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Epigenetic variation predicts regional and local intraspecific functional diversity in a perennial herb

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Abstract

The ecological significance of epigenetic variation has been generally inferred from studies on model plants under artificial conditions, but the importance of epigenetic differences between individuals as a source of intraspecific diversity in natural plant populations remains essentially unknown. This paper investigates the relationship between epigenetic variation and functional plant diversity by conducting epigenetic (methylation-sensitive amplified fragment length polymorphisms, MSAP) and genetic (amplified fragment length polymorphisms, AFLP) marker-trait association analyses for 20 whole-plant, leaf and regenerative functional traits in a large sample of wild-growing plants of the perennial herb *Helleborus foetidus* from ten sampling sites in southeastern Spain. Plants differed widely in functional characteristics, and exhibited greater epigenetic than genetic diversity, as shown by percent polymorphism of MSAP fragments (92%) or markers (69%) greatly exceeding that for AFLP ones (41%). After controlling for genetic structuring and possible cryptic relatedness, every functional trait considered exhibited a significant association with at least one AFLP or MSAP marker. A total of 27 MSAP (13.0% of total) and 12 AFLP (4.4%) markers were involved in significant associations, which explained on average 8.2% and 8.0% of trait variance, respectively. Individual MSAP markers were

more likely to be associated with functional traits than AFLP markers. Between-site differences in multivariate functional diversity was directly related to variation in multilocus epigenetic diversity after multilocus genetic diversity was statistically accounted for. Results suggest that epigenetic variation can be an important source of intraspecific functional diversity in *H. foetidus*, possibly endowing this species with the capacity to exploit a broad range of ecological conditions despite its modest genetic diversity.

Introduction

The crucial evolutionary importance of variation within species has been long acknowledged and thoroughly scrutinized from an endless variety of perspectives (Bowler 2005; Herrera 2009). In contrast, emphasis on the ecological consequences of intraspecific variation is a relatively recent phenomenon, largely bound to the emergence of community genetics and trait-based community ecology as two burgeoning, interrelated ecological subdisciplines (Neuhauser *et al.* 2003; Whitham *et al.* 2006; Violle *et al.* 2012). Intraspecific trait variability enhances the ecological breadth and distributional range of species (Sides *et al.* 2014), and contributes to amplify the functional diversity of plant communities, a key component of biodiversity with important implications for species coexistence and ecosystem functioning (de Bello *et al.* 2011; Albert *et al.* 2012). Genetic diversity of populations, through its effects on trait-dependent functional variability, also influences community and ecosystem processes (Hughes *et al.* 2008; Hersch-Green *et al.* 2011). In plant communities, genetic diversity of dominant species can be as important or more than overall species richness in shaping the diversity and abundance of associated consumers. Intraspecific genetic differences may condition the structure of herbivore communities (Whitham *et al.* 2006; Tack & Roslin 2011), and distinct genotypes may possess distinct functional features and play different ecological roles as if they were separate species (Crawford & Rudgers 2012).

The current community genetics framework rests on the unstated assumption that genetic variation (i.e., arising from allelic differences due to DNA sequence variants) is the only source of heritable, trait-based functional variation among conspecific genotypes (Whitham *et al.* 2006; Violle *et al.* 2012). Nevertheless, considerable evidence has accumulated in recent years showing that epigenetic variation (heritable phenotypic changes unrelated to variation in DNA sequence; Richards 2006) can also account for phenotypic differences between conspecific plants that are stably transmitted from parents to offspring (Jablonka & Raz 2009; Johannes *et al.* 2009; Verhoeven *et al.* 2010; Becker & Weigel 2012; Cortijo *et al.* 2014). Cytosine methylation is an important mechanism for stable epigenetic modification of DNA in plants, and heritable individual variation in phenotypic traits has been induced artificially by manipulating the pattern (distribution across specific sites in the genome) and/or level (proportion of total cytosines that are methylated) of cytosine methylation (Grant-Downton & Dickinson 2005, 2006; Jablonka & Raz 2009). Artificial modifications of patterns and/or levels of cytosine methylation can generate heritable intraspecific variation in a broad array of functional plant traits, including size, growth rate, seed size, seed production, flowering phenology, leaf size and shape, and stomatal features (Sano *et al.* 1990; King 1995; Finnegan *et al.* 1996; Fieldes & Amyot 1999; Tatra *et al.* 2000; Kondo *et al.* 2006; Amoah *et al.* 2012; Tricker *et al.* 2012). Results of these experiments provide justification for the hypothesis that, in addition to genetic variation, epigenetic differences between individuals might be acting as an hitherto unrecognized source of intraspecific functional diversity in natural plant populations (Bossdorf *et al.* 2008). Additional motivation is provided by observations indicating that (i) wild plant populations harbor considerable epigenetic diversity, which often exceeds genetic diversity (Li *et al.* 2008; Herrera & Bazaga 2010; Lira-

Medeiros *et al.* 2010); (ii) intraspecific variation in global DNA cytosine methylation may be associated with differences in functional traits (Alonso *et al.* 2014); and (iii) epigenetic diversity may enhance the colonizing ability, productivity, recruitment and stability of plant populations (Richards *et al.* 2012; Latzel *et al.* 2013; Herrera *et al.* 2014). All these findings point to a role of epigenetic variation as a source of intraspecific functional diversity.

With few exceptions, studies on the ecological significance of epigenetic variation have been conducted on model plants under artificial conditions, and the hypothesis relating epigenetic variation to intraspecific functional diversity remains largely unexplored in natural populations (but see Richards *et al.* 2012; Alonso *et al.* 2014; Schulz *et al.* 2014). In this paper, we undertake epigenetic marker-trait association analyses on a large sample of wild-growing plants of the herb *Helleborus foetidus* to test the predicted relationship between epigenetic variation and functional diversity in this species. Individual epigenetic differences may or may not be independent of individual genetic differences (i.e., DNA sequence-based) (Richards 2006; Herrera & Bazaga 2010; Herrera *et al.* 2014), hence genetic markers were also included in the association analyses. This will allow, on one side, to evaluate the association between epigenetic variation and trait variation while controlling for the effects of genetic heterogeneity and, on the other, to compare the quantitative importance of genetic and epigenetic variation as predictors of intraspecific functional diversity. Epigenetic and genetic marker-trait associations will be sought for a total of 20 whole-plant, leaf and regenerative traits (listed in Table 1) measured on individual wild-growing plants. All plant features considered here qualify as functional traits, as they may directly or indirectly affect the fitness or the environment of individuals (Pérez-Harguindeguy *et al.* 2013).

Materials and methods

Study plant and field sampling

Helleborus foetidus L. (Ranunculaceae) is a perennial, evergreen herb widely distributed in western and southwestern Europe, where it can be found from sea level to 2100 m elevation in a broad variety of habitat types ranging from open scrub to conifer and broad-leaved forests (Mathew 1989). Adult plants generally consist of vegetative and reproductive ramets arising from a small, weakly developed rhizome (Werner & Ebel 1994). After several seasons of vegetative growth, each vegetative ramet produces a single terminal inflorescence and dies following fruit maturation and seed shedding. In our study area (see below), flowering mostly takes place during February-April. Each inflorescence produces 25-75 flowers over its 1.5-2.5 months flowering period, and bumble bees are the main pollinators. Fruit maturation and seed shedding occur in June-early July.

Field sampling for this study was conducted during 2012 and 2013 in the Sierra de Cazorla, a well-preserved mountain area in Jaén province, southeastern Spain. *Helleborus foetidus* is widely distributed there over a broad range of elevations and habitat types. Plants were sampled at ten locations, chosen to encompass the entire ecological range of the species in the region (Appendix S1). Sites included the three localities studied by Herrera *et al.* (2013, 2014). At each locality, 20 widely spaced, inflorescence-bearing plants were randomly selected during February-May 2012, marked with permanent tags, and georeferenced using a GPS receiver. Sampled plants were distributed over roughly similar areas at all sites (Appendix S1). Elevational differences between sites resulted in phenological variation. To avoid developmental variation in DNA methylation confounding individual differences in methylation patterns, leaf samples for molecular analyses were collected at each site during the local flowering peak. Young expanding leaves were collected from each plant, placed in paper envelopes and dried immediately at ambient temperature in sealed containers with silica gel.

This material was used for genetic and epigenetic fingerprinting of plants, and also for leaf carbon isotope ratio measurements (see below). The following traits were recorded for every plant at the time of leaf collection in 2012: number of vegetative and reproductive ramets, diameter of inflorescence at the base, number of flowers per inflorescence, and age in years of flowering ramets as determined from counts of annual marks left on stems by the abruptly shrinking late-season internodes (Werner & Ebel 1994). Length of floral perianth ('corolla length' in Herrera *et al.* 2002) was measured on two randomly chosen flowers from each plant, and the mean used as an estimate of flower size. The number of follicles eventually developing into ripe fruits was determined for each plant shortly before fruit maturation. For each plant, a sample of ripe seeds were collected from 2-9 different fruits (range = 10-15 seeds per plant), weighed individually to the nearest 0.1 mg, and a mean seed mass value obtained.

Sampling sites were revisited in spring 2013 to collect additional leaf material from marked plants for measuring functional leaf traits related to foliar size and density, and characteristics of stomata (see below). Some plants had died or lost their tags, and could not be sampled again. *Helleborus foetidus* bear pedate, deeply-divided leaves, and the number, size and morphology of constituent segments ('leaflets' hereafter) vary within and among leaves of the same plant (Mathew 1989; Werner & Ebel 1994). To account for this variation and obtain figures that are comparable between plants, foliar trait measurements were taken on the central leaflet of leaves from different parts of the plant, sampled using a stratified scheme. The two longest vegetative ramets were selected from each plant. From each ramet, the central leaflets of two non-adjacent, undamaged, mature leaves were collected, labeled, and kept into sealed plastic bags in a cooler until processed in the laboratory.

Laboratory methods

Genetic and epigenetic characteristics of *H. foetidus* plants sampled were assessed by fingerprinting them using amplified fragment length polymorphism (AFLP; Weising *et al.* 2005; Meudt & Clarke 2007) and methylation-sensitive amplified polymorphism (MSAP; Schulz *et al.* 2013; Fulneček & Kovařik 2014) techniques. Total genomic DNA was extracted from dry leaf samples using Qiagen DNeasy Plant Mini Kit and the manufacturer protocol. AFLP and MSAP analyses were conducted on the same DNA extracts. The AFLP analysis was performed using standard protocols involving the use of fluorescent dye-labeled selective primers (Weising *et al.* 2005). Restriction-ligation was conducted using *Pst*I / *Mse*I endonuclease mixture and double-stranded adaptors. After an initial screening of primer pair combinations, a total of eight *Pst*I + 2 / *Mse*I + 3 primer pairs were chosen that provided reliable, consistently scorable results, and each plant was fingerprinted using these combinations (Table S1). Fragment separation and detection was made using an ABI PRISM 3130xl DNA sequencer, and the presence or absence of each AFLP fragment in each individual plant was scored manually by visualizing electropherograms with GeneMapper 3.7 software. Only fragments ≥ 150 base pairs in size were considered to reduce possible biases arising from size homoplasy (Vekemans *et al*. 2002; Caballero *et al.* 2008). AFLP genotyping error rates were determined for each primer combination by running repeated, independent analyses for 27 (combinations 1-4, Table S1; 13.5% of total plants) or 20 plants (combinations 5-8, Table S1; 10% of total), and estimated as the ratio of the number of discordant scores in the two analyses (all plants and markers combined) to the product of the number of plants by the number of scored markers (Herrera & Bazaga 2009). Average genotyping error rate (± SE) for the eight AFLP primer combinations used was 1.7 ± 0.3% (Table S1).

MSAP is a modification of the standard AFLP technique that uses the methylation-sensitive restriction enzymes *Hpa*II and *Msp*I in parallel runs in combination with another restriction enzyme, commonly *Eco*RI or *Mse*I. *Mse*I was used here because of better repeatability of results (see also

Verhoeven *et al.* 2010, Herrera *et al.* 2013, for earlier MSAP implementations based on *Mse*I). The recognition sequence of *Mse*I (5'-TTAA-3') is shorter than that of *Eco*RI (5'-GTTAAC-3'), which leads to more frequent cuts and hence an expected reduction in the incidence of blind internal 5'-CCGG-3' targeted sites (Fulneček & Kovařic 2014). More importantly, *Mse*I cleavage site does not contain any cytosine residue, which produces a 'methylation-indifferent cutting' independent of cytosine presence and methylation status. *Hpa*II and *Msp*I are isoschizomers that recognize the same tetranucleotide 5'-CCGG but have differential sensitivity to methylation at the inner or outer cytosine. Differences in the products obtained with *Hpa*II and *Msp*I thus reflect different methylation states at the cytosines of the CCGG sites recognized by *Hpa*II or *Msp*I cleavage sites (see Schulz *et al.* 2013, Fulneček & Kovařic 2014, for references and further details). MSAP assays were conducted on DNA samples from all *H. foetidus* plants sampled using four *Hpa*II-*Msp*I + 2 / *Mse*I + 3 primer combinations (Table S1). Fragment separation and detection was made using an ABI PRISM 3130xl DNA sequencer, and the presence or absence of *Hpa*II/*Mse*I and *Msp*I/*Mse*I fragments in each sample was scored manually by visualizing electropherograms with GeneMapper 3.7 software. MSAP genotyping error rates were estimated for each primer combination by running repeated *Hpa*II/*Mse*I and *Msp*I/*Mse*I analyses for 17 plants (8.5% of total), and computed as the ratio of the number of discordant scores in the two analyses (all plants and markers, and the two enzyme pairs, combined) to twice the product of the number of plants by the number of scored markers. Mean genotyping error rate (± SE) for the four MSAP primer combinations used was 3.7 ± 0.5% (Table S1).

Leaf carbon isotope ratios were measured following standard protocols (Pérez-Harguindeguy *et al.* 2013) on the same leaf material used for DNA extraction. Weighed powdered leaf samples were placed into tin capsules and combusted at 1020 ºC using continuous flow isotope-ratio mass spectrometry by means of a Flash HT Plus elemental analyzer coupled to a Delta-V Advantage isotope ratio mass spectrometer via a CONFLO IV interface (Thermo Fisher Scientific, Bremen, Germany). Results were expressed relative to the Pee Dee Belemnite standard as $\delta^{13}C$ in per mil units (‰) (Pérez-Harguindeguy *et al.* 2013).

All collected leaflets from marked plants were mounted individually on paper sheets while still in fresh condition, digitally scanned, and then desiccated. After calibration of digital images, total area, maximum length and maximum width of each leaflet were measured using SigmaScan Pro (version 5.0; Systat Software Inc., San Jose, CA, USA). Dried leaflets were weighed on an analytical balance to the nearest 0.01 mg, and specific area calculated as the area to dry mass ratio (Pérez-Harguindeguy *et al.* 2013). The impression approach (e.g., Peterson *et al.* 2012) was used to measure stomatal traits. Transparent impressions of the widest portion of the abaxial surface of each leaflet were created using clear nail polish, and mounted on microscope slides. Stomatal density (number of stomata per mm^2) was estimated for five fields of view widely spaced across each impression at 400× magnification (field of view = 0.283 mm^2). Two photomicrographs were taken from haphazardly selected, non-overlapping areas of each impression at 100 × magnification using Nomarski differential interference contrast optics. Counts of stomata and epidermal cells were performed on two non-adjacent quadrats of a 0.0625 mm^2 grid overimposed on each image, and the area independent stomatal index (SI) was calculated as SI = [s/(e + s)] x 100], where s is the number of stomata and e is the number of epidermal cells (Salisbury 1927). Guard cells were not included in the number of epidermal cells. Stomatal length, defined as the distance between the junctions of guard cells at opposite ends of stomata, was measured on 20 randomly-chosen, open stomata per impression (10 per photomicrograph). Replicate measurements of leaflet and stomatal traits from the same plant were averaged to obtain single values per trait and individual.

Data analysis

Two presence-absence matrices for MSAP fragments were obtained with the four *Hpa*II-*Mse*I and *Msp*I-*Mse*I primer combination pairs (Table S1). Different workflows (MSAP 'scoring' methods) have been proposed to obtain from these raw data the sample x marker matrix with the information on the methylation status of cytosines at the CCGG end of fragments (MSAP 'fingerprint' matrix) (Herrera & Bazaga 2010; Schulz *et al.* 2013; Fulneček & Kovařic 2014). The optimal MSAP scoring approach will presumably vary depending on genomic features of the species under study and the restriction enzymes used (Messeguer *et al.* 1991; Schulz *et al.* 2013; Fulneček & Kovařic 2014). We adopted here the 'Mixed Scoring 2' transformation scheme of Schulz *et al*. (2013), where details and justification can be found. MSAP fragments were transformed into three distinct sets of markers corresponding to unmethylated (*u*-type in Schulz *et al.*'s [2013] terminology), ^{HMe}CG + ^{Me}CG methylation (internal methylation plus hemimethylation, *m*-type) and ^{HMe}CCG methylation (external hemimethylation, *h*-type) markers. All *H. foetidus* plants sampled were characterized epigenetically by means of the presence-absence scores for *u*-type (N = 105), *h*-type (N = 120) and *m*-type (N = 71) MSAP markers (Table S1), using the Extract_MSAP_epigenotypes function from Schulz *et al.* (2013). The predominance of *h*-type markers found here was at odds with findings of the only previous study on plants adopting this scoring method (Schulz *et al.* 2014), which may stem from differences in genomic characteristics of species and/or the restriction enzymes used.

To determine whether, and the extent to which, differences between individual *H. foetidus* plants in functional features were associated with their genetic and/or epigenetic characteristics, we looked for AFLP and MSAP markers significantly associated with the 20 functional traits considered (Table 1). For each trait, separate linear mixed-effects models were fit for each AFLP and MSAP marker using REML estimation. Computations were done using the lme function from the nlme package for the R environment (R Development Core Team 2012). In each model, the functional trait was the dependent variable and marker presence-absence the single fixed-effect, two-level factor. Application of Bayesian clustering to the AFLP fingerprint data revealed that plants sampled were genetically structured, falling into one of two genetically distinct clusters (Appendix S2; clusters comprised the six northernmost and four southernmost sampling sites, respectively). Genetic stratification and possible relatedness of sampled plants could produce spurious marker-trait associations (Price *et al.* 2010; Sillanpää 2011). To correct, at least in part, for these possible confounding effects, genetic cluster, and sampling site nested within genetic cluster, were incorporated as random effects in the mixed models (Price *et al.* 2010). *P*-values for the effect of marker presence-absence on a given trait were used to identify significant associations. Given the large number of models fit for every trait, Storey & Tibshirani's (2003) *q*-value method was applied to estimate false discovery rates. Using the qvalue package (Storey & Tibshirani 2003), we calculated for every trait the set of *q*-values for all marker-trait models fitted, and found the largest *q*-value leading to an expectation of less than one falsely significant model [i.e., *q*-value x (number of models accepted as significant) < 1].

In addition to identifying AFLP and MSAP markers significantly associated with the functional traits considered, we were also interested in quantifying the explanatory value of these significant markers as predictors of intraspecific functional diversity in *H. foetidus*. Whenever applicable, three separate linear mixed-effects models were fit for each trait, which had trait value as the response variable, and included all significant AFLP markers, all significant MSAP markers, and all significant AFLP + MSAP markers, respectively, as fixed effects (predictors). As done in models fitted to identify significant markers, genetic cluster and sampling site nested within genetic cluster were also included as random effects. The marginal R^2 for each model, which represents the variance explained by fixed

factors alone (Nakagawa & Schielzeth 2013), was used to evaluate the explanatory value of significant epigenetic and genetic markers, taken separately and in combination.

The within- and between-site components of sample-wide variance in functional traits was computed by fitting random effects models to the data using REML estimation, and confidence intervals of variance estimates obtained by bootstraping. Between-site differences in functional diversity of *H. foetidus* plants, and their relationship to local genetic and epigenetic diversity, were tested using a multivariate version of Levene's test for homogeneity of variances, which tests the mean absolute deviation rather than the variance (Van Valen 2005). Principal coordinates analyses of pairwise distance matrices were used to obtain plant coordinates on each of five reduced-dimensionality spaces, defined respectively by functional traits and the scores for significant AFLP markers, nonsignificant AFLP markers, significant MSAP markers and nonsignificant MSAP markers. Individual distances to the respective group centroids were then computed on each of these spaces. Site means were used as measurements of multivariate dispersion, and significance of between-site differences was tested using an analysis of variance approach. Computations were performed with function betadisper of the vegan package. Relationships across sites between multivariate functional diversity, on one side, and multilocus genetic and epigenetic diversity of significant and nonsignificant markers, on the other, were tested by fitting ordinary linear models to site means.

Results

Genetic and epigenetic diversity

All *H. foetidus* plants sampled were fingerprinted using 674 AFLP and 155 MSAP fragments (Table S1). After scoring, the vast majority of MSAP fragments (91.6%) led to one or more distinct MSAP marker types, and a combined total of 296 *u*-, *h*- and *m*-type markers were obtained (Table S1). Only the 270 AFLP and 207 MSAP (64 *u*-type, 99 *h*-type, 44 *m*-type) polymorphic markers (at least 2% of samples showing a variant score) were retained for study (Table S1). Percent marker polymorphism per primer combination was considerably higher for MSAP (68.6 ± 3.2% polymorphism, $N = 12$, *u*-, *m*- and *h*-type markers combined) than for AFLP markers (41.1 ± 3.4% polymorphism, $N = 8$), the difference being statistically significant (chi-squared = 15.25, df = 1, $P < 0.0001$; Kruskal-Wallis rank sum test).

Intraspecific variation in functional traits

Plants of *H. foetidus* differed widely in most of the 20 functional traits considered, as denoted by broad ranges and large coefficients of variation (CV = 100 x standard deviation/mean) of individual values (Table 1). There was a trend for increasing individual variability from leaf (mean CV ± SE = 23 ± 5 %; means are reported ± SE throughout this paper) through regenerative (44 ± 15%) to whole plant (53 ± 7%) functional traits, but differences between trait classes did not reach statistical significance (chi-squared = 4.07, df = 2, $P = 0.13$; Kruskal-Wallis rank sum test). Flower length (CV = 5.8%), leaf carbon isotope ratio (6.0%), and stomata length (6.6%) were the least variable traits. On the opposite extreme, number of follicles ripened (CV = 102.2%), number of flowers produced (82.8%), and number of vegetative ramets (66.6%), were the most variable traits (Table 1).

Although means for all traits considered differed significantly among sampling sites (results not shown), most variation occurred within sites. On average, 70.7 ± 3.6 % ($N = 20$ traits) of sample-wide variance was due to individual variation within sites. For 15 traits, within-site variance component was greater than 50% and the 95% confidence interval did not include that value, thus denoting that within-site variance significantly exceeded between-site variance (Fig. 1). Four leaf-related traits (width, length, area and specific area) exhibited the smallest proportions of within-site functional variance (range = 39.4–52.6%; Fig. 1). On the opposite extreme, three regenerative traits were among

those exhibiting the highest levels of within-site variance (number of flowers, number of seeds, number of follicles; range = 85.3–93.5%; Fig. 1).

Marker-trait associations

A total of 477 polymorphic markers (270 AFLP, 207 MSAP) were tested for significant associations with the 20 functional traits considered, and 50 instances were found (Table 2). Every trait had at least one significantly associated MSAP or AFLP marker (mean ± SE = 2.5 ± 0.3 associated markers per trait, or 0.52% of markers assayed per trait; Table 2). Instances of significant AFLP and MSAP marker-trait associations were non-randomly distributed across traits (P = 0.00011, Fisher's exact probability test). Individual traits tended to be associated exclusively with either MSAP (e.g., vegetative ramets, stomatal density, leaf carbon isotope ratio, follicles per flower) or AFLP (e.g., reproductive ramets, specific leaf area, stomatal index) markers more often than would be expected by chance (Table 2).

The 50 instances of significant marker-trait associations involved 20 distinct MSAP fragments (12.9% of total), 27 distinct MSAP markers (13.0% of total) and 12 distinct AFLP markers (4.4% of total) (Table S2). On a per-fragment or per-marker basis, therefore, the probability of MSAP markers being significantly associated with some functional trait roughly triplicated that for AFLP markers, the difference being statistically significant (P = 0.0011, Fisher's exact probability test).

Explanatory value of significant genetic and epigenetic markers

After statistically controlling for genetic background heterogeneity and possible cryptic relatedness of plants from the same site, significant AFLP and MSAP markers combined explained on average 9.8 ± 1.0% (marginal R^2 from mixed models; range = 2.2–17.9%, N = 20 traits) of trait variance, while significant AFLP and MSAP markers considered separately explained on average 8.0 ± 1.4% (range = 2.2–16.8%) and 8.2 ± 0.9% (range = 3.3–17.9%) of trait variance, respectively (Table 2). Individual traits differed widely, however, in the relative explanatory value of significantly associated AFLP and MSAP markers, as estimated by the marginal R^2 of the corresponding models (Fig. 2). Certain traits had a considerable amount of variance explained by either MSAP (e.g. vegetative ramets, stomatal density, leaf carbon isotope ratio, flower length) or AFLP markers alone (e.g., stomatal index, reproductive ramets, inflorescence basal diameter), while in other cases MSAP and AFLP markers had roughly similar explanatory values (e.g., leaflet dry mass, stomata length, leaflet area) (Fig. 2). There was no discernible relationship between functional trait class and the explanatory value of significant AFLP and MSAP markers.

Functional, genetic and epigenetic diversity across sampling sites

Multivariate functional diversity of locally coexisting *H. foetidus* plants, estimated by the mean distance of individuals to the corresponding site centroid in the reduced-dimensionality functional space, differed significantly between sampling localities (chi-squared = 47.6, df = 9, $P << 0.0001$; Kruskal-Wallis rank sum test). Differences between sites in functional diversity were positively and significantly related to variation in local multilocus diversity of significant genetic (AFLP) and epigenetic (MSAP) markers, but unrelated to differences in local multilocus diversity of nonsignificant markers of any type (Table 3). Between-site differences in local epigenetic and genetic diversity accounted for 83% of variation in local functional diversity (Table 3), which suggests a major predictive value of variations in genetic and epigenetic diversity as determinants of population differences in functional diversity.

Discussion

Intraspecific variation in the wild populations of *H. foetidus* sampled was extensive, implicated the vast majority of the 20 traits considered, and occurred predominantly at the within-population level. These results corroborate and extend those of recent studies which, although generally based on

limited sets of traits, have also documented the quantitative importance of intraspecific diversity in wild plant populations (Iannetta *et al.* 2007; Boucher *et al.* 2013; Mitchell & Bakker 2014). The magnitude of intraspecific variation exhibited by *H. foetidus* is well illustrated by comparing, for example, the ranges of individual values for specific leaf area (a moderately variable trait, range = 8-26 mm^2 mg^{-1}, Table 1) and leaf carbon isotope ratio (a relatively constant trait, range = -30 – -22 ‰, Table 1) with the corresponding interspecific ranges reported for large multispecies samples worldwide (1–69 mm^2 mg^{-1}, 2370 species from Wright *et al.* 2004; -33 – -23 ‰; 146 species from Körner *et al.* 1988). For these two traits, the extent of intraspecific variation over the relatively small spatial scale of this study was thus large enough to encompass a major fraction of the corresponding ranges of interspecific variation worldwide. All traits examined here are expected to be consequential for the plants' fitness or their immediate environment, as discussed below. Consequently, the finding that intraspecific variation can sometimes be nearly as large as interspecific differences stresses once more the importance of considering intraspecific variation in studies of community and ecosystem function (de Bello *et al.* 2011; Violle *et al.* 2012; Mitchell & Bakker 2014; Sides *et al.* 2014).

Traits considered in this study can have direct or indirect functional consequences for plants, and their variation at the regional and within-population levels will be associated with intraspecific functional diversity. Among leaf traits, for instance, carbon isotope composition reflects intrinsic water-use efficiency; specific leaf area is directly related to mass-based photosynthetic rate; variations in leaf area and linear dimensions are related to life span and thermal balance; and size and density of stomata are key factors in water economy, gas exchange and net carbon assimilation (Ackerly & Reich 1999; Westoby *et al.* 2002; Wright *et al.* 2004; Pérez-Harguindeguy *et al.* 2013). Variation in life history (e.g., age of flowering ramets, plant size) and fecundity-related traits (e.g., fruit and seed production, seed size) will directly influence the turnover, recruitment, age structure, productivity and persistence of populations (Harper 1977). Variations in size of inflorescences and individual flowers can influence fecundity through effects on pollinator attractiveness and pollination success, since seed production by winter-flowering *H. foetidus* is often pollen-limited in the study region (Herrera 2002).

After statistically controlling for the potential confounding effects of genetic structuring and possible relatedness of sampled plants, all functional traits considered exhibited a significant association with at least one AFLP or MSAP marker. Interpretation of these results is subject to the usual caveat that significant marker-trait associations provide only indicative evidence, and are not by themselves a conclusive proof of causality (e.g., Platt *et al.* 2010). Keeping this in mind, circumstantial evidence does support the interpretation that significant marker-trait associations found here can stem from the markers involved being linked to genomic regions directly controlling the associated traits in causative ways. In plant genomes, AFLP markers are often positioned within gene sequences or linked to QTLs of known phenotypic effects, including some of the traits considered here such as leaf area, specific leaf area, carbon isotope discrimination and seed size (Teulat *et al.* 2002; Scalfi *et al.* 2004; Caballero *et al.* 2013). Although they have been investigated much less often, there are also clear indications that MSAP markers can be stably associated across generations and environments with genes or QTL^{epi} of diverse phenotypic effects, including some of the traits considered here (Long *et al.* 2011; Tricker *et al.* 2012). For instance, transgenerationally heritable variations in stomatal development and water use efficiency are due to stable alterations in the methylation status of specific genes or genomic sites (Wang *et al.* 2011; Tricker *et al.* 2012). Regardless of the underlying mechanistic basis, however, marker-trait associations revealed by this study indicate that, in addition to genetic variation, individual differences in the methylation status of specific zones in the genome also predict intraspecific variation in life history, fecundity and leaf traits of functional significance.

Results of this study support the hypothesis that, apart from the usually acknowledged effects of genetic diversity, natural epigenetic variation can also contribute to enhance intraspecific functional diversity in wild plant populations (Bossdorf *et al.* 2008; Richards *et al.* 2012; Alonso *et al.* 2014). In addition to the marker-trait relationships identified at the regional scale, another result supporting this hypothesis was the finding that between-site variation in multivariate functional diversity of local *H. foetidus* populations was directly related to differences in multilocus epigenetic diversity after multilocus genetic diversity was statistically accounted for. Given the low statistical power of the test due to the limited number of sites sampled, this result suggests that the effect of local epigenetic diversity on local functional diversity should be quantitatively important. The importance of epigenetic variation in explaining intraspecific functional diversity varied widely among traits. Individual traits tended to be predominantly associated with either MSAP or AFLP markers alone, which led to intraspecific trait variance being mostly explained by either epigenetic or genetic variation, respectively (Fig. 2). Although it is not possible at present to propose a mechanistic basis for these results, further evidence on the independence (orthogonality) of AFLP and MSAP markers as predictors of functional traits is furnished by the almost perfect additivity of their respective contributions to total marginal R^2 in the case of traits that were significantly related to markers of both types (Table 2) (Rencher & Schaalje 2008). Averaged over all traits, significant AFLP and MSAP markers had roughly similar explanatory value (marginal R^2 = 8.0% and 8.2%, respectively), which would perhaps suggest quantitatively similar roles of genetic and epigenetic variation as predictors of intraspecific functional diversity in *H. foetidus*. Our results, however, may slightly underestimate the predictive value of epigenetic relative to genetic variation, since the number of polymorphic AFLP markers assayed (270) exceeded that of variable MSAP fragments (142) and markers (207). The per-marker probability of being significantly associated with some trait was considerably higher for MSAP (0.130) than for AFLP markers (0.044). Had we assayed an equivalent number of MSAP and AFLP markers, the number of MSAP markers significantly associated with traits, and hence their overall predictive value, would possibly have been higher.

Studies on model plants under artificial conditions have firmly established that DNA methylation patterns at specific genomic sites most often are stably transmitted from parents to offspring (Johannes *et al.* 2009; Cortijo *et al.* 2014; Li *et al.* 2014), but comparatively little is known on the transgenerational transmissibility of methylation patterns in wild plant populations. Prior investigations conducted at three of the *H. foetidus* populations studied here found that, averaged over plants, 84% of MSAP markers had their methylation status unchanged from plant to pollen (i.e., sporophyte to gametophyte stages), thus demonstrating extensive post-meiotic epigenetic stability in this species (Herrera *et al.* 2013, 2014). In addition, multilocus epigenetic differentiation between *H. foetidus* populations was preserved from the sporophyte to the gametophyte stage despite a certain amount of epigenetic reprogramming during gametogenesis (Herrera *et al.* 2013). Although the set of MSAP markers considered in the present study only partly overlap those used in these prior investigations on transmissibility, some shared markers found here significantly associated with functional traits had transmissibilities >90% (C. M. Herrera and M. Medrano, Unpublished). Methylation patterns could be reprogrammed during early embryo development, and methylation patterns of pollen grains might differ from methylations of sperm cells (see Herrera *et al.* 2013, for review and discussion), yet these earlier results lead us to tentatively suggest that, insofar as marker-trait associations found here reflect causal relationships, population and individual variability of epigenetically-influenced traits will stably persist across a number of generations in *H. foetidus* in our study region. In this way, epigenetically-mediated functional variability would propagate

transgenerationally in a way similar to variability in genetically-influenced traits. Long-term field experiments are currently underway to test this prediction. It must be stressed, however, that even if individual and population differences in methylation patterns were quite imperfectly transmitted across generations, the relationship between epigenetic variation and intraspecific functional diversity documented in this study would still retain its ecologically relevance, as discussed in the next paragraph.

Intraspecific trait variability may enhance the ecological breadth and distributional range of species, as illustrated by Sides *et al.* (2014) for a set of 21 mountain plants whose elevational ranges were directly related to variability in specific leaf area, one of the traits considered here. Consistent with this finding are the extensive variability in functional traits exhibited by *H. foetidus* in our study region, and the broad range of elevations and habitat types inhabited by the species there and elsewhere (Mathew 1989), which presumably denotes an ability to exploit wide environmental gradients. Our finding that intraspecific functional variability at the regional (all sites pooled) and local (within sites) levels was significantly predicted by epigenetic variation points to an effective role of epigenetic diversity in allowing *H. foetidus* to exploit contrasting environments. In addition to the higher per-marker probability of MSAP markers of predicting functional variation relative to AFLP ones discussed above, additional evidence likewise suggests that epigenetic variation might be at least as important as genetic variation in explaining the broad ecological niche and high functional diversity of *H. foetidus*. Percent polymorphism of MSAP fragments and markers greatly exceeded that of AFLP markers, denoting considerably greater epigenetic than genetic diversity as found in other species (see references in Introduction). In addition, *H. foetidus* has characteristically low levels of genetic variation, as revealed not only by the modest polymorphism of AFLP markers shown here (41%), but also by the low polymorphisms obtained in screenings of other genetic markers using samples from broad geographical areas (50% polymorphism for 26 nuclear microsatellites, 7% polymorphism for 13 allozyme loci; Consortium MERPD *et al.* 2013; M. Medrano, Unpublished). We therefore interpret results of this study as an indication that, by contributing significantly to the broad intraspecific functional diversity of *H. foetidus*, epigenetic variation possibly allows this species to exploit a broad range of ecological conditions despite its modest genetic diversity.

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References

Ackerly DD, Reich PB (1999) Convergence and correlations among leaf size and function in seed plants: a comparative test using independent contrasts. *American Journal of Botany*, **86**, 1272–1281.

Albert CH, de Bello F, Boulangeat I *et al.* (2012) On the importance of intraspecific variability for the quantification of functional diversity. *Oikos*, **121**, 116–126.

Alonso C, Pérez R, Bazaga P, Medrano M, Herrera CM (2014) Individual variation in size and fecundity is correlated with differences in global DNA cytosine methylation in the perennial herb *Helleborus foetidus* (Ranunculaceae). *American Journal of Botany*. doi:10.3732/ajb.1400126

Amoah S, Kurup S, López CMR *et al.* (2012) A hypomethylated population of *Brassica rapa* for forward and reverse epi-genetics. *BMC Plant Biology*, **12**, 193.

Becker C, Weigel D (2012) Epigenetic variation: origin and transgenerational inheritance. *Current*

Opinion in Plant Biology, **15**, 562–567.
Bossdorf O, Richards CL, Pigliucci M (2008) Epigenetics for ecologists. *Ecology Letters*, **11**, 106–115.
Boucher FC, Thuiller W, Arnoldi C, Albert CH, Lavergne S (2013) Unravelling the architecture of functional variability in wild populations of *Polygonum viviparum* L. *Functional Ecology*, **27**, 382–391.
Bowler PJ (2005) Variation from Darwin to the Modern Synthesis. In: *Variation. A Central Concept in Biology* (eds Halgrímsson B, Hall BK). pp. 29–47, Elsevier, Amsterdam.
Caballero A, Quesada H, Rolán-Alvarez E (2008) Impact of amplified fragment length polymorphism size homoplasy on the estimation of population genetic diversity and the detection of selective loci. *Genetics*, **179**, 539–554.
Caballero A, García-Pereira MJ, Quesada H (2013) Genomic distribution of AFLP markers relative to gene locations for different eukaryotic species. *BMC Genomics*, **14**, 528.
Consortium MERPD, Aksoy S, Almeida-Val VMF *et al.* (2013) Permanent genetic resources added to Molecular Ecology Resources database 1 October 2012–30 November 2012. *Molecular Ecology Resources*, **13**, 341–343.
Cortijo S, Wardenaar R, Colomé-Tatché M *et al.* (2014) Mapping the epigenetic basis of complex traits. *Science*, **343**, 1145–1148.
Crawford KM, Rudgers JA (2012) Plant species diversity and genetic diversity within a dominant species interactively affect plant community biomass. *Journal of Ecology*, **100**, 1512–1521.
de Bello F, Lavorel S, Albert CH *et al.* (2011) Quantifying the relevance of intraspecific trait variability for functional diversity. *Methods in Ecology and Evolution*, **2**, 163–174.
Fieldes MA, Amyot LM (1999) Epigenetic control of early flowering in flax lines induced by 5-azacytidine applied to germinating seed. *Journal of Heredity*, **90**, 199–206.
Finnegan EJ, Peacock WJ, Dennis ES (1996) Reduced DNA methylation in *Arabidopsis thaliana* results in abnormal plant development. *Proceedings of the National Academy of Sciences of the United States of America*, **93**, 8449–8454.
Fulneček J, Kovařik A (2014) How to interpret Methylation Sensitive Amplified Polymorphism (MSAP) profiles? *BMC Genetics*, **15**, 2.
Grant-Downton RT, Dickinson HG (2005) Epigenetics and its implications for plant biology. 1. The epigenetic network in plants. *Annals of Botany*, **96**, 1143–1164.
Grant-Downton RT, Dickinson HG (2006) Epigenetics and its implications for plant biology 2. The 'epigenetic epiphany': Epigenetics, evolution and beyond. *Annals of Botany*, **97**, 11–27.
Harper JL (1977) *Population Biology of Plants*. Academic Press, London.
Herrera CM (2002) Censusing natural microgametophyte populations: variable spatial mosaics and extreme fine-graininess in winter-flowering *Helleborus foetidus* (Ranunculaceae). *American Journal of Botany*, **89**, 1570–1578.
Herrera CM (2009) *Multiplicity in Unity. Plant Subindividual Variation and Interactions with Animals*. University of Chicago Press, Chicago, Illinois.
Herrera CM, Bazaga P (2009) Quantifying the genetic component of phenotypic variation in unpedigreed wild plants: tailoring genomic scan for within-population use. *Molecular Ecology*, **18**, 2602–2614.
Herrera CM, Bazaga P (2010) Epigenetic differentiation and relationship to adaptive genetic divergence in discrete populations of the violet *Viola cazorlensis*. *New Phytologist*, **187**, 867–876.
Herrera CM, Cerdá X, García MB *et al.* (2002) Floral integration, phenotypic covariance structure and pollinator variation in bumblebee-pollinated *Helleborus foetidus*. *Journal of Evolutionary Biology*,

15, 108–121.

Herrera CM, Medrano M, Bazaga P (2013) Epigenetic differentiation persists after male gametogenesis in natural populations of the perennial herb *Helleborus foetidus* (Ranunculaceae). *PLoS One*, **8**, e70730.

Herrera CM, Medrano M, Bazaga P (2014) Variation in DNA methylation transmissibility, genetic heterogeneity and fecundity-related traits in natural populations of the perennial herb *Helleborus foetidus*. *Molecular Ecology*, **23**, 1085–1095.

Hersch-Green EI, Turley NE, Johnson MTJ (2011) Community genetics: what have we accomplished and where should we be going? *Philosophical Transactions of the Royal Society B-Biological Sciences*, **366**, 1453–1460.

Hughes AR, Inouye BD, Johnson MTJ, Underwood N, Vellend M (2008) Ecological consequences of genetic diversity. *Ecology Letters*, **11**, 609–623.

Iannetta PPM, Begg G, Hawes C, Young M, Russell J, Squire GR (2007) Variation in *Capsella* (shepherd's purse): an example of intraspecific functional diversity. *Physiologia Plantarum,* **129**, 542–554.

Jablonka E, Raz G (2009) Transgenerational epigenetic inheritance: prevalence, mechanisms, and implications for the study of heredity and evolution. *Quarterly Review of Biology*, **84**, 131–176.

Johannes F, Porcher E, Teixeira FK *et al.* (2009) Assessing the impact of transgenerational epigenetic variation on complex traits. *PloS Genetics* **5**. e1000530.

King GJ (1995) Morphological development in *Brassica oleracea* is modulated by *in vivo* treatment with 5-azacytidine. *Journal of Horticultural Science*, **70**, 333–342.

Kondo H, Ozaki H, Itoh K, Kato A, Takeno K (2006) Flowering induced by 5-azacytidine, a DNA demethylating reagent in a short-day plant, *Perilla frutescens* var. *crispa*. *Physiologia Plantarum*, **127**, 130–137.

Körner C, Farquhar GD, Roksandic Z (1988) A global survey of carbon isotope discrimination in plants from high altitude. *Oecologia*, **74**, 623–632.

Latzel V, Allan E, Silveira AB, Colot V, Fischer M, Bossdorf O (2013) Epigenetic diversity increases the productivity and stability of plant populations. *Nature Communications*, **4**, 2875.

Li Q, Eichten SR, Hermanson PJ, Springer NM (2014) Inheritance patterns and stability of DNA methylation variation in maize near-isogenic lines. *Genetics*, **196**, 667–676.

Li YD, Shan XH, Liu XM, Hu LJ, Guo WL, Liu B (2008) Utility of the methylation-sensitive amplified polymorphism (MSAP) marker for detection of DNA methylation polymorphism and epigenetic population structure in a wild barley species (*Hordeum brevisubulatum*). *Ecological Research*, **23**, 927–930.

Lira-Medeiros CF, Parisod C, Fernandes RA, Mata CS, Cardoso MA, Ferreira PCG (2010) Epigenetic variation in mangrove plants occurring in contrasting natural environment. *PLoS One* **5**, e10326.

Long Y, Xia W, Li RY *et al.* (2011) Epigenetic QTL Mapping in *Brassica napus*. *Genetics*, **189**, 1093–1102.

Mathew B (1989) *Hellebores*. Alpine Garden Society, St. John's Woking, Surrey, UK.

Messeguer R, Ganal MW, Steffens JC, Tanksley SD (1991) Characterization of the level, target sites and inheritance of cytosine methylation in tomato nuclear DNA. *Plant Molecular Biology*, **16**, 753–770.

Meudt HM, Clarke AC (2007) Almost forgotten or latest practice? AFLP applications, analyses and advances. *Trends in Plant Science*, **12**, 106–117.

Mitchell RM, Bakker JD (2014) Quantifying and comparing intraspecific functional trait variability: a case study with *Hypochaeris radicata*. *Functional Ecology*, **28**, 258–269.

Nakagawa S, Schielzeth H (2013) A general and simple method for obtaining R^2 from generalized linear mixed-effects models. *Methods in Ecology and Evolution*, **4**, 133–142.

Neuhauser C, Andow DA, Heimpel GE, May G, Shaw RG, Wagenius S (2003) Community genetics: expanding the synthesis of ecology and genetics. *Ecology*, **84**, 545–558.

Pérez-Harguindeguy N, Díaz S, Garnier E *et al.* (2013) New handbook for standardised measurement of plant functional traits worldwide. *Australian Journal of Botany*, **61**, 167–234.

Peterson CA, Fetcher N, McGraw JB, Bennington CC (2012) Clinal variation in stomatal characteristics of an arctic sedge, *Eriophorum vaginatum* (Cyperaceae). *American Journal of Botany*, **99**, 1562–1571.

Platt A, Vilhjálmsson BJ, Nordborg M (2010) Conditions under which genome-wide association studies will be positively misleading. *Genetics*, **186**, 1045–1052.

Price AL, Zaitlen NA, Reich D, Patterson N (2010) New approaches to population stratification in genome-wide association studies. *Nature Reviews Genetics*, **11**, 459–463.

R Development Core Team (2012) *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna.

Rencher AC, Schaalje GB (2008) *Linear Models in Statistics*. 2nd edition. Wiley, Hoboken, New Jersey.

Richards CL, Schrey AW, Pigliucci M (2012) Invasion of diverse habitats by few Japanese knotweed genotypes is correlated with epigenetic differentiation. *Ecology Letters*, **15**, 1016–1025.

Richards EJ (2006) Inherited epigenetic variation - revisiting soft inheritance. *Nature Reviews Genetics*, **7**, 395–401.

Salisbury EJ (1927) On the causes and ecological significance of stomatal frequency, with special reference to the woodland flora. *Philosophical Transactions of the Royal Society of London B*, **216**, 1–65.

Sano H, Kamada I, Youssefian S, Katsumi M, Wabiko H (1990) A single treatment of rice seedlings with 5-azacytidine induces heritable dwarfism and undermethylation of genomic DNA. *Molecular & General Genetics*, **220**, 441–447.

Scalfi M, Troggio M, Piovani P *et al.* (2004) A RAPD, AFLP and SSR linkage map, and QTL analysis in european beech (*Fagus sylvatica* L.). *Theoretical and Applied Genetics*, **108**, 433–441.

Schulz B, Eckstein RL, Durka W (2013) Scoring and analysis of methylation-sensitive amplification polymorphisms for epigenetic population studies. *Molecular Ecology Resources*, **13**, 642–653.

Schulz B, Eckstein RL, Durka W (2014) Epigenetic variation reflects dynamic habitat conditions in a rare floodplain herb. *Molecular Ecology*, **14**, 3523–3537.

Sides CB, Enquist BJ, Ebersole JJ, Smith MN, Henderson AN, Sloat LL (2014) Revisiting Darwin's hypothesis: Does greater intraspecific variability increase species' ecological breadth? *American Journal of Botany*, **101**, 56–62.

Sillanpää MJ (2011) Overview of techniques to account for confounding due to population stratification and cryptic relatedness in genomic data association analyses. *Heredity*, **106**, 511–519.

Storey JD, Tibshirani R (2003) Statistical significance for genomewide studies. *Proceedings of the National Academy of Sciences USA,* **100**, 9440–9445.

Tack AJM, Roslin T (2011) The relative importance of host-plant genetic diversity in structuring the associated herbivore community. *Ecology*, **92**, 1594–1604.

Tatra GS, Miranda J, Chinnappa CC, Reid DM (2000) Effect of light quality and 5-azacytidine on genomic methylation and stem elongation in two ecotypes of *Stellaria longipes*. *Physiologia Plantarum*, **109**, 313–321.

Teulat B, Merah O, Sirault X *et al.* (2002) QTLs for grain carbon isotope discrimination in field-grown barley. *Theoretical and Applied Genetics*, **106**, 118–126.

Tricker PJ, Gibbings JG, Lopez CMR, Hadley P, Wilkinson MJ (2012) Low relative humidity triggers RNA-

directed de novo DNA methylation and suppression of genes controlling stomatal development. *Journal of Experimental Botany*, **63**, 3799–3813.

Van Valen L (2005) The statistics of variation. In: *Variation. A Central Concept in Biology* (eds Halgrímsson B, Hall BK). pp. 29–47, Elsevier, Amsterdam.

Vekemans X, Beauwens T, Lemaire M, Roldán-Ruiz I (2002) Data from amplified fragment length polymorphism (AFLP) markers show indication of size homoplasy and of a relationship between degree of homoplasy and fragment size. *Molecular Ecology,* **11**, 139–151.

Verhoeven KJF, Jansen JJ, van Dijk PJ, Biere A (2010) Stress-induced DNA methylation changes and their heritability in asexual dandelions. *New Phytologist*, **185**, 1108–1118.

Violle C, Enquist BJ, McGill BJ *et al.* (2012) The return of the variance: intraspecific variability in community ecology. *Trends in Ecology & Evolution*, **27**, 244–252.

Wang WS, Pan YJ, Zhao XQ *et al.* (2011) Drought-induced site-specific DNA methylation and its association with drought tolerance in rice (*Oryza sativa* L.). *Journal of Experimental Botany*, **62**, 1951–1960.

Weising K, Nybom H, Wolff K, Kahl G (2005) *DNA Fingerprinting in Plants. Principles, Methods, and Applications*. 2nd ed. CRC Press, Boca Raton, Florida.

Werner K, Ebel F (1994) Zur Lebensgeschichte der Gattung *Helleborus* L. (Ranunculaceae). *Flora*, **189**, 97–130.

Westoby M, Falster DS, Moles AT, Vesk PA, Wright IJ (2002) Plant ecological strategies: some leading dimensions of variation between species. *Annual Review of Ecology and Systematics*, **33**, 125–159.

Whitham TG, Bailey JK, Schweitzer JA *et al.* (2006) A framework for community and ecosystem genetics: from genes to ecosystems. *Nature Reviews Genetics*, **7**, 510–523.

Wright IJ, Reich PB, Westoby M *et al.* (2004) The worldwide leaf economics spectrum. *Nature*, **428**, 821–827.

Data accessibility

AFLP, MSAP and functional trait data used in this study deposited at DRYAD: doi:10.5061/dryad.fr2k8

Author contributions

Conceived and designed the experiments: CMH MM. Performed the experiments: CMH MM PB. Analyzed the data: CMH MM PB. Wrote the paper: CMH MM.

Supporting information

Additional supporting information may be found in the online version of this article.

Appendix S1

Location and characteristics of sampling sites.

Appendix S2

Genetic structure of *Helleborus foetidus* plants sampled for the study.

Table S1

Primer combinations, scoring errors, number of markers and polymorphism levels for AFLP and MSAP analyses.

Table S2

AFLP and MSAP markers significantly associated with functional traits.

Table 1. Individual variation in 20 quantitative functional traits in the sample of *Helleborus foetidus* plants from 10 locations in the Sierra de Cazorla region (southeastern Spain; see Appendix S1) considered in this study. Functional trait classes follow Perez-Harguindeguy *et al.* (2013).

					Individual variation	
Trait class	Functional trait	Trait code	Measurement unit	Number of plants measured	Range	CV * (%)
Whole plant	Vegetative ramets	RAME.VEG	number	201	0–22	66.6
	Reproductive ramets	RAME.REP	number	201	1–5	53.1
	Total ramets	RAME.NUM	number	201	1–25	58.2
	Age of flowering ramets	INFL.AGE	years	201	2–9	33.4
Leaves	Leaflet length	LEAF.LEN	mm	147	44–201	26.6
	Leaflet width	LEAF.WID	mm	147	9–26	24.3
	Leaflet area	LEAF.ARE	mm^2	147	326–3368	49.4
	Leaflet dry mass	LEAF.MAS	mg	147	19–261	44.0
	Specific leaf area	LEAF.SLA	$mm^2 \cdot mg^{-1}$	147	8–26	25.6
	Stomata length	STOM.LEN	µm	147	34–51	6.6
	Stomatal density	STOM.DEN	mm^{-2}	147	69–161	16.5
	Stomatal index ¶	STOM.IND	per cent	147	20–32	8.3
	Leaf carbon isotope ratio	CARB.DIS	$\delta\,^{13}C$ per mil	201	-30 – -22	6.0
Regenerative	Inflorescence basal diameter	INFL.DIA	mm	201	7–22	21.9
	Flower length	FLOW.LEN	mm	201	14–18	5.8
	Follicles per flower	FLOW.FOL	number	197	1.6–3.9	16.0
	Total flowers produced	FLOW.NUM	number	201	10–372	82.8
	Total follicles ripened	FOLL.NUM	number	197	10–783	102.2
	Total seeds produced	SEED.NUM	number	197	52–2132	62.2
	Seed mass	SEED.MAS	mg	194	8–17	13.9

* CV = coefficient of variation, ratio of standard deviation to the mean expressed as percentage.

¶ Stomatal index = 100 * (stomatal density) / (stomatal density + epidermal cell density).

Table 2. Number of epigenetic (MSAP) and genetic (AFLP) markers significantly associated with functional traits in the sample of *Helleborus foetidus* plants studied (see Table S2 for marker identification and further details), and proportion of sample-wide variance explained, as assessed with the marginal R^2 of the corresponding mixed-effects models.

	Significantly associated markers				Marginal R^2 (%)		
Functional trait	MSAP	AFLP	Total	*P*-value threshold *	MSAP markers	AFLP markers	MSAP + AFLP markers
Vegetative ramets	5	0	5	0.0012	17.90		17.90
Reproductive ramets	0	3	3	0.0019		13.72	13.72
Total ramets ¶	2	0	2	0.0029	9.42		9.42
Age of flowering ramets	1	0	1	0.00046	5.39		5.39
Leaflet length	1	0	1	0.0039	3.26		3.26
Leaflet width	0	1	1	0.0017		2.24	2.24
Leaflet area	2	1	3	0.0021	5.96	4.51	9.11
Leaflef dry mass	2	1	3	0.0015	10.52	7.81	16.80
Specific leaf area	0	2	2	0.0012		5.68	5.68
Stomata length	1	1	2	0.0012	6.29	5.49	8.87
Stomatal density	3	0	3	0.0034	10.31		10.31
Stomatal index	0	3	3	0.0026		16.76	16.76
Leaf carbon isotope ratio	5	0	5	0.0018	10.12		10.12
Inflorescence basal diameter	0	2	2	0.00062		7.92	7.92
Flower length	1	0	1	0.00021	9.81		9.81
Follicles per flower	5	0	5	0.0021	7.17		7.17
Total flowers produced ¶	1	1	2	0.00010	6.87	7.71	14.55
Total follicles ripened ¶	1	1	2	0.000072	7.67	7.94	15.66
Total seeds produced ¶	1	0	1	0.0032	4.02		4.02
Seed mass	3	0	3	0.0012	7.70		7.70

* For each functional trait, all markers deemed significant had associated *P*-values ≤ than the trait-specific threshold shown, and taken together the expected number of false positives was < 1.

¶ Data were $\log_{10}$-transformed for the analyses.

Table 3. Relationship across the 10 sampling sites between multivariate functional diversity of *Helleborus foetidus* plants and multilocus epigenetic and genetic diversity, tested separately for subsets of markers significantly and nonsignificantly related to functional traits (Tables 2 and S2).

		Linear model fit		
	Predictor	Parameter estimate ± SE	$F_{1,7}$	*P*-value
Significant markers				
Model fit: $F_{2,7}$ = 23.79, adjusted R^2 = 0.83, *P* = 0.0007				
	Epigenetic diversity	0.267 ± 0.105	6.39	0.038
	Genetic diversity	0.898 ± 0.159	31.76	0.00078
Nonsignificant markers				
Model fit: $F_{2,7}$ = 0.76, adjusted R^2 = 0.02, *P* = 0.50				
	Epigenetic diversity	0.141 ± 0.133	1.12	0.32
	Genetic diversity	0.014 ± 0.050	0.078	0.79

Legends to figures

Fig. 1 Proportion of total sample-wide variance accounted for by within-site variation for each of the 20 functional traits considered. Horizontal dashed line denotes the threshold above which within-site variance exceeds among-site variance. Vertical segments represent 95% confidence intervals of estimates. Trait codes and classes as in Table 1.

Fig. 2 Proportion of variance of the different functional traits considered that was explained by the respective sets of significantly associated epigenetic (MSAP) and genetic (AFLP) markers (see Tables 2 and S2), as estimated by marginal R^2 from mixed-effects models. Trait codes and classes as in Table 1.