*Sites and plant material*

The sampling included four locations of *A. halleri* in southern Poland: two metalliferous (M) locations at low altitude in the Olkusz region (M\_PL22 and M\_PL27), one sub-alpine non-metalliferous location at the northern foothills of the Tatra Mts (NM\_PL35), and one non-metalliferous location at low altitude in Niepołomice Forest (NM\_PL14). In August 2014, 10 *A. halleri* individuals were sampled at each site, every 4 m along transects to avoid potential clones. Plants have subsequently been grown in a greenhouse environment (photoperiod: 14 h day, 10 h night; temperature: 20°C day, 18°C night; irradiance at plant level: 300 µmol photons m-2 s-1). Pots have been repeatedly randomized and plants were propagated several times via cuttings to minimize carry-over effects of the native population environment. As plants grew and expanded, each genotype was further divided to obtain clonal cuttings for two reciprocal transplant experiments: in the field (F) and under controlled (C) condition.

*Reciprocal transplant experiment in the field*

The reciprocal transplantations consisted of planting individuals from each population to the site of origin (sympatric) and to three sites in the foreign region (allopatric). Accordingly, each site received plants from its local population and from three foreign populations, in a randomized block design with three plots per site. Two months prior planting, natural vegetation in the experimental plots was mechanically removed. In May 2015 (t0), four-week old rooted cuttings were transplanted directly into the local soil, on an evenly-spaced square grid with a 0.3 m spacing. Each plot contained 40 individuals represented by 10 genotypes per population. A total of 480 individuals was used in this experiment (4 populations x 10 genotypes x 4 clonal replicates x 3 plots = 480 plants). The time until the following spring was considered as a period to eliminate carry-over effects of the greenhouse conditions on transplants (Latimer 1991). The experiment run from March 2016 (t1) to September 2016 (t2). The experimental plots were hand-weeded through the entire experiment.

The survival after the acclimatization was first assessed in March 2016 (at t1), and monitored during the growing season 2016 (until t2). At the peak of the growing season we scored 64 phenotypic traits, including variables representing growth, reproduction, elemental composition, and foliar properties of each plant. For the list of all traits and details on the trait measurements see Supplementary Table S1 and Supplementary Methods.

*Reciprocal transplant experiment under controlled condition*

160 1.5 l pots were filled with substrate (topsoil) collected directly at study sites (40 pots x 2 soil types x 2 sites). Four-week old rooted cuttings were individually placed into pots in April 2018. Each treatment received plants from its local population and from three foreign populations (4 populations x 10 genotypes x 4 clonal replicates = 160 plants). With some genotypes being sterile, the final number of genotypesin the experiment was 142 (i.e. 10 to 18 genotypes per location; Table 1).

This experiment was conducted in a controlled growth chamber, with a day/night temperature regime of 20/18° C, 65% humidity, photoperiod of 13h/11h, and a light intensity of 100 μmol photons m-2·s-1. Pots have been watered with deionized water and randomized weekly.

After six weeks of culture we scored 50 phenotypic traits, including variables representing growth, elemental composition, and foliar properties of each plant. For the list of all traits and details on the trait measurements see Supplementary Table S1 and Supplementary Methods.

*DNA extraction whole-genome sequencing, and bioinformatic analyses*

For DNA extraction, 15 mg of silicalgel-dried leaf tissue of each clone were used. Extraction was performed with a KingFisher Flex 96 (Thermo Fisher Scientific, Waltham, USA) and the sbeadex maxi plant kit (LGC Genomics, Berlin, Germany). DNA quality was checked on 1.5% agarose gels stained with GelRed and a Nanodrop 1000 (Thermo Fisher Scientific). DNA quantity was assessed with a Quantus fluorometer (Promega, Madison, USA). Library preparation of the 40 samples was done with the KAPA HyperPrep Kit (Roche, Basel, Switzerland) and whole-genome sequencing (2x150 bp paired-end reads) was performed on four lanes of an Illumina HiSeq 2500 with high output mode at the Quantitative Genomics Facility (D-BSSE, ETH Basel, Switzerland).

From the obtained reads, we removed low quality reads (Q<15 along a sliding window of 4 bp, length <50) with Trimmomatic 0.35 (Bolger et al. 2014). Only read pairs for which both forward and reverse reads passed the quality criterion were further considered. We then mapped the remaining reads to the reference genome of *A. halleri* ssp. *halleri* (Sailer et al. 2018) using BWA 0.7.12 (Li and Durbin 2009) and a mapping quality threshold of 10. Freebayes 1.1.0 (Garrison 2012) was used to perform the SNP calling, with ploidy set to 2, minimum alternative allele proportion to 0.2, and minimum count of the reference allele to 2. Using VCFtools (Danecek et al. 2011) and mainly following the dDocent pipeline (Puritz et al. 2014), the SNP set was then reduced to loci with mapping quality ≥20, minimum depth ≥3, mean depth ≥10, minor allele count ≥3, minor allele frequency ≥0.05, and proportion of missing data ≤0.5. Moreover, we excluded SNPs exhibiting a proportion of missing data per population >0.2. From this SNP set we only kept loci with an allele balance between 0.25 and 0.75, a mapping quality/alternate allele count ratio ≥10, and support from both forward and reverse reads (PAIRED and PAIREDR, resp.). To exclude potentially paralogous regions, we excluded SNPs with a coverage > 100 x. We decomposed complex variants and removed InDels. We finally only kept bi-allic SNPs and missing data proportion of ≤0.2. We then produced two SNP sets; the complete SNP set and one SNP with loci in Hardy-Weinberg equilibrium (HWE) in all populations (*p*<0.05).