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Characterisation of Swiss wild hops (*Humulus lupulus*): agronomic, genetic, phytochemical and aromatic diversity compared with commercial varieties

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Abstract

Why was the work done: Wild hop populations represent an underexplored resource for the development of new hop varieties with distinctive flavour profiles and improved agronomic performance. This study evaluated the potential of Swiss wild hops as both breeding material and as candidates for use in brewing.

How was the work done: Wild hop accessions (62) from diverse biogeographical regions of Switzerland were characterised and compared with 14 commercial hop cultivars. Genetic diversity, agronomic performance, and chemical composition, including essential oils and bittering compounds, were analysed.

What are the main findings: Swiss wild hops exhibited high genetic diversity and were differentiated from commercial cultivars. On average, wild accessions showed higher yields than commercial varieties. Although essential oil content was generally lower in wild hops, some selected accessions displayed promising aromatic profiles, with several genotypes surpassing commercial cultivars in specific compounds. However, commercial cultivars typically contained higher levels of bittering compounds, but several wild genotypes achieved a comparable concentration.

Why is the work important: These findings highlight the potential of Swiss wild hops as a resource for breeding and for diversifying the raw materials used in brewing. The identified variability in agronomic and chemical traits supports the development of more sustainable hop varieties with novel flavour characteristics, contributing to innovation in the brewing industry.

Keywords

wild hops; genetic diversity; essential oils; brewing quality; hop breeding.

Introduction

Hop (*Humulus lupulus* L.) is a dioecious, wind-pollinated hemicryptophyte belonging to the Cannabaceae family, which is widely distributed across the Northern Hemisphere, primarily in temperate zones (Murakami et al. 2006). The adaptability of hop plants to a diverse range of environments, from coastal regions to mountainous areas, has allowed them to spread over vast geographical regions, leading to considerable genetic diversity. Molecular phylogenetic studies have suggested that wild hops exhibit high genetic variability, which presents an invaluable resource for germplasm conservation and breeding programs aimed at improving traits such as yield, disease resistance, and chemical composition (Murakami et al. 2006; Hagemann et al. 2023). Such genetic diversity is essential for the sustainable cultivation of hops, particularly considering increasing environmental stressors due to climate change.

The variability of biogeographical environments in which hop genotypes grow and, their remarkable adaptability to these environments, contribute to the creation of a pool of diversity. In particular, Switzerland, with its unique topography and microclimates, provides a natural laboratory for studying the genetic and phenotypic diversity of wild hop populations. Switzerland's small yet ecologically diverse territory, is home to a wide range of ecosystems, each characterised by different climatic and environmental conditions that can affect plant growth and adaptation (FOEN 2022, Herkenhoff et al. 2024). These environmental factors shape the genetic and agronomic properties of wild hop populations, making Switzerland an ideal location to investigate the diversity of hops that grow in various habitats, from lowland to subalpine zones (Hess et al. 1976). Such studies can contribute to a deeper understanding of how different hop genotypes may perform under varying environmental conditions.

Hops are primarily cultivated for their cones, which are the female inflorescences of the plant. These cones are a key raw ingredient in the brewing industry, where they are prized for their characteristic bitterness, aroma, and antimicrobial properties (Neve 1991; Zanolli and Zavatti 2008; Iniu et al. 2013; Almaguer et al. 2014; Dresel et al. 2016; Lafontaine and Shellhammer 2018; McCallum et al.

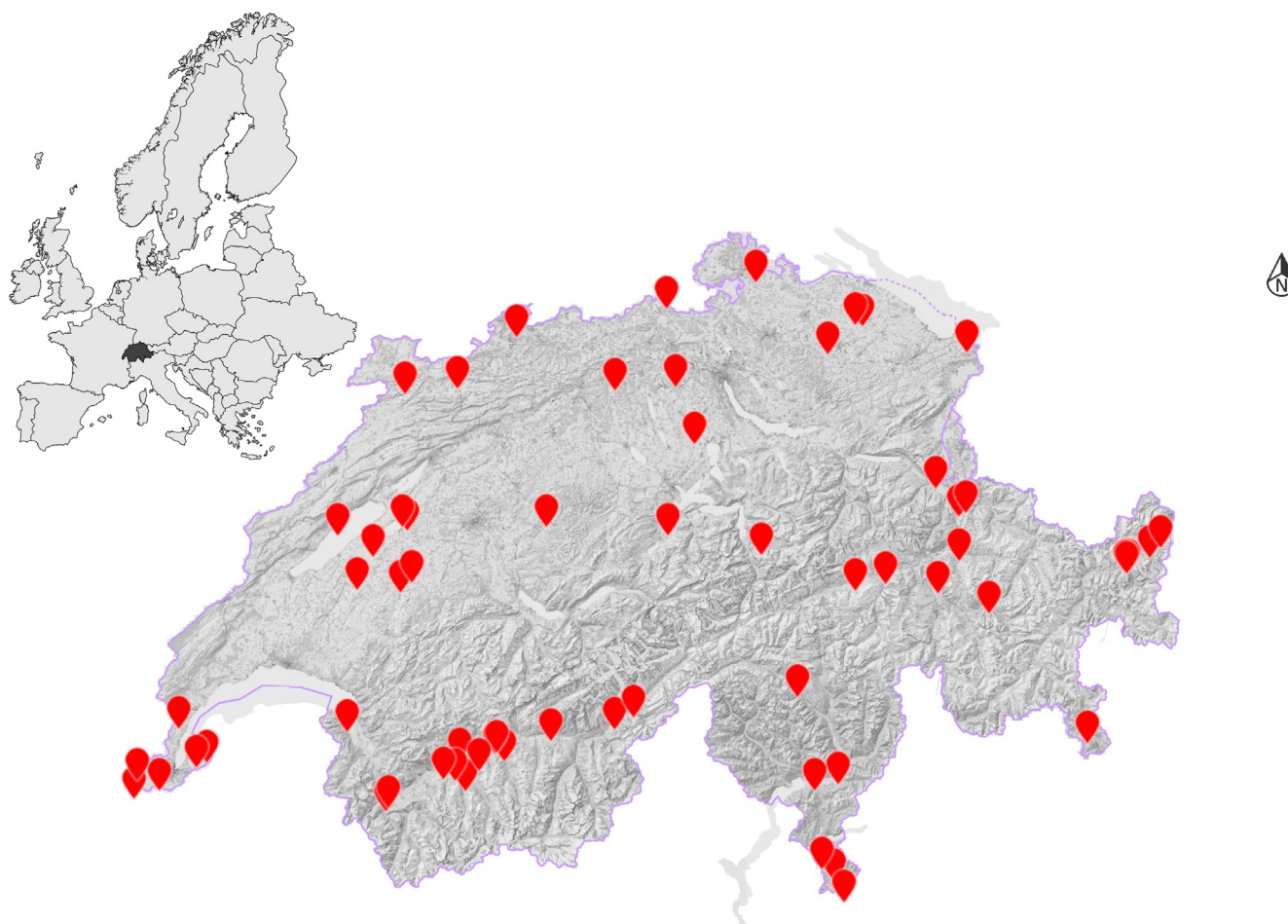
2019; Borges Martins da Silva et al. 2024). The compounds responsible for these properties include prenylflavonoids, polyphenolic compounds, and acyl phloroglucides. In addition to their use in brewing, hops contain bioactive compounds such as flavanones, chalcones, and phloroglucinol derivatives that have medicinal and pharmacological benefits (Zanolli et al. 2008). These compounds are of interest due to their antioxidant, anti-inflammatory, and anti-cancer properties (Kowalska 2022; Tamia et al. 2024). Accordingly, hop plants are important for the brewing industry but also have potential in the pharmaceutical and nutraceutical sectors.

European wild hop populations have gained interest due to their aromatic profiles and potential use in brewing (Mongelli et al. 2016; Machado et al. 2021; Riccioni et al. 2021; Paguet et al. 2023; Tegopoulos et al. 2023). These studies focus on evaluating the aromatic and chemical composition of hops grown in different European regions for their suitability in the production of beer. While much of this research has focused on wild hops from Germany and the Czech Republic, the native hop populations in Switzerland have remained underexplored. However, it is noteworthy that in Europe, Switzerland has one of the highest proportions of breweries relative to its population, with a demand for local beer made with Swiss ingredients.

In 2022, an unpublished sensory and olfactometric study was undertaken to assess the potential of wild hop populations from different bioclimatic regions in Switzerland. This work evaluated their suitability for use in brewing and provided the first comprehensive analysis of Swiss wild hops from various ecological zones. Here, in this study, the work was extended by investigating the genomic, chemical, and agronomic variability of 62 wild hop accessions collected in Switzerland from a range of altitudes, from the lowest zone of a mountain range (colline zone) to the subalpine level (Hess et al. 1976) (Figure 1). These wild hop accessions were compared with 14 commercial hop varieties, selected given their prominent role in the global brewing industry.

This research provides a comprehensive characterisation of Swiss wild hops, with an analysis of their genetic, chemical, sensory and

Figure 1. The top-left inset shows Europe in grey, with Switzerland in black. The main map displays the collection sites of the 62 wild hop accessions. These originate from lowland to subalpine environments, reflecting the ecological diversity contributing to their genetic and phenotypic variation.



agronomic traits. By comparing these wild hops with commercial varieties, the study seeks to identify potentially valuable genotypes for future breeding programs, not only for brewing but also for medicinal and plant protection purposes. Ultimately, this research seeks to contribute to the preservation of Swiss hop germplasm and to the development of breeding programs that enhance the sustainability and quality of Swiss hop production in the face of changing environmental conditions.

Materials and methods

Plant material and cultivation conditions

Sixty-two wild hop accessions ('wild') were collected from six different bioclimatic regions in Switzerland, at altitudes ranging from 281 to 1,190 meters above sea level ('masl') between 2019 and 2021 (Table 1). Wild hop rootstocks were propagated in glasshouses from cuttings and grown under controlled conditions for two years in pots before being transplanted in 2022 into a hop field in Conthey (latitude

46.21089, longitude 7.30123, altitude 480 masl). Four clones of each accession were planted randomly in the experimental field. Fourteen commercial cultivars (Table 1) were propagated from cuttings and grown in the same field conditions.

Based on preliminary agronomic results at harvest 2022, 15 wild accessions exhibiting promising traits were selected (primarily) by sensory analysis and classified as 'wild-selected' (Table 1). In the text and figures, accessions are referred to as 'commercial', 'wild-selected', and 'wild'.

Phenology

The phenological development of the hop plants was monitored in 2022 by weekly field observations from early July to mid-September. For each of the wild and cultivated hop accessions, four individual plants were observed by the same observer to ensure consistency. Each plant was assigned to a BBCH ('Biologische Bundesanstalt, Bundessortenamt, and

Chemical industry') growth stage following the guidelines of Meier et al (2009). This allowed for the reconstruction of individual phenological trajectories and facilitated comparisons between wild and cultivated types.

Yield analysis

The inflorescences (cones) were harvested at physiological maturity from each accession. After harvest, the cones were dried at 40°C for 12 hours to < 8% moisture, vacuum sealed in plastic bags and stored in the dark at -1 °C until analysis. Each accession was labelled with a unique code and the name of origin. Yield was the total dry weight of inflorescences per plant.

Genetic analysis

In all, 74 hop samples were analysed. DNA was extracted from leaf tissue using the DNeasy Plant Mini Kit from Qiagen starting with 100 mg of fresh leaf material. A set of 14 microsatellite markers were chosen for those analyses: 5-2, 11a59, 7-82, 3a88 (Brady et al. 1996); CO653778-GA9, GA4-P11-9, CO653957-TCCCA4 (Jakse et al. 2011); HI-ACA3, HI-AGA4, HIAGA6, HIAGA7, HIGT2, HIGT14 (Stajner et al. 2005); HIAGA8 (Korbecka-Glinka et al. 2016). Markers were amplified by PCR independently with every forward primer labelled with either DY682 or DY782. Amplified microsatellites were separated and visualised on denaturing urea polyacrylamide gel (10%) with a Licor 4300 DNA Analyzer at 160V/cm for 2h 50 mins. Distance based clustering was performed using DARwin version 6.0.21 (Perrier et al. 2003) by calculating simple matching coefficient of dissimilarity and constructing a dendrogram by unweighted neighbour-joining method based on the distance measure (Jaccard's coefficient).

Measurement of alpha and beta acids

Measurement was performed using the certified methodology of Mitteleuropäische Brautechnische Analysenkommission (MEBAK). Whole hop cones were ground to a fine powder using a blender and a volume of liquid nitrogen. Chemical extraction was performed by mixing 10 g of hop powder in 250 ml glass bottles with 20 ml HPLC grade methanol (Fisher Scientific, Whaltham, USA), 100 ml diethylether (Thommen F rler, Switzerland) and 40 ml HCl 0.1M (Fisher Scientific). Bottles were tightly capped and shaken at room temperature at 2.5 x g for 40 min.

After 10 minutes - to allow - phase separation, 2.5 ml of the upper ether phase was collected and diluted 10-fold with methanol and 1 ml inserted in HPLC vials through 13mm, 0.45µm hydrophobic PTFE filters (BGB analytic, B ckten, Switzerland).

A calibration extract was prepared using the International Calibration Extract (ICE-3) standard (Labor Veritas, Z rich, Switzerland). About 0.5 g was dissolved using an ultrasonic bath in HPLC grade methanol for 5 minutes at 25°C. The standard stock solution was adjusted to 100ml with methanol and stored in the dark for up to 48 hours at 4°C. After a fivefold dilution with methanol, the calibration extract was filtered and added to HPLC vials for standard injections.

Separation was performed using an Agilent HPLC 1100 system: EC250/4 Nucleosil 100-5 C18 column (Macherey Nagel, D ren, Germany), isocratic elution with a mobile phase composed by 850 HPLC methanol/170 DI water/2.5 phosphoric acid (vol/vol/vol), runtime of 13.5 minutes, measurement at a wavelength of 314 nm against a reference set at 420 nm. Co-humulone, n+ad-humulone, co-lupulone, and n+ad-lupulone were quantified against values in the ICE-3 standard datasheet (Labor Veritas), using chemstation software (Agilent).

Measurement of essential oil content

The essential oil content of dried hop cones was determined by hydrodistillation as described in the European Pharmacopoeia 11.0 (Council of Europe 2023). Approximately 50 g of coarsely ground, air-dried hop material was subjected to hydrodistillation for 3 hours using a Clevenger-type apparatus. This consisted of hops in a round bottom flask, a separator for the distilled solution and a condenser. The essential oil was collected and measured volumetrically and expressed as dry matter (%). All samples were analysed in duplicate, and the results averaged.

Volatile compounds - GC MS analysis

Hop samples (100 mg), dried and ground to a fine powder, were added to 20 mL headspace vials (Macherey-Nagel, Oensingen, Switzerland) which were hermetically sealed with a cap fitted with a Silicon Teflon septum (Macherey-Nagel). Samples were randomised (Excel RAND function)

Table 1. Accessions by name, type (commercial, wild-selected, or wild), and collection altitude (meters above sea level, masl).

Accession Name	Type	Altitude	Accession Name	Type	Altitude
101_Centennial	commercial	NA	64_St Margrathen	wild	445
102_Chinook	commercial	NA	66_Sion	wild	1072
103_Perle	commercial	NA	67_Schlatt	wild	394
105_Hersbrucker	commercial	NA	68_Hérémece	wild	1317
106_Willamette	commercial	NA	69_Aarau	wild	406
108_Saaz	commercial	NA	6_Martigny	wild	457
110_Galena	commercial	NA	70_Rietheim	wild	320
111_Glacier	commercial	NA	72_Trey	wild	547
92_Cascade	commercial	NA	75_Galmiz	wild	432
93_Tettnanger	commercial	NA	76_Nax	wild	1040
94_Magnum	commercial	NA	77_Confignon	wild	402
95_Herkules	commercial	NA	78_Chancy	wild	345
10_Mörel-Filet	wild	857	7_Fully	wild	460
11_Chessel	wild	380	81_Bürglen	wild	800
13_Delémont	wild	403	83_Strada	wild	1075
17_Cortailod	wild	431	84_Ramosch	wild	1190
20_Fribourg	wild	554	86_Scuol	wild	1335
22_Hauterive	wild	611	87_Ftan	wild	1395
23_Emmenmatt	wild	636	89_Coire	wild	784
25_Locarno	wild	198	90_Waltensburg	wild	756
26_Vico Morcote	wild	394	91_Hohtenn	wild	1094
27_Chiasso	wild	243	9_Arbaz	wild	922
35_Bogis Bossey	wild	466	12_Saint-Ursanne	wild-selected	432
39>Weinfelden	wild	432	18_Muttenz	wild-selected	281
3_Sierre	wild	523	28_Sulz	wild-selected	355
41_Alpnach	wild	447	36_Sugiez	wild-selected	432
46_Poschiavo	wild	1035	37_Sirnach	wild-selected	522
47_Schmitten	wild	1154	48_Paspels	wild-selected	804
49_Ilanz	wild	686	4_Sierre	wild-selected	524
51_Conthey	wild	478	50_Ernen	wild-selected	997
52_Pontis	wild	948	53_Dardagny	wild-selected	455
54_Meinier	wild	431	59_Hünenberg	wild-selected	441
55_Gy	wild	472	60_Malans	wild-selected	630
56_Mendrioso	wild	341	62_Landquart	wild-selected	568
57_Bellinzona	wild	277	65_Bürglen	wild-selected	486
58_Faido	wild	669	73_Domdidier	wild-selected	439
61_Sargans	wild	568	88_Taraps	wild-selected	1199

and stored at -20°C until analysis.

The extraction of volatile compounds was based on the Vacuum transfer in-Tube technique (VTT)

described in Fuchsmann et al. (2019). Samples were extracted using an MPS Robotic autosampler (Gerstel, Sursee, Switzerland) fitted with the ITEX (In-Tube Extraction) module and a needle packed

with Tenax TA, 80/100 mesh/Carbosieve S III, 60/80 mesh (ITEX2, BGB Analytics, Switzerland). The Vacuum in-Tube Extraction (V-ITEX) module developed by CTC Analytics (CTC Analytics, Zwingen, Switzerland) and connected to a Büchi V300 pump with an I300 interface (Büchi, Flawil, Switzerland) was connected to the autosampler.

Volatile compounds were extracted as follows: the extraction needle was conditioned (300°C, 60min) under a nitrogen flow (220 mL/min). The samples were incubated for 10 min at 60°C without agitation and then extracted for 10 min at 60°C under a 5 mbar vacuum. Throughout the extraction, the extraction needle was kept at 30°C. The ITEX needle was then desorbed in a CIS4 injector (Gerstel, Sursee, Switzerland) fitted with a liner filled with Tenax TA for 2 min at 300°C under a flow of hydrogen carrier gas. The injector in solvent vent with a flow of 10 mL/min was maintained at 10°C during injection and then heated to 240°C at a rate of 12°C/s. The purge flow to split vent was fixed at 7 mL/min at 0.02 min. After injection, the ITEX needle was reconditioned at 300°C for 10 min under a flow of nitrogen (220mL/min).

The volatile compounds were separated in an Agilent 7890B gas chromatograph GC (Agilent Technology, Santa Clara, CA USA) coupled to an Agilent 5977B mass selective detector MSD (Agilent). The column was a MN-FFAP fused silica capillary column (100% polyethylene glycol PEG with nitroterephthalic acid, bonded and cross-linked, 60 m × 0.20 mm × 0.25 µm film - Macherey-Nagel, Switzerland). The oven was at an initial temperature of 40°C for 10 min and then heated to 175°C at a rate of 5°C/min. The heating rate was increased to 20°C/min up to 220°C with a plateau of 0.75 min. The total run time was 40 min, with the transfer line maintained at 230°C. The hydrogen flow rate was 1.3 mL/min corresponding to a velocity of 42.804 cm/sec at constant flow. The MS source temperature was set at 230°C with a gain factor of 0.5. The mass range analysed was 40–400 Da. Volatile compounds were identified using the NIST 17 library.

Sensory analysis

Sensory analyses of 20 powder samples of different hop varieties (15 wild-selected + 5 commercial) were performed at Changins (University of Applied

Sciences and Arts Western Switzerland). The samples were maintained at room temperature (20°C ± 1°C), anonymously with a three-digit code in a glass jar for each of the 20 varieties. The first methodology used was Free Sorting task, the aim of which is to obtain groupings of products with olfactory similarities. Panellists were instructed to create as many groups as they wished (between two and 19 groups). Each group was made of products with olfactory similarities.

A second methodology - the Check-All-That-Apply (CATA) - with a panel of 27 trained panellists (14 female, 13 male, aged 26–65) who evaluated orthonasally the aroma of 20 hop powders. During training sessions, standard reference and commercial hop varieties were presented to familiarise the panel with hop attributes (Van Doorn 2020; Machado et al. 2021). After the training sessions, the tasters performed the evaluation sessions (Monday 27/03/2023 with 10 panellists and Thursday 30/03/2023 with 17 panellists). For this, each panellist smelt each hop powder and selected the terms that characterise each product. To do this, panellists were provided with a list of odour terms, including 13 terms characterising the main olfactory families: 'tropical fruits'; 'red berries'; 'citrus'; 'menthol'; 'spicy'; 'floral'; 'dry grass/hay'; 'fresh grass'; 'vegetal/soil'; 'woody'; 'lactic'; 'green fruit' and 'defaults'.

FIZZ software (Biosystemes, Couternon, France), version 2.50A, was used for the collection of the data. The FreeSortR package of the R-software was used to treat the data of the Free Sorting task (R development Core Team, 2014). To process the data of the CATA, a Chi-square distance to test the independence between the hops and attributes was applied using XLSTAT software version 2024.4.0 (Addinsoft, Paris, France, 2021). Then a Correspondence Factorial Analysis (CFA) was carried out using XLSTAT software to create a graphical representation of the 20 hop powders and the olfactory terms characterising each product.

Results

Plant growth and phenology

The wild hop accessions and the 14 commercial cultivars were planted in 2022. By September, all cultivars reached maturity and were ready for

harvest. There were no significant differences in the phenology between the wild and commercial cultivars (Figure 2).

A slightly faster development was observed with the wild hop varieties, particularly during the early stages of growth, to approximately BBCH stage 60 ('flowering') Meier et al (2009). During this period, the wild cultivars exhibited quicker growth compared to the commercial varieties, although this difference was not pronounced after flowering. On reaching full maturity, around harvest time, the development of both wild and commercial cultivars was indistinguishable.

All hop cultivars were harvested within a 10 day window in September 2022, reflecting similar ripening times across the different genotypes. This suggests that the wild hop accessions - despite originating from diverse biogeographical regions - adapted well to field conditions with maturation synchronised with the commercial cultivars. Such a uniform harvest window simplifies the management of production and potential breeding programs.

Genetic dissimilarity

Genetic analysis revealed a significant level of diversity among the Swiss wild hop accessions,

clearly distinguishing them from the commercial cultivars (Figure 3). While the wild hops were spread across a wide genetic range, the commercial cultivars were clustered together, indicating a much narrower genetic diversity. This genetic separation suggests that the wild hop populations in Switzerland have maintained distinct genetic traits, possibly due to adaptation to local biogeographical environments. In contrast, the commercial cultivars, which have been selectively bred for consistent traits (such as yield and aroma), exhibit less genetic variation.

This genetic dissimilarity highlights the potential of Swiss wild hops as a useful resource for breeding programs. The genetic profiles of the wild accessions could be leveraged to introduce novel traits into commercial breeding programs, such as improved disease resistance, climate adaptability, or unique aromatic compounds.

Agronomic hop performance traits

The wild and wild-selected hop cultivars showed, on average, higher yields compared to the commercial cultivars (Figure 4). This finding was both surprising and encouraging for selection and breeding, as it suggests that some of the wild accessions may offer improved productivity. Overall, the yields of both the wild and wild-selected cultivars

Figure 2. BBCH growth stages over time, from vegetative development in July until harvest, for individual accessions (thin lines) grouped by type: commercial cultivars (blue), wild accessions (green), and wild-selected cultivars (orange). Solid lines indicate the mean BBCH stage per group at each time point.

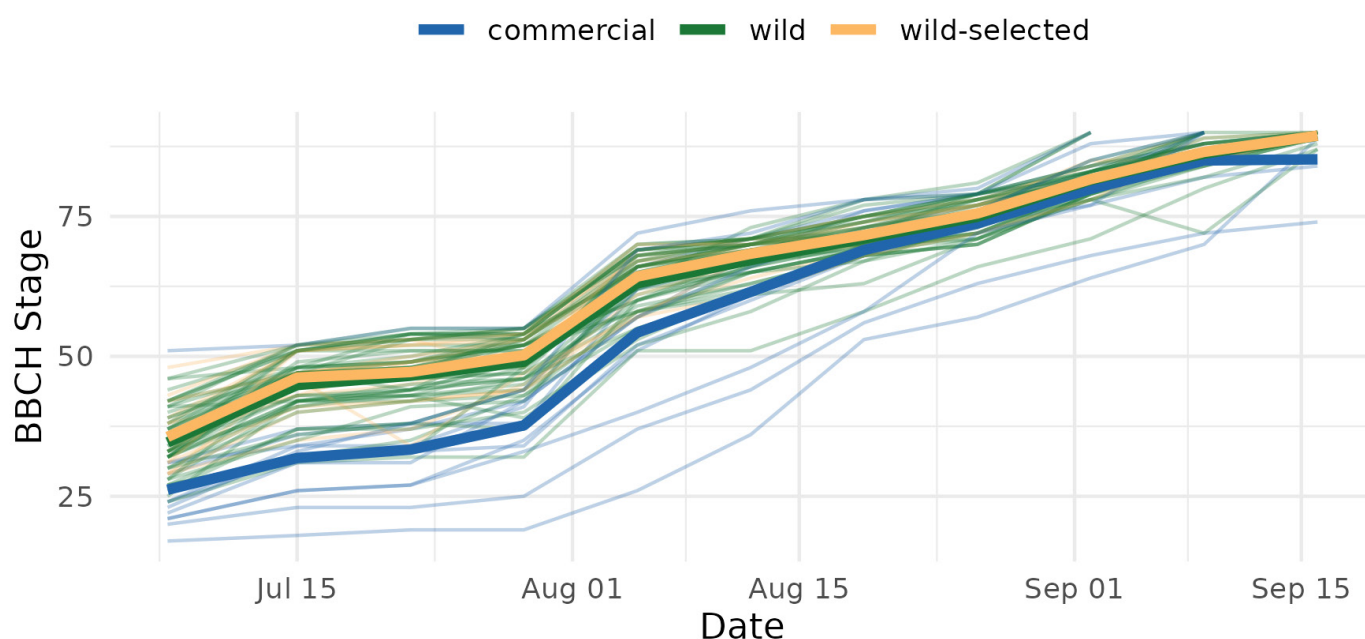
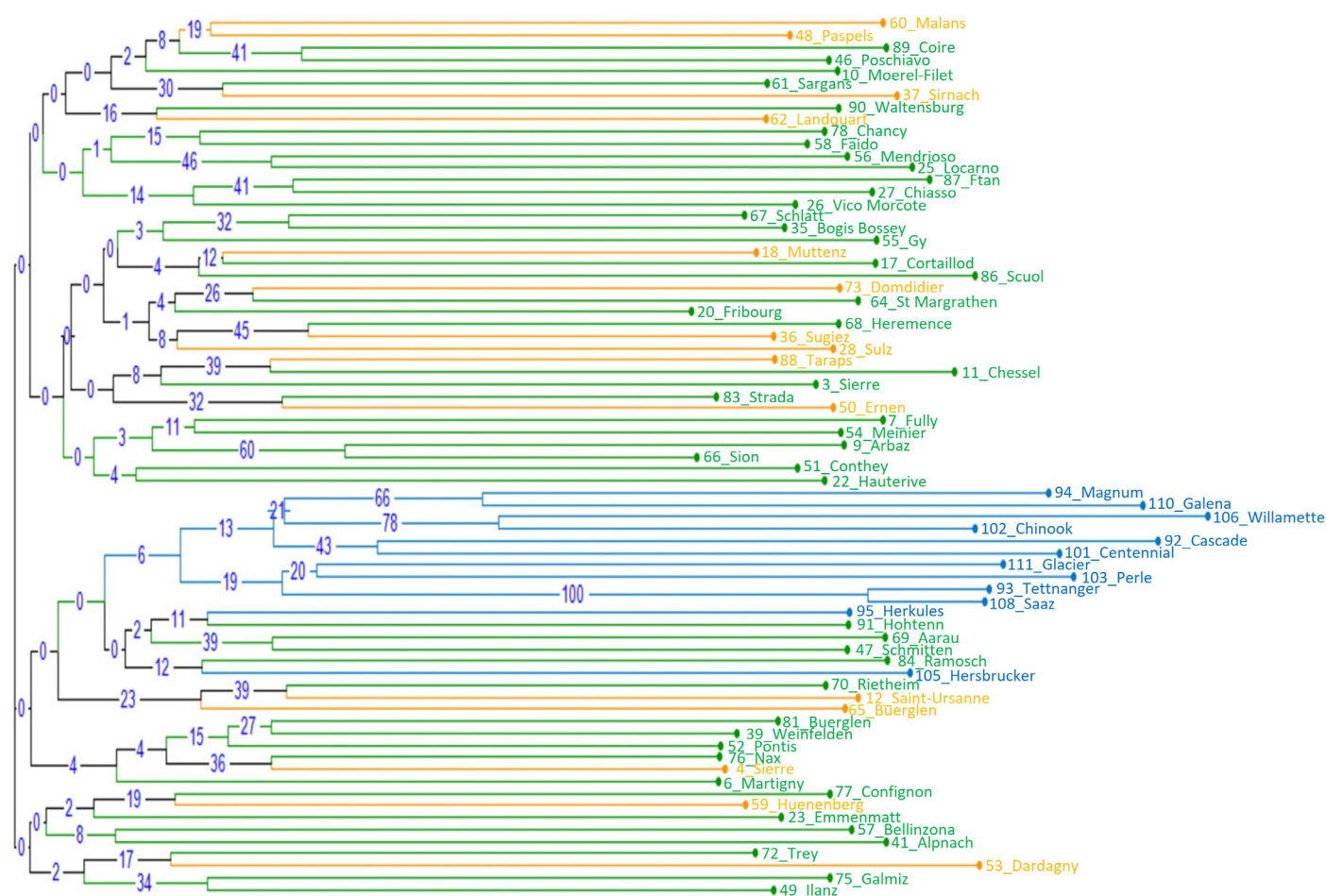


Figure 3. Genetic dissimilarity tree of the 74 hop accessions with commercial cultivars (blue), wild accessions (green), and wild-selected cultivars (orange). Distance based clustering was performed by calculating simple matching coefficient of dissimilarity across 14 microsatellite regions and constructing a dendrogram by unweighted neighbour-joining method based on distance measure. The score on each branch indicates the reliability level of each matching.



were good, indicating that these genotypes perform well under the tested field conditions.

With regard to the content of essential oils, the commercial cultivars and wild-selected hop accessions were similar, with some wild-selected cultivars outperforming the commercial varieties. This suggests that some of the wild genotypes may produce essential oils with a comparable or superior aromatic profile to the commercial cultivars. However, on average, the wild hop accessions had a lower essential oil content compared to the selected cultivars. This may be attributed to the natural variability of wild hop populations and could be an area of focus for breeding programs to increase essential oil production.

For alpha and beta acids, both key parameters for brewing, a similar trend was observed. The

commercial cultivars generally had higher levels of both alpha and beta acids, but there was considerable variability. Interestingly, some of the wild-selected cultivars achieved the same levels of alpha and beta acids as the commercial varieties, suggesting that selection from wild populations could yield hops with appropriate brewing characteristics. On the other hand, the wild hop accessions generally had lower concentrations of these acids, possibly a reflection of adaptation to local environmental conditions rather than selection for brewing traits.

Heatmap analysis of volatile compounds

As part of the characterisation of the volatile compounds in hops, a comparative analysis of commercial cultivars and wild Swiss hop populations from the 2022 harvest was performed. Fifty-three volatiles were selected to establish the aroma profile based on chromatographic intensity

and known odour-active properties, with emphasis on molecules with high sensory impact.

Compound identification used the NIST mass spectral library with a minimum match factor of 80. The data are presented as a heatmap (Figure 5) of normalised intensities (0–1 scale), where each cell represents the relative abundance of a compound in each variety. Rows span chemical classes (terpenes, esters, alcohols, aldehydes, ketones) and columns represent hop varieties; with commercial cultivars highlighted in blue, wild Swiss accessions in green and others in black. To reveal chemically coherent groupings, hierarchical clustering was performed on both compounds and samples using Euclidean distance and Ward.D2 linkage.

Interpreting these structures, three dominant chemical-sensory axes describe most of the variation: (i) a citrus/green-resin axis driven by monoterpene hydrocarbons (β -myrcene, D-limonene, α/β -pinene, ocimenes, p/m-cymene); (ii) a woody/spicy-balsamic axis dominated by sesquiterpenes (α -humulene, β -caryophyllene,

selinenes, γ/δ -cadinene); and (iii) a floral-fruity/estery vs. green-waxy axis associated with oxygenated monoterpenes and mid-chain carbonyls/esters (linalool; 2-nonanone/2-decanone/2-undecanone; methyl octanoate/nonanoate/4-decenoate/6-methyl-heptanoate, isobutyl and butyl isobutyrate).

Along the axes, the U.S. resin-citrus cluster - notably 92_Cascade, 101_Centennial, 102_Chinook (with 106_Willamette moderate) - exhibits bright citrus peel/pith (D-limonene, cymenes), pine/resin (α/β -pinene, β -myrcene), and green herbal ocimene notes, sometimes with a light floral lift (linalool) (Herkenhoff et al. 2026). The European noble-like cluster (108_Saaz, 93_Tettnanger) trends herbal-spicy with cleaner citrus-terpene top notes and is less resinous than the U.S. group. An intermediate commercial set (103_Perle, 94_Magnum, 95_Herkules) is anchored by woody/spicy sesquiterpenes (α -humulene, β -caryophyllene; selinenes/cadinenes) with a subtle citrus overlay consistent with structured bitterness and brewhouse versatility.

Figure 4. This shows - from top to bottom - yield, essential oil content, alpha acid and beta acid concentration for the hop accessions, grouped by type: commercial cultivars (blue), wild accessions (green), and wild-selected cultivars (orange). Each point represents a single accession. Horizontal bars indicate the mean value for each group within the respective trait.

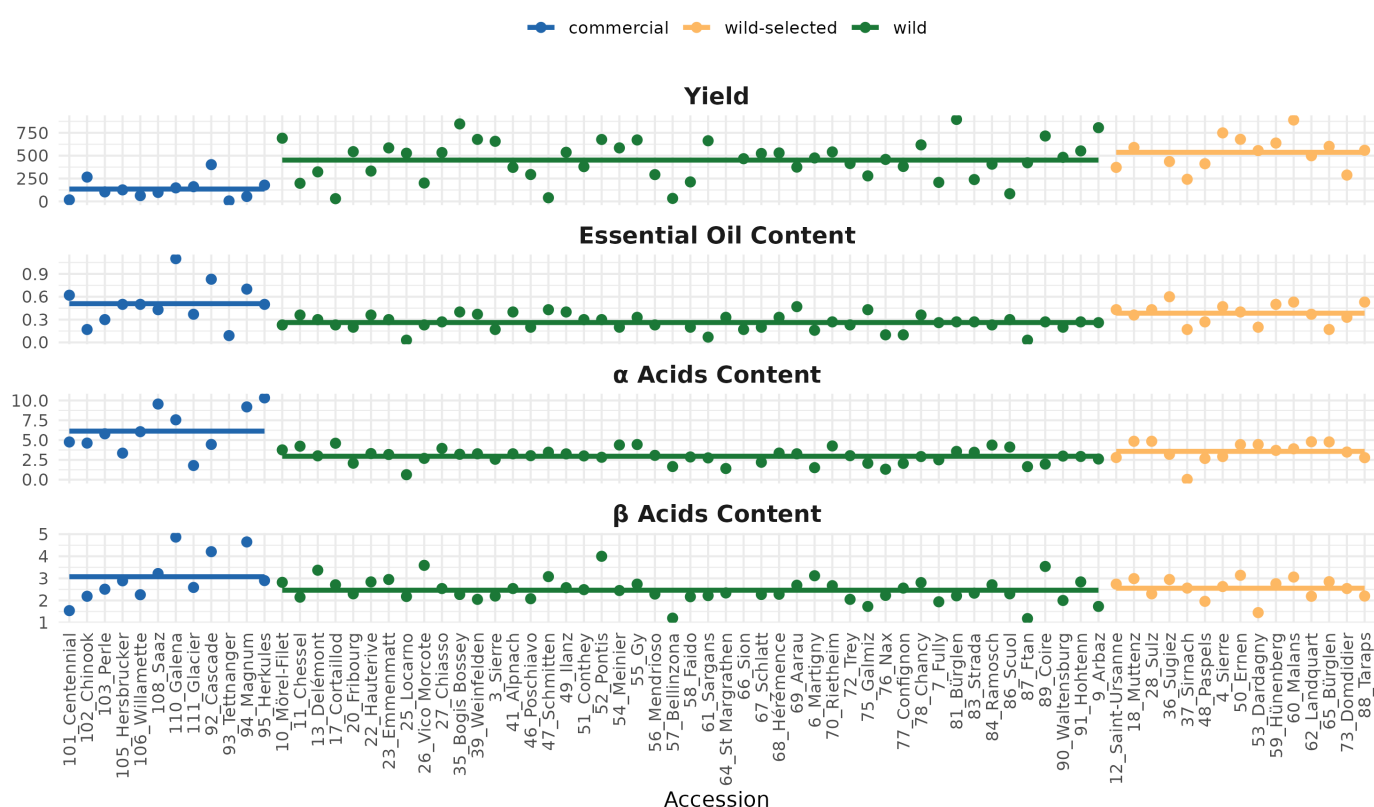
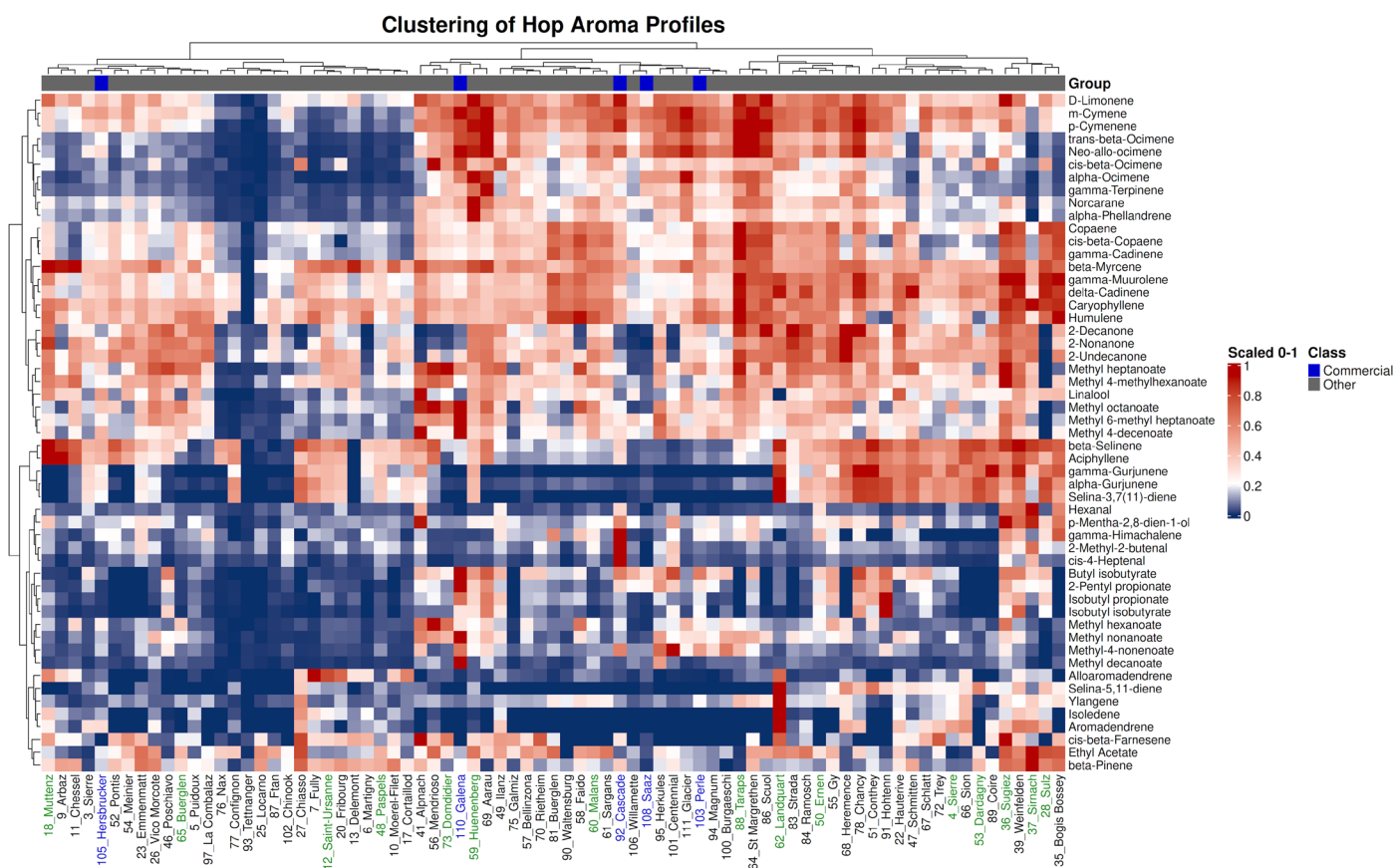


Figure 5. Heatmap of volatile compounds (scaled 0–1) across commercial (blue), wild (green), and selected hop varieties (black). Clustering was performed using Euclidean distance and Ward.D2 linkage. Commercial varieties group together and display characteristic terpene-rich profiles (β -myrcene, humulene, caryophyllene), while wild varieties form separate clusters with higher variability and unique ester signatures. Selected varieties are positioned intermediately, reflecting a combination of commercial-like aroma traits and the metabolic diversity of local wild hops.



Two of the commercial cultivars behave as sensory outliers. 105_Hersbrucker is separated from other commercial hops due to elevated linalool together with C9–C11 ketones (2-nonanone/2-decanone/2-undecanone), yielding a floral (lavender/orange blossom) character over a green-waxy, citrus-peel base. 110_Galena, enriched in cymenes and mid-chain methyl esters, leans toward citrus-peel/terpene with a sweet, ripe-fruity (apple, pear, pineapple) overlay, contrasting with the drier resin profile of Cascade/Centennial/Chinook.

The wild Swiss accessions populate all three axes and provide useful diversity around commercial reference spaces. Several lines - 75_Galmiz, 100_Burgaeschi, 73_Domdidier, 25_Locarno, 76_Nax - have noble hop like signatures (herbal-spicy with citrus-terpene lift), bridging toward Saaz/Tettnanger or Perle/Magnum/Herkules. 3 & 4_Sierre and 48_Paspels align Hersbrucker-like, combining floral linalool with green-waxy ketones, providing a bouquet without heavy resin. Lines adjacent to the

Galena space (e.g., 69_Aarau, and 100_Burgaeschi, 73_Domdidier) show stronger sweet-fruity ester signatures that could add 'juicy' top-notes to otherwise woody or spicy bases. Other wild hops (57_Bellinzona, 61_Sargans) carry higher sesquiterpene load, emphasizing woody/spicy-balsamic.

In terms of sensory translation, key marker aroma links include: β -myrcene (green/resinous), D-limonene (orange/lemon), α/β -pinene (pine), ocimenes (green-herbal/citrus), p/m-cymene (citrus peel/terpene), linalool (floral), α -humulene/ β -caryophyllene/selinene/cadinene (woody/spicy-balsamic), hexanal/cis-4-heptenal (cut grass/fatty-green), C9–C11 ketones (waxy/green-peel), and mid-chain esters (sweet-fruity, shifting toward waxy/oily with chain length). Together with the clustering, these signatures suggest that commercial hops are metabolically cohesive and terpene-forward, while wild populations offer ester rich, floral, or sesquiterpene dense profiles that

broaden the sensory space. The outlier status of both 105_Hersbrucker (floral/green-waxy) and the 110_Galena ester/terpenic tilt are relevant for blending. Although formal odour-activity ratios would refine quantitative impact, the present matrix delineates clear chemotype trajectories for breeding and recipe development - ranging from bright citrus/pine, through herbal/spicy, to floral and juicy-fruity - and identifies wild accessions that can be paired with commercial hops to achieve targeted aromatic outcomes.

Sensory analysis

The results of the Check-All-That-Apply (CATA) following a Correspondence of Factorial Analysis are presented in Figure 6. The plane with dimensions 1 and 2 accounts for 65.53% of the total variance. On the first dimension (45.81%) of the total genetic or chemical differences between some of the wild hops and commercial varieties is shown. A clustering of five commercial varieties on the left and upper part of the product map, with 92_Cascade, 103_Perle, 105_Hersbrucker, 108_Saaz and 110_Galena close to each other. 92_Cascade is characterised at the level at 5% by the term 'tropical fruits', with sample 105_Hersbrucker is described as 'citrus' and 'floral'. Hop 110_Galena is perceived as 'red berries' and 'tropical fruits'.

Some wild varieties were sensorially characterised as being close to these commercial varieties. For example, 53_Dardagny is perceived as having

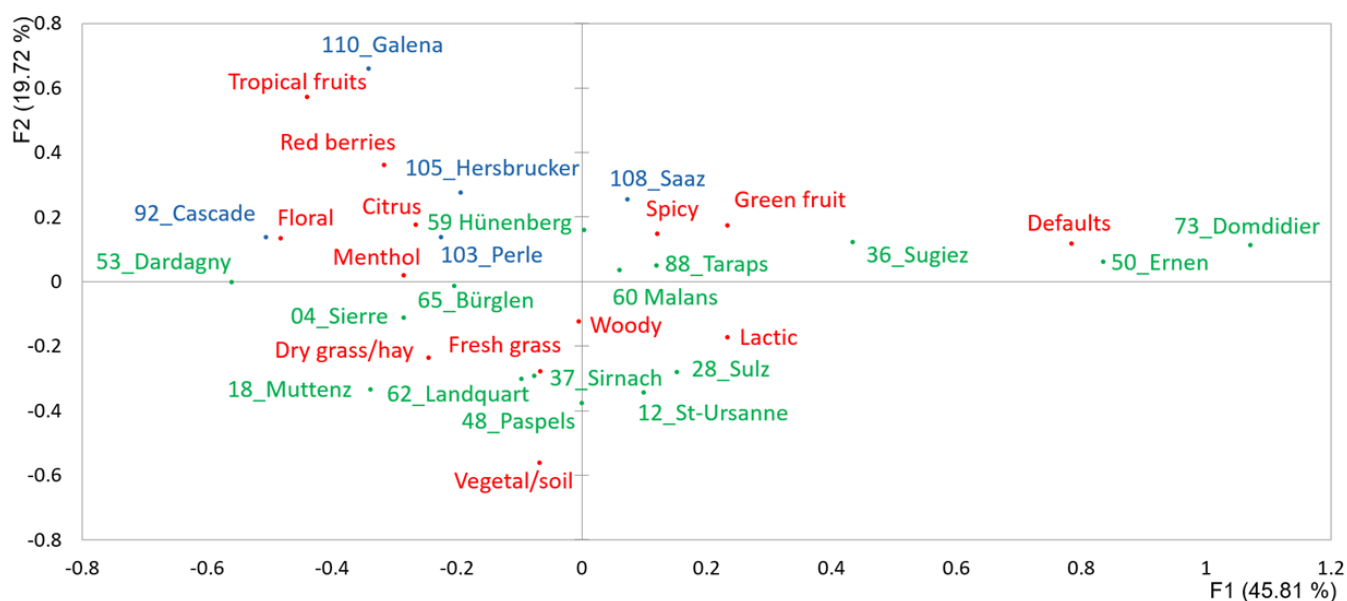
'floral' and 'menthol' notes with 12_Saint-Ursanne described as 'dry grass/hay'. Conversely, some wild varieties are distinguished from commercial varieties by having other aromatic profiles, as with 48_Paspels characterised as being 'vegetal/soil'.

Discussion

This study represents the largest and most comprehensive collection of Swiss wild hop accessions to date, detailing their genetic, agronomic, and chemical diversity. Analysis of 62 wild hop accessions has expanded the understanding the genetic pool of wild hops in this region. This information can serve as will be a useful resource for both brewing and other uses.

The results show a high level of genetic variability among the Swiss wild hop accessions, differentiating them from commercial cultivars. Such genetic diversity offers potential for unique aromatic profiles, improved resistance to environmental stresses, the development of hops with enhanced resistance tolerance together brewing or medicinal applications. Several wild genotypes exhibited promising characteristics, including unique aromatic profiles, which could be explored further in the context of new product development. Further, resistance traits to pests or diseases, could be of value in more sustainable agricultural practices. Additionally, the wide genetic diversity of the wild hop accessions can be used to breed hops with characteristics that meet

Figure 6. Map of sensory attributes and hop powders on dimensions 1 and 2 following Correspondence Factor Analysis. The sensory descriptors are in red, commercial varieties in blue and wild varieties in green.



the needs of diverse markets.

In terms of agronomic performance, the wild and wild-selected hop cultivars exhibited comparable results to the commercial varieties. These include plant development, yield, essential oil content, and concentration of alpha and beta acids. The wild hops performed well in terms of yield, showing potential for use in production systems. Moreover, while the essential oil content and the levels of alpha and beta acids were typically lower than those found in the commercial cultivars, some wild-selected genotypes matched or even exceeded the commercial varieties in terms of these brewing parameters. This indicates that wild hop populations have agronomic potential and could contribute to the development of cultivars with similar or superior qualities compared to commercially cultivated hops. This is also relevant from a brewing perspective, as hop chemistry can influence microbial behaviour in high-hopped beers (da Silva et al. 2024).

With regard to sensory analysis, the commercial cultivars clustered together in terms of aromatic profiles. This is consistent with their widespread use and breeding for specific, stable characteristics. In contrast, some wild hop accessions, particularly those with unique or under-explored aromatic profiles, could meet consumer demands for hops with flavours similar to popular varieties like Cascade (Herkenhoff et al. 2026). Additionally, there is potential for these wild hops to contribute to the development of novel tastes that could appeal to emerging markets or niche brewing sectors. Given the growing trend for innovation in the brewing industry, the unique sensory profiles of Swiss wild hops could provide brewers with options for creating new beers.

While this study provides insights into the genetic, agronomic, and chemical potential of Swiss wild hops, questions remain that warrant further investigation. One is the pathogen resistance of the wild hop accessions. Given the increasing challenges posed by pests and diseases in hop cultivation, identifying wild hop genotypes with natural resistance could play a role in developing more sustainable hop varieties. Understanding the genetic basis of these resistance traits and their potential application in breeding programs could

reduce the use of chemical pesticides and improve the resilience of hops to environmental pressures.

Another consideration is the between year variability in the performance of the wild hop accessions. While the current study provides baseline data, it is necessary to evaluate the stability of these traits across multiple growing seasons. This will determine whether the performance - yield, essential oil content, and alpha/beta acids - is consistent year to year or impacted by environmental factors (Herkenhoff et al. 2024). Long-term studies across different locations and climatic conditions will provide a more comprehensive understanding of the suitability of wild hops for large-scale cultivation.

In addition to yield and chemical composition, it is important to consider how these wild hop accessions can be tailored for specific uses. Understanding how to best utilise wild hops for different types of products - such as brewing, medicinal applications, or plant protection - will be necessary for integration into commercial systems. This includes which wild hop traits are most valuable for each application, whether it be a high aromatic content for brewing or bioactive compounds for medicinal purposes. Additional research on the functional properties of these hops will enable more targeted use and breeding strategies.

Given the challenge of climate change, the ability of wild hop accessions to tolerate higher temperatures and adapt to varying climatic conditions is of importance. Heat tolerance is of relevance as global temperatures rise, affecting hop production in traditional growing regions. Identification of wild hop genotypes that exhibit heat tolerance could be of value for regions experiencing warmer climates or more erratic weather patterns. Additionally, understanding how these hops respond to other environmental stressors, such as drought or soil salinity, could broaden their potential use in different geographic locations.

Adaptability to different regions is another factor in determining the future utility of Swiss wild hops. While this study was conducted in a specific field environment, evaluating the performance of these wild hop accessions in diverse geographical locations and soil types will be critical for understanding

their broader applicability. Exploring the potential for cultivation of these hops in other areas, both within Switzerland and internationally, could help diversify hop production systems and reduce reliance on commercial cultivars.

As the brewing industry continues to seek innovation and sustainability, the wild hop accessions explored here offer exciting possibilities for breeding programs aimed at improving hop quality, yield, and resilience. Further research and long-term trials will be necessary to realise the potential of these genetic resources in the face of evolving agricultural challenges and market demands.

Conclusions

This study considers the genetic, agronomic, and chemical diversity within Swiss wild hop populations, offering valuable insights for future breeding programs. The wild hop accessions exhibited promising characteristics in terms of yield, essential oil content, and brewing parameters, with comparable or, in some cases, superior traits to commercial cultivars. The high genetic variability presents an opportunity for discovering new aromatic profiles, disease resistance, and adaptability to changing environmental conditions. While there are questions regarding pathogen resistance, climate adaptability, and between-year variability, the findings of this study underline the potential of Swiss wild hops for both brewing and emerging applications. Further research and long-term trials will be required to fully exploit the genetic resources of these wild hops and to address the challenges posed by climate change and market demands.

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Conflict of interest

The authors declare there are no conflicts of interest.

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Sophia Corsi: investigation, data curation, writing (original draft), writing (review and editing).

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