E. H. A. Rikkerink, D. S. Tustin, J. Zhou and S. E. Gardiner (2008). "Genome mapping of three major resistance genes to woolly apple aphid (*Eriosoma lanigerum* Hausm.)." *Tree Genetics & Genomes* 4(2): 223-236.
- Soufflet-Freslon, V., L. Gianfranceschi, A. Patocchi and C. E. Durel (2008). "Inheritance studies of apple scab resistance and identification of *Rvi14*, a new major gene that acts together with other broad-spectrum QTL." *Genome* 51(8): 657-667.
- Stoeckli, S., K. Mody, C. Gessler, A. Patocchi, M. Jermini and S. Dorn (2008). "QTL analysis for aphid resistance and growth traits in apple." *Tree Genetics & Genomes* 4(4): 833-847.

2009

- Broggini, G. A. L., P. Galli, G. Parravicini, L. Gianfranceschi, C. Gessler and A. Patocchi (2009). "*HcrVf* paralogs are present on linkage groups 1 and 6 of *Malus*." *Genome* 52(2): 129-138.
- Patocchi, A., F. Fernandez-Fernandez, K. Evans, D. Gobbin, F. Rezzonico, A. Boudichevskaia, F. Dunemann, M. Stankiewicz-Kosyl, F. Mathis-Jeanneteau, C. E. Durel, L. Gianfranceschi, F. Costa, C. Toller, V. Cova, D. Mott, M. Komjanc, E. Barbaro, L. Kodde, E. Rikkerink, C. Gessler and W. E. van de Weg (2009). "Development and test of 21 multiplex PCRs composed of SSRs spanning most of the apple genome." *Tree Genetics & Genomes* 5(1): 211-223.
- Patocchi, A., A. Frei, J. E. Frey and M. Kellerhals (2009). "Towards improvement of marker assisted selection of apple scab resistant cultivars: *Venturia inaequalis* virulence surveys and standardization of molecular marker alleles associated with resistance genes." *Molecular Breeding* 24(4): 337-347.
- Stoeckli, S., K. Mody, A. Patocchi, M. Kellerhals and S. Dorn (2009). "Rust mite resistance in apple assessed by quantitative trait loci analysis." *Tree Genetics & Genomes* 5(1): 257-267.
- Szankowski, I., S. Waidmann, J. Degenhardt, A. Patocchi, R. Paris, E. Silfverberg-Dilworth, G. Brogginini and C. Gessler (2009). "Highly scab-resistant transgenic apple lines achieved by introgression of *HcrVf2* controlled by different native promoter lengths." *Tree Genetics & Genomes* 5(2): 349-358.

2010

- Galli, P., G. A. L. Brogginini, C. Gessler and A. Patocchi (2010). "Phenotypic Characterization of the *Rvi15* (*Vr2*) Apple Scab Resistance." *Journal of Plant Pathology* 92(1): 219-226.
- Galli, P., G. A. L. Brogginini, M. Kellerhals, C. Gessler and A. Patocchi (2010). "High-resolution genetic map of the *Rvi15* (*Vr2*) apple scab resistance locus." *Molecular Breeding* 26(4): 561-572.
- Galli, P., A. Patocchi, G. A. L. Brogginini and C. Gessler (2010). "The *Rvi15* (*Vr2*) Apple Scab Resistance Locus Contains Three TIR-NBS-LRR Genes." *Molecular Plant-Microbe Interactions* 23(5): 608-617.
- Hilber-Bodmer, M., M. Bunter and A. Patocchi (2010). "First report of brown rot caused by *Monilinia fructicola* on apricot in a Swiss orchard." *Plant Disease* 94(5): 643-643.

Le Roux, P. M. F., M. A. Khan, G. A. L. Broggin, B. Duffy, C. Gessler and A. Patocchi (2010). "Mapping of quantitative trait loci for fire blight resistance in the apple cultivars 'Florina' and 'Nova Easygro'." *Genome* 53(9): 710-722.

2011

Evans, K. M., A. Patocchi, F. Rezzonico, F. Mathis, C. E. Durel, F. Fernandez-Fernandez, A. Boudichevskaia, F. Dunemann, M. Stankiewicz-Kosyl, L. Gianfranceschi, M. Komjanc, M. Lateur, M. Madduri, Y. Noordijk and W. E. van de Weg (2011). "Genotyping of pedigreed apple breeding material with a genome-covering set of SSRs: trueness-to-type of cultivars and their parentages." *Molecular Breeding* 28(4): 535-547.

Flachowsky, H., P. M. Le Roux, A. Peil, A. Patocchi, K. Richter and M. V. Hanke (2011). "Application of a high-speed breeding technology to apple (*Malus x domestica*) based on transgenic early flowering plants and marker-assisted selection." *New Phytologist* 192(2): 364-377.

Parravicini, G., C. Gessler, C. Denance, P. Lasserre-Zuber, E. Vergne, M. N. Brisset, A. Patocchi, C. E. Durel and G. A. L. Broggin (2011). "Identification of serine/threonine kinase and nucleotide-binding site-leucine-rich repeat (NBS-LRR) genes in the fire blight resistance quantitative trait locus of apple cultivar 'Evereste'." *Molecular Plant Pathology* 12(5): 493-505.

Weger, J., M. Schanze, M. Hilber-Bodmer, T. H. M. Smits and A. Patocchi (2011). "First report of the beta-Tubulin E198A mutation conferring resistance to methyl benzimidazole carbamates in European isolates of *Monilinia fructicola*." *Plant Disease* 95(4): 497-497.

2012

Freiman, A., L. Shlizerman, S. Golobovitch, Z. Yablovitz, R. Korchinsky, Y. Cohen, A. Samach, E. Chevreau, P. M. Le Roux, A. Patocchi and M. A. Flaishman (2012). "Development of a transgenic early flowering pear (*Pyrus communis* L.) genotype by RNAi silencing of *PcTFL1-1* and *PcTFL1-2*." *Planta* 235(6): 1239-1251.

Gusberti, M., A. Patocchi, C. Gessler and G. A. L. Broggin (2012). "Quantification of *Venturia inaequalis* Growth in *Malus x domestica* with Quantitative Real-Time Polymerase Chain Reaction." *Plant Disease* 96(12): 1791-1797.

Hilber-Bodmer, M., V. Knorst, T. H. M. Smits and A. Patocchi (2012). "First Report of Asian brown rot caused by *Monilia polystroma* on apricot in Switzerland." *Plant Disease* 96(1): 146-146.

Jansch, M., J. E. Frey, M. Hilber-Bodmer, G. A. L. Broggin, J. Weger, G. Schnabel and A. Patocchi (2012). "SSR marker analysis of *Monilinia fructicola* from Swiss apricots suggests introduction of the pathogen from neighbouring countries and the United States." *Plant Pathology* 61(2): 247-254.

Le Roux, P. M., H. Flachowsky, M. V. Hanke, C. Gessler and A. Patocchi (2012). "Use of a transgenic early flowering approach in apple (*Malus x domestica* Borkh.) to introgress fire blight resistance from cultivar Evereste." *Molecular Breeding* 30(2): 857-874.

Le Roux, P. M. F., D. Christen, B. Duffy, S. Tartarini, L. Dondini, T. Yamamoto, C. Nishitani, S. Terakami, Y. Lespinasse, M. Kellerhals and A. Patocchi (2012). "Redefinition of the map position and validation of a major quantitative trait locus for fire blight resistance of the pear cultivar 'Harrow Sweet' (*Pyrus communis* L.)." *Plant Breeding* 131(5): 656-664.

Mouron, P., B. Heijne, A. Naef, J. Strassemeier, F. Hayer, J. Avilla, A. Alaphilippe, H. Hohn, J. Hernandez, G. Mack, G. Gaillard, J. Sole, B. Sauphanor, A. Patocchi, J. Samietz, E. Bravin, C. Lavigne, M. Bohanec, B. Golla, C. Scheer, U. Aubert and F. Bigler (2012). "Sustainability assessment of crop protection systems: SustainOS methodology and its application for apple orchards." *Agricultural Systems* 113: 1-15.

Socquet-Juglard, D., A. Patocchi, J. Pothier, D. Christen, B. Duffy B (2012) Evaluation of *Xanthomonas arboricola* pv. *pruni* inoculation techniques to screen for bacterial spot resistance in peach and apricot. *Journal of Plant Pathology*. 94:91-96.

2013

Costa, F., L. Cappellin, E. Zini, A. Patocchi, M. Kellerhals, M. Komjanc, C. Gessler and F. Biasioli (2013). "QTL validation and stability for volatile organic compounds (VOCs) in apple." *Plant Science* 211: 1-7.

Socquet-Juglard, D., D. Christen, G. Devenes, C. Gessler, B. Duffy and A. Patocchi (2013). "Mapping architectural, phenological, and fruit quality QTLs in apricot." *Plant Molecular Biology Reporter* 31(2): 387-397.

Socquet-Juglard, D., B. Duffy, J. F. Pothier, D. Christen, C. Gessler and A. Patocchi (2013). "Identification of a major QTL for *Xanthomonas arboricola* pv. *pruni* resistance in apricot." *Tree Genetics & Genomes* 9(2): 409-421.

Socquet-Juglard, D., T. Kamber, J. F. Pothier, D. Christen, C. Gessler, B. Duffy and A. Patocchi (2013). "Comparative RNA-Seq analysis of early-infected peach leaves by the invasive phytopathogen *Xanthomonas arboricola* pv. *pruni*." *Plos One* 8(1):e54196

2014

- Bink, M. C. A. M., J. Jansen, M. Madduri, R. E. Voorrips, C. E. Durel, A. B. Kouassi, F. Laurens, F. Mathis, C. Gessler, D. Gobbin, F. Rezzonico, A. Patocchi, M. Kellerhals, A. Boudichevskaia, F. Dunemann, A. Peil, A. Nowicka, B. Lata, M. Stankiewicz-Kosyl, K. Jeziorek, E. Pitera, A. Soska, K. Tomala, K. M. Evans, F. Fernandez-Fernandez, W. Guerra, M. Korbin, S. Keller, M. Lewandowski, W. Plochanski, K. Rutkowski, E. Zurawicz, F. Costa, S. Sansavini, S. Tartarini, M. Komjanc, D. Mott, A. Antofie, M. Lateur, A. Rondia, L. Gianfranceschi and W. E. van de Weg (2014). "Bayesian QTL analyses using pedigreed families of an outcrossing species, with application to fruit firmness in apple." *Theoretical and Applied Genetics* 127(5): 1073-1090.
- Broggini, G. A. L., T. Wohner, J. Fahrentrapp, T. D. Kost, H. Flachowsky, A. Peil, M. V. Hanke, K. Richter, A. Patocchi and C. Gessler (2014). "Engineering fire blight resistance into the apple cultivar 'Gala' using the FB_MR5 CC-NBS-LRR resistance gene of *Malus x robusta* 5." *Plant Biotechnology Journal* 12(6): 728-733.
- Jansch, M., R. Paris, F. Amoako-Andoh, W. Keulemans, M. W. Davey, G. Pagliarani, S. Tartarini and A. Patocchi (2014). "A Phenotypic, molecular and biochemical characterization of the first cisgenic scab-resistant apple variety 'Gala'." *Plant Molecular Biology Reporter* 32(3): 679-690.
- Padmarasu, S., D. J. Sargent, M. Jaensch, M. Kellerhals, S. Tartarini, R. Velasco, M. Troggio and A. Patocchi (2014). "Fine-mapping of the apple scab resistance locus *Rvi12* (*Vb*) derived from 'Hansen's baccata #2'." *Molecular Breeding* 34(4): 2119-2129.

2015

- Baumgartner, I. O., A. Patocchi, J. E. Frey, A. Peil, and M. Kellerhals (2015) Breeding elite lines of apple carrying pyramided homozygous resistance genes against apple scab and resistance against powdery mildew and fire blight. *Plant Molecular Biology Reporter*: 10.1007/s11105-015-0858-x
- Caffier, V., Patocchi, A., Expert, P., Bellanger, M. N., Durel, C. E., Hilber-Bodmer, M., GAL Broggin, G.A.L, Groenwold, R. and Bus, V. (2014). Virulence characterization of *Venturia inaequalis* reference isolates on the differential set of *Malus* hosts. *Plant Disease*, 99(3):370-375.
- Cova V., Lewke Bandara N., Liang W., Tartarini S., Patocchi A., Troggio M., Velasco R., and M. Komjanc (2015) Fine mapping of the *Rvi5* (*Vm*) apple scab resistance locus in the 'Murray' apple genotype. *Molecular breeding* 35 (10): 200.
- Jansch, M., G. A. L. Broggin, J. Weger, V. G. M. Bus, S. E. Gardiner, H. Bassett and A. Patocchi (2015). "Identification of SNPs linked to eight apple disease resistance loci." *Molecular Breeding* 35(1). 10.1007/s11032-015-0242-4
- Kost T., Gessler C., Jäensch M., Flachowsky H., Patocchi A., and G.A.L. Broggin (2015) Development of the first cisgenic apple with increased resistance to fire blight. *PLoS one* 10 (12): e0143980

2016

- Lambert P., Campoy J.A., Pacheco I., Mauroux J. B., Da Silva Linge C., Micheletti D., Bassi D., Rossini L., Dirlewanger E., Pascal T., Troggio M., Aranzana M.-J., Patocchi A., and P. Arús (2016) Identifying SNP markers tightly associated with six major genes in peach [*Prunus persica* (L.) Batsch] using a high-density SNP array with an objective of marker-assisted selection (MAS). *Tree Genetics & Genomes* 12 (6): 121.
- Baumgartner, I. O., Kellerhals, M., Costa, F., Dondini, L., Pagliarani, G., Gregori, R., Tartarini, S., Leumann, L., Laurens, F., and Patocchi, A. (2016). Development of SNP-based assays for disease resistance and fruit quality traits in apple (*Malus x domestica* Borkh.) and validation in breeding pilot studies. *Tree genetics & genomes*, 12(3), 1-21.

2017

- Cova, V., Paris, R., Toller, C., Patocchi, A., Velasco, R., and Komjanc, M. (2017). Apple genes involved in the response to *Venturia inaequalis* and salicylic acid treatment. *Scientia Horticulturae*, 226, 157-172.

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Major Scientific Achievements in apple breeding

1) Enabling classical durable resistance breeding in apple

Throughout my scientific career, my primary aim was to develop tools to expedite resistance breeding in apple and thereby promote a more sustainable production of this important fruit. The two most important diseases of apple are, apple scab caused by *Venturia inaequalis* and fire blight caused by *Erwinia amylovora*. For these two diseases, I identified molecular markers that are tightly associated to several resistance loci often originating from small-fruited crab apple. To advance progress in marker-assisted selection, I continuously updated the type of molecular markers in order to be compatible with time and economically-efficient, high-throughput screening technology. However, it became apparent to me that, in order to breed for cultivars with durable apple scab resistance, it was crucial to map the geographical distribution of strains of *V. inaequalis* that could overcome resistance genes. In order to fill this gap, in 2010 I established the VINQUEST project (www.vinquest.ch). Currently the programme has 26 partners in 14 countries, providing and sharing publicly-accessible data. These data allow identifying highly promising apple scab resistance genes for breeding (Patocchi et al. 2020).

To be successful on the market, resistant cultivars must at least preserve the same fruit quality and agronomic performance as their susceptible progenitors. Given that fruit quality, yield and other important traits are polygenic, genomic selection is the method of choice to assist complex breeding. As such, at the end of the European-funded 'FruitBreedomics' project, a consortium of European-based apple breeding institutions and companies decided to select, multiply and plant at six sites (Belgium, France, Italy, Poland, Spain and Switzerland) the material necessary for the development of genomic selection in apple. In the scope of a PhD programme that I co-supervised as well as three PostDoc projects in my team, models for genomic selection for fruit and tree traits have been developed (Jung et al. 2020, Roth et al. 2020, Jung et al. 2022, Keller et al. *MS in preparation*). These models will be validated and then applied in three Swiss apple breeding programs (Lubera, PomaCulta and Agroscope) in the framework of the FOAG-funded "Apfelzukunft dank Züchtung" (AZZ) project that I am co-leading.

2) Development of disease-resistant cultivars using new plant breeding technologies

Conventional apple breeding programmes face two major challenges: the lengthy (4-5 yr) juvenile phase of seedlings, and the high level of heterozygosity due to self-incompatibility. The long juvenile phase delays both the assessment of fruit traits and the introduction of desired traits from wild apples (e.g. disease resistance) in new cultivars. Together, this means it can take, an incredible, a quarter of a century to breed a new apple variety carrying a so far not deployed resistance of wild origin. The translational development of genomic selection models by team members will increase the percentage of seedlings with favourable traits to assess in the orchard and thus increasing the selection efficiency of new resistant commercially competitive cultivars. In addition, using molecular tools for early flower induction, in collaboration with international partners we demonstrated that a (pseudo)backcross per year is possible, which reduced the time needed to produce fifth generation genotypes to just seven years (Schlathölter et al. 2018) and that the early flowering line used in the experiment contains only one transgenic insertion and shows no further partial insertions of the transformation vector (Patocchi et al. 2021). Importantly, the final plants developed using this method were null-segregant i.e. they lacked introduced, foreign DNA.

Null segregant plants have been deregulated in the US and other countries but the legal status and material exchange/trade policies in Switzerland and Europe remains unclear.

Another new plant breeding technology that allow a fast introduction of (cloned) genes into commercially successfully cultivars is cisgenesis. My team and I, by cloning several resistance genes, set the basis for the establishment of this technology for the apple and participated in the transformation and development of the first worldwide fire blight resistant cisgenic apple line (Kost et al. 2015).

3) Testing of potential and ecological risks of new plant breeding technologies

A significant achievement in the last five years was the establishment and running of a field trial to investigate the cisgenic line developed by Kost et al. (2015) (SNF grant 31003A_163386). After obtaining permission and adhering to strict conditions imposed by from the Federal Office for the Environment, we performed a multi-year, comprehensive study, including the measuring of tree, flower and fruit traits, as well as genomics, transcriptomics, proteomics and metabolomics of the leaves and a metabolomics study of the fruits. Importantly, no controversial side-effects of the cisgenic line compared from the wild-type and control plants were found (Schlathölter et al., MSs *in preparation*). These results indicate a substantial equivalence of the cisgenic line to the natural mutants of the cultivar of origin. Complementing this important field trial and of high relevance for this SNF project proposal, is the *de novo* diploid assembly of the genome of the apple cultivar, ‘Gala Galaxy’ (Broggini et al. 2020). This genomic data is of exceptional quality for apple research and will provide unprecedented capacity for allele mining.