## **Vascular Plant Metric Names and Descriptions**

## **Key Information for reading Table 2:**

- Unless otherwise indicated, vegetation metrics are summarized to site level. Metrics are calculated based on data from five 100-m² plots in the Assessment Area (AA) for the site (or if fewer than 5 plots were sampled, then the total number plots sampled). In the metric descriptions or formulas provided in this appendix, the phrase 'five 100-m² plots' can be assumed to mean the 5 plots in the AA or the total number of plots sampled if less than 5. Rarely were fewer than 5 vegetation plots sampled at the AA.
- The term 'Species' as typically used in this appendix refers to taxonomic species or lowest identifiable taxonomic unit (e.g., variety, genus, family, growth habit).
- **GRAY BANNER,** heading each major group of metrics, lists the NWCA Field Data Form from which the validated field data that is used in metrics originated.
- **COLORED BANNERS**, under each major metric group, provide section and subsection headings for sets of metrics that describe related ecological components.
- METRIC NAME column corresponds to the metric name in the NWCA vegetation metrics data set.
- **DESCRIPTION column** provides narrative description of each metric.
- CALCULATION/TRAIT INFORMATION column provides:
  - o In white metric rows:
    - § A general formula for calculation of the metric, if not evident in text in the DESCRIPTION column, is provided. PARAMETER NAMES representing raw data that are included in calculations are highlighted in BLUE and are defined in **Table 1**.
    - § Some calculated metrics listed in the METRIC NAME column are, in turn, used as components of other calculated metrics.
    - § Some calculated metrics use species trait information to aggregate species level data. Where traits are used, trait names are indicated in the calculation column using GREEN font.
  - o *In colored banner rows defining metric sets* General categories of species trait information used in calculating a particular series of metrics are listed, if applicable. Codes for specific traits are indicated in GREEN font. *For metrics that use species traits, trait designations are applied as follows:* 
    - § Growth Habit, Duration, and Taxonomic Category are applied by species.
    - § Wetland Indicator Status is applied to taxa-region pairs based on species values for the National Wetland Plant List Regions (U.S. Army Corps of Engineers regions.
    - § Native status designations are applied to taxa-site pairs based on state-level native status for each species.
    - § Coefficients of Conservatism (CCs, aka C-values) are applied to taxa-site pairs based on state specific C-values for each species.
- **METRIC TYPE column** indicates whether the candidate metric describes ecological condition or stress.
- Metrics of the National Vegetation Multimetric Index (VMM) are highlighted in blue bold font.
- Metrics included in the Nonnative Plant Stressor Indicator (NPSI) are highlighted in red bold font.

Table 1. Parameter names from NWCA 2011 Form V-2 (from Appendix B in NWCA 2011 Technical Report)

PARAMETER NAME	DESCRIPTION	RESULT	VALID RANGE/ LEGAL VALUES
Form V-2a and V	/-2b: NWCA Vascular Species P	resence and Cover	
-	· •	each vascular plant species observed our component nested quadrats for ea	
SPECIES	Scientific Name for each species (taxon) encountered in the Veg Plot. Scientific names reconciled to USDA_PLANTS nomenclature. Unknowns are named using growth form codes.	Typically the genus and species name. In some cases: lower taxonomic levels (e.g., subspecies, varieties) or higher taxonomic levels (e.g., genus, family, growth form)	Taxon name
SW	For each species present, the smallest scale at which it is first observed: 1-m² or 10-m² quadrat in SW corner or in larger 100-m² Veg Plot	One of: S = 1-m <sup>2</sup> quadrat, M = 10- m <sup>2</sup> quadrat, or L = entire 100-m <sup>2</sup> Veg Plot	S, M, or L
NE	For each species present, the smallest scale at which it is first observed: 1-m2 or 10-m2 quadrat in NE corner or in larger 100-m <sup>2</sup> Veg Plot	One of: S = 1-m <sup>2</sup> quadrat, M = 10- m <sup>2</sup> quadrat, or entire L = 100-m <sup>2</sup> Veg Plot	S, M, or L
HEIGHT	Predominant height class for each species present across a Veg Plot	One Height Class: 1 = < 0.5m, 2 = > 0.5m-2m, 3 = > 2-5m, 4 = > 5-15m, 5 = > 15-30m, 6 = > 30m, or E = Liana, vine, or epiphyte species	1, 2,3, 4, 5, 6, or E
COVER	Percent cover of each species across a Veg Plot	Cover value for each species present is estimated as a direct percentage of the spatial area of the plot overlain by that species and can range from 0 to 100%.	0-100%

Table 2. Metric names and descriptions (from Appendix D in NWCA 2011 Technical Report)

		•	•
METRIC NAME	METRIC DESCRIPTION	CALCULATION (listed in White Metric Row), SPECIES TRAIT TYPE (if applicable, indicated in Colored Banners)	METRIC TYPE (C = condition, S = stress)
SECTIONS 1 - 5	Metrics based on field data: FORI SPECIES PRESENCE AND COVER	M V-2 – NWCA VASCULAR	
SECTION 1	TAXA COMPOSITION (RICHNESS, FREQUENCY, COVER, DIVERSITY)		
Section 1.1	All Species/Taxonomic Groups		
TOTN_SPP	Richness - Total number of unique species across all 100-m <sup>2</sup> plots	Count unique species across all plots	С
XN_SPP	Mean number of species across all 100-m <sup>2</sup> plots		С
MEDN_SPP	Median number of species across all 100-m <sup>2</sup> plots		С
SDN_SPP	Standard deviation in number of species across all 100-m <sup>2</sup> plots		С
TOTN_GEN	Total number of unique genera across all 100-m <sup>2</sup> plots	Count unique genera across all plots	С
XN_GEN	Mean number of unique genera across all 100-m <sup>2</sup> plots		С
MEDN_GEN	Median number of genera across all 100-m <sup>2</sup> plots		С
SDN_GEN	Standard deviation in number of genera across 100-m <sup>2</sup> plots		С
TOTN_FAM	Total number of families across 100-m <sup>2</sup> plots	Count unique families observed across all plots	С
XN_FAM	Mean number of families across 100-m <sup>2</sup> plots		С
MEDN_FAM	Median number of families across 100-m <sup>2</sup> plots		С
SDN_FAM	Standard deviation in number of families across 100-m <sup>2</sup> plots		С
XTOTABCOV (summary data used in calculation of other metrics)	Mean total absolute cover summed across all species across 100-m <sup>2</sup> plots	S COVER of all individual taxa across 5 plots/5 plots	
H_ALL	Shannon-Wiener Diversity Index - All species  S = number of species observed, i = species i, p = proportion of individuals (relative cover) belonging to species i	$H' = -\sum_{i}^{s} p_{i} \ln p_{i}$	С
J_ALL	Evenness (Pielou) - All species  S = number of species observed	$J = \frac{H'}{\ln S}$	С

METRIC NAME	METRIC DESCRIPTION	CALCULATION (listed in White Metric Row), SPECIES TRAIT TYPE (if applicable, indicated in Colored Banners)	METRIC TYPE (C = condition, S = stress)
D_ALL	Simpson Diversity Index - All species  S = number of species observed, i = species i, p = proportion of individuals (relative cover) belonging to species i	$D=1-\sum_{i}^{s}p_{i}^{2}$	С
XBCDIST_SPP	Within Assessment Area dissimilarity based on species composition = Mean of between-plot Bray-Cutis (BC) Distance (Dissimilarity) based on all species.	Calculate between-plot Bray Curtis Distance for all plot pairs based on species and plot level cover values. Calculate mean of these values to get mean within AA distance: $BC_{ih} = 1 \ \frac{2 \ \sum_{j=1}^{p} MIN(a_{ij}, a_{hj})}{\sum_{j=1}^{p} a_{ij} + \sum_{j=1}^{p} a_{hj}}$	С

SECTIONS 1.2 - 1.3	NATIVE STATUS	Trait Information = Native Status (see Table 5-4)	
Section 1.2	Native (NAT) Species/Taxonomic Groups		
TOTN_NATSPP	Native Richness: Total number of unique native species across all 100- m <sup>2</sup> plots	Count unique native (NAT) species across all plots	С
XN_NATSPP	Mean number of native species across 100-m <sup>2</sup> plots		С
MEDN_NATSPP	Median number of native species across 100-m <sup>2</sup> plots		С
SDN_NATSPP	Standard deviation in number of native species across 100-m <sup>2</sup> plots		С
PCTN_NATSPP	Percent richness of native species observed across 100-m <sup>2</sup> plots	(TOTN_NATSPP/TOTN_SPP) x 100	С
RFREQ_NATSPP	Relative frequency of occurrence for native species as a percent of total frequency (sum of all species)	∑ Frequencies of all (NAT species/∑ Frequencies of all species) x 100; Frequency for individual species = % of 100-m² plots in which it occurs.	С
XABCOV_ NATSPP	Mean total absolute cover of native species across 100-m <sup>2</sup> plots	∑ COVER of all individual native (NAT) taxa across 5 plots/5 plots	С
XRCOV_NATSPP	Mean relative cover of native species across 100-m² plots as a percentage of total cover	(XABCOV_NATSPP/XTOTABCOV) x 100	С
RIMP_NATSPP	Mean relative importance of all native species	(RFREQ_NATSPP + XRCOV_NATSPP)/2	C, Used in VMMI
H_NAT	Shannon-Wiener Diversity Index – Native species only	See H_ALL	С
J_NAT	Evenness (Pielou) – Native species only	See J_ALL	С

METRIC NAME	METRIC DESCRIPTION	CALCULATION (listed in White Metric Row), SPECIES TRAIT TYPE (if applicable, indicated in Colored Banners)	METRIC TYPE (C = condition, S = stress)
D_NAT	Simpson Diversity Index – Native species only	See D_NAT	С
XBCDIST_ NATSPP	Within AA dissimilarity based on native species only composition = Mean of between plot Bray-Cutis Distance (Dissimilarity) based on native species only	See XBCDIST_SPP	С
Section 1.3	Introduced (INTR), Adventive (ADV), ALIEN (INTR + ADV), Cryptogenic (CRYP)	Trait Information = Native Status (see Table 5-4)	
TOTN_INTRSPP	Introduced Richness: Total number of unique introduced species across all 100-m <sup>2</sup> plots	Count unique introduced (INTR) species across all plots	S
XN_INTRSPP	Mean number of introduced species across 100-m <sup>2</sup> plots		S
MEDN_INTRSPP	Median number of introduced species across 100-m <sup>2</sup> plots		S
SDN_INTRSPP	Standard deviation in number of introduced species across 100-m <sup>2</sup> plots		S
PCTN_INTRSPP	Percent richness introduced species observed across 100-m <sup>2</sup> plots	(TOTN_INTRSPP/TOTN_SPP) x 100	S
RFREQ_INTRSPP	Relative frequency of occurrence for introduced species as a percent of total frequency (sum of all species)	( $\Sigma$ Frequencies of all introduced (INTR) species/ $\Sigma$ Frequencies of all species) x 100; Frequency for individual species = % of 100-m <sup>2</sup> plots in which it occurs.	S
XABCOV_ INTRSPP	Mean total absolute cover of all introduced species across 100-m <sup>2</sup> plots	S COVER of all individual INTR taxa across 5 plots/5 plots	S
XRCOV_INTRSPP	Mean relative cover of all INTR species across 100-m² plots as a percentage of total cover	(XABCOV_INTRSPP/XTOTABCOV) x 100	S
RIMP_INTRSPP	Mean relative importance of all introduced species	(RFREQ_INTRSPP + XRCOV_INTRSPP)/2	S
TOTN_ADVSPP	Adventive Richness: Total number of adventive species across 100-m <sup>2</sup> plots	Count unique adventive (ADV) species across all plots	S
XN_ADVSPP	Mean number of adventive species across 100-m <sup>2</sup> plots		S
MEDN_ADVSPP	Median number of adventive species across 100-m <sup>2</sup> plots		S
SDN_ADVSPP	Standard deviation in number of adventive species across 100-m <sup>2</sup> plots		S
DCTN ADVCDD	Descent richness adventive species	/TOTAL ADV/SDD/TOTAL SDD/ v 100	

Percent richness adventive species (TOTN\_ADVSPP/TOTN\_SPP) x 100

observed across all 100-m² plots

PCTN\_ADVSPP

S

METRIC NAME	METRIC DESCRIPTION	CALCULATION (listed in White Metric Row), SPECIES TRAIT TYPE (if applicable, indicated in Colored Banners)	METRIC TYPE (C = condition, S = stress)
RFREQ_ADVSPP	Relative frequency of adventive species occurrence across 100-m <sup>2</sup> plots	(∑ Frequencies of all adventive (ADV) species/∑ Frequencies of all species) x 100; Frequency for individual species = % of 100-m² plots in which it occurs.	S
XABCOV_ ADVSPP	Mean total absolute cover of all ADV species across 100-m <sup>2</sup> plots	S COVER of all individual ADV taxa across 5 plots/5 plots	S
XRCOV_ADVSPP	Mean relative cover of all ADV species or lowest taxonomic unit across 100-m <sup>2</sup> plots as a percentage of total cover	(XABCOV_ADVSPP/XTOTABCOV) x 100	S
RIMP_ADVSPP	Mean relative importance of all adventive species	(RFREQ_ADVSPP + XRCOV_ADVSPP)/2	S
TOTN_ALIENSPP	Alien Richness: Total number of unique alien (INTR + ADV) species across 100-m <sup>2</sup> plots	TOTN_ADVSPP + TOTN_INTRSPP	S
XN_ALIENSPP	Mean number of alien (INTR + ADV) species across 100-m <sup>2</sup> plots		S
MEDN_ALIENSPP	Median number of alien (INTR + ADV) species across 100-m <sup>2</sup> plots		S
SDN_ALIENSPP	Standard deviation in number of alien (INTR + ADV) species		S
PCTN_ALIENSPP	Percent richness alien species across 100-m <sup>2</sup> plots	(TOTN_ALIENSPP/TOTN_SPP) x 100	S
RFREQ_ ALIENSPP	Relative frequency of alien (INTR + ADV) species occurrence across 100-m <sup>2</sup> plots	(∑ Frequencies of all ALIEN species/∑ Frequencies of all species) x 100; Frequency for individual species = % of 100-m² plots in which it occurs.	S
XABCOV_ ALIENSPP	Mean total absolute cover of ALIEN (INTR + ADV) species across 100-m <sup>2</sup> plots	S COVER of all individual ALIEN taxa across 5 plots/5 plots	S
XRCOV_ ALIENSPP	Mean relative cover of all ALIEN (INTR + ADV) species across 100-m <sup>2</sup> plots as a percentage of total cover	(XABCOV_ALIENSPP/XTOTABCOV) x 100	S
RIMP_ALIENSPP	Mean relative importance of all ALIEN (INTR + ADV) species	(RFREQ_ALIENSPP + XRCOV_ALIENSPP)/2	S
H_ALIEN	Shannon-Wiener Diversity Index	See H_ALL	S
J_ALIEN	Evenness (Pielou)	See J_ALL	S
D_ALIEN	Simpson Diversity Index	See D_NAT	S
TOTN_CRYPSPP	Cryptogenic Richness: Total number of unique cryptogenic species across 100-m <sup>2</sup> plots	Count unique cryptogenic (CRYP) species across all plots	S
XN_CRYPSPP	Mean number of cryptogenic species across 100-m <sup>2</sup> plots		S
MEDN_CRYPSPP	Median number of cryptogenic species across 100-m² plots		S

METRIC NAME	METRIC DESCRIPTION	CALCULATION (listed in White Metric Row), SPECIES TRAIT TYPE (if applicable, indicated in Colored Banners)	METRIC TYPE (C = condition, S = stress)
SDN_CRYPSPP	Standard deviation in number of cryptogenic species across 100-m <sup>2</sup> plots	·	S
PCTN_CRYPSPP	Percent richness cryptogenic species across 100-m <sup>2</sup> plots	(TOTN_CRYPSPP/TOTN_SPP) x 100	S
RFREQ_CRYPSPP	Relative frequency of cryptogenic species occurrence across 100-m <sup>2</sup> plots	(∑ Frequencies of all cryptogenic (CRYP) species/∑ Frequencies of all species) x 100; Frequency for individual species = % of 100-m² plots in which it occurs.	S
XABCOV_ CRYPSPP	Mean total absolute cover of all CRYP species across 100-m² plots	S COVER of all CRYP taxa across 5 plots/5 plots	S
XRCOV_CRYPSPP	Mean relative cover of all CRYP species across 100-m <sup>2</sup> plots as a percentage of total cover	(XABCOV_CRYPSPP/XTOTABCOV) x 100	S
RIMP_CRYPSPP	Mean relative importance of all CRYP species	(RFREQ_CRYPSPP + XRCOV_CRYPSPP)/2	S
TOTN_AC	AC Richness: Total number of unique alien and cryptogenic species across 100-m² plots	TOTN_CRYPSPP + TOTN_ALIENSPP	S, Used in NPSI
XN_AC	Mean number of AC (ALIEN + CRYP) species across 100-m <sup>2</sup> plots		S
MEDN_AC	Median number of AC (ALIEN + CRYP) species across 100-m² plots		S
SDN_AC	Standard deviation number of AC (ALIEN + CRYP) species across 100- m <sup>2</sup> plots		S
PCTN_AC	Percent Richness AC species (ALIEN + CRYP) across 100-m <sup>2</sup> plots	(TOTN_CRYPSPP + TOTN- ALIENSPP/TOTN_SPP) x 100	S
RFREQ_AC	Relative frequency of alien and cryptogenic species occurrence in flora based on five 100-m <sup>2</sup> plots	(∑ Frequencies of all ALIEN + CRYP species/∑ Frequencies of all species) x 100; Frequency for individual species = % of 100-m² plots in which it occurs.	S, Used in NPSI
XABCOV_AC	Mean total absolute cover of all AC (ALIEN + CRYP) species across 100- m <sup>2</sup> plots	S COVER of all ALIEN + CRYP taxa across 5 plots/5 plots	S
XRCOV_AC	Mean relative cover of all AC (ALIEN + CRYP) species across 100- m² plots as a percentage of total cover	(XABCOV_AC/XTOTABCOV) x 100	S, Used in NPSI
RIMP_AC	Mean relative importance of all AC (ALIEN + CRYP) species	(RFREQ_AC + XRCOV_AC)/2	S
H_AC	Shannon-Weiner Diversity Index	See H_ALL	S
J_AC	Evenness (Pielou)	See J_ALL	S
D_AC	Simpson Diversity Index	See D_NAT	S

METRIC NAME Section 2	METRIC DESCRIPTION FLORISTIC QUALITY	CALCULATION (listed in White Metric Row), SPECIES TRAIT TYPE (if applicable, indicated in Colored Banners) Trait Information = Coefficients of Conservatism (see Section 5.9); Native Status (see Table 5-4)	METRIC TYPE (C = condition, S = stress)
Equation 1	General formula for Mean C $CC_{ij}$ – coefficient of conservatism for each unique species $i$ at site $j$ , $N =$ number of species at site $j$	$\overline{C} = (\mathring{a}_{CC_{ij}})/N_{j}$	
Equation 2	General formula for FQAI $CC_{ij}$ – coefficient of conservatism for each unique species $i$ at site $j$ , $N =$ number of species at site $j$	$FQAI = $ å $CC_{ij}/\sqrt{N_{j}}$	
Equation 3	For weighted Mean C or FQAI Replace $CC_{ij}$ with $wCC_{ij}$ , where $p_{ij}$ = relative frequency or relative cover	$wCCij = p_{ij}CC_{ij}$	
XC_NAT	Mean Coefficient of Conservatism with native species only	Equation 1	С
XC_ALL	Mean Coefficient of Conservatism with all species	Equation 1	С
XC_FREQ_NAT	Relative frequency-weighted Mean Coefficient of Conservatism with native species only	Equation 1, Equation 3	С
XC_FREQ_AII	Relative frequency-weighted Mean Coefficient of Conservatism with all species only	Equation 1, Equation 3	С
XC_COV_NAT	Relative cover-weighted Mean Coefficient of Conservatism with native species only	Equation 1, Equation 3	С
XC_COV_AII	Relative cover-weighted Mean Coefficient of Conservatism with all species	Equation 1, Equation 3	С
FQAI_NAT	Floristic Quality Index with native species only	Equation 2	С
FQAI_ALL	Floristic Quality Index with all species	Equation 2	C, Used in VMMI
FQAI_FREQ_NAT	Proportional frequency-weighted Floristic Quality Assessment Index with native species only	Equation 2, Equation 3	С
FQAI_FREQ_ALL	Proportional frequency-weighted Floristic Quality Assessment Index with all species only	Equation 2, Equation 3	С
FQAI_COV_NAT	Proportional cover-weighted Floristic Quality Assessment Index with native species only	Equation 2, Equation 3	С
FQAI_COV_ALL	Proportional cover-weighted Floristic Quality Assessment Index with all species	Equation 2, Equation 3	С

		CALCULATION (listed in White	
		Metric Row),	METRIC TYPE
		SPECIES TRAIT TYPE (if applicable,	(C = condition,
METRIC NAME	METRIC DESCRIPTION	indicated in Colored Banners)	S = stress)
Section 3	STRESS	Trait Information =	
	TOLERANCE/SENSITIVITY	Coefficients of Conservatism	
	10 EnAiteLy SEItSITIVITI	(Section 5.9)	
N_HSEN	Number (Richness) Highly Sensitive	Count unique species that meet	С
	Species; C-value >= 9	criterion across 100-m <sup>2</sup> plots	
N_SEN	Number (Richness) Sensitive	Count unique species that meet	С
	Species; C -value >= 7	criterion across 100-m² plots	
N_ISEN	Number (Richness) Intermediate	Count unique species that meet	С
	Sensitivity Species; C-value = 5 to 6	criterion across 100-m <sup>2</sup> plots	
N_TOL	Number (Richness) Tolerant	Count unique species that meet	С
	Species; C -value <= 4	criterion across 100-m <sup>2</sup> plots	
N_HTOL	Number (Richness) Highly Tolerant	Count unique species that meet	С
	Species; C-value <= 2	criterion across 100-m² plots	
PCTN_HSEN	Percent Richness Highly Sensitive		С
	Species; C-value >= 9	(N_HSEN/TOTN_SPP) x 100	
PCTN_SEN	Percent Richness Sensitive Species;	(	С
DOTAL 10511	C-value >= 7	(N_SEN/TOTN_SPP) x 100	
PCTN_ISEN	Percent Richness Intermediate	(N. 1851) (TOTAL 800) 400	С
DOTAL TOL	Sensitivity Species; C-value = 5 to 6	(N_ISEN/TOTN_SPP) x 100	
PCTN_TOL	Percent Richness Tolerant Species;	(N. TOL /TOTAL CDD) 400	С
DOTAL LITOL	C-value <= 4	(N_TOL/TOTN_SPP) x 100	
PCTN_HTOL	Percent Richness Highly Tolerant	(N. LITOL/TOTAL CDD) v 100	С
VADCOV LISEN	Species; C-value <= 2	(N_HTOL/TOTN_SPP) x 100	
XABCOV_HSEN	Absolute Mean Cover Highly Sensitive Species; C-value >= 9	S COVER of species with C-value	С
VADCOV SEN	Absolute Mean Cover Sensitive	>= 9 across 5 plots/5 plots	
XABCOV_SEN	Species; C-value >= 7	S COVER of species with C-value	С
XABCOV_ISEN	Absolute Mean Cover Intermediate	>= 7 across 5 plots/5 plots	
AABCOV_ISEN		S COVER of species with C-value =	С
VARCOV TO	Sensitivity Species; C-value= 5 to 6	5 or 6 across 5 plots/5 plots	
XABCOV_TOL	Absolute Mean Cover Tolerant	S COVER of species with C-value	С
VARCOV LITO	Species; C-value <= 4	<= 4 across 5 plots/5 plots	
XABCOV_HTOL	Absolute Mean Cover Highly	S COVER of species with C-value	С
VDCOV LICEN	Tolerant Species; C-value <= 2	<= 2 across 5 plots/5 plots	
XRCOV_HSEN	Relative Mean Cover Highly	(XABCOV_HSEN/XTOTABCOV) x	С
VDCOV CEN	Sensitive Species; C >= 9	100	
XRCOV_SEN	Relative Mean Cover Sensitive	(VARCOV, CENT/VTOTARCOV) -: 100	С
VDCOV ICEN	Species; C-value >= 7	(XABCOV_SEN/XTOTABCOV) x 100	
XRCOV_ISEN	Relative Mean Cover Intermediate	(XABCOV_ISEN/XTOTABCOV) x 100	С
VPCOV TO	Sensitivity Species; C-value = 5 to 6 Relative Mean Cover Tolerant	100	
XRCOV_TOL		(XABCOV TOL/XTOTABCOV) x 100	С
XRCOV_HTOL	Species; C-value <= 4 Relative Mean Cover Highly	(XABCOV_TOL/XTOTABCOV) x 100	
VUCOA LIOF	Tolerant Species; C-value <= 2	100	С
-	Totel allt Species, C-Value <- 2	100	

METRIC NAME	METRIC DESCRIPTION	CALCULATION (listed in White Metric Row), SPECIES TRAIT TYPE (if applicable, indicated in Colored Banners)	METRIC TYPE (C = condition, S = stress)
SECTION 4	HYDROPHYTIC STATUS	Trait Information = Wetland	
	Obligate (OBL), Facultative Wetland	Indicator Status (WIS) from	
	(FACW), Facultative (FAC),	National Wetland Plant List	
	Facultative Upland (FACU), Upland	(Table 5-3); Native Status	
	(UPL + Not Listed (NL))	(Table 5-4)	
N_OBL	Richness (number) of Obligate species	Count unique OBL species across 100-m² plots	С
N_FACW	Richness (number) of Facultative Wetland species	Count unique FACW species across 100-m <sup>2</sup> plots	С
N_FAC	Richness (number) of Facultative species	Count unique FACU species across 100-m <sup>2</sup> plots	С
N_FACU	Richness (number) of Facultative Upland species	Count unique FAC species across 100-m <sup>2</sup> plots	С
N_UPL	Richness (number) of UPL species = UPL	Count unique UPL species across 100-m² plots	С
PCTN_OBL	Percent richness of Obligate species	(N_OBL/TOTN_SPP) x 100	С
PCTN_FACW	Percent richness of Facultative Wetland species	(N_FACW/TOTN_SPP) x 100	С
PCTN_FAC	Percent richness of Facultative species	(N_FAC/TOTN_SPP) x 100	С
PCTN_FACU	Percent richness of Facultative Upland species	(N_FACU/TOTN_SPP) x 100	С
PCTN_UPL	Percent richness of UPL (= UPL + NL) species	(N_UPL/TOTN_SPP) x 100	С
XABCOV_OBL	Mean Absolute Cover of Obligate species	S COVER of OBL species across 5 plots/5 plots	С
XABCOV_FACW	Mean Absolute Cover of Facultative Wetland species	S COVER of FACW species across 5 plots/5 plots	С
XABCOV_FAC	Mean Absolute Cover of Facultative species	S COVER of FAC species across 5 plots/5 plots	С
XABCOV_FACU	Mean Absolute Cover of Facultative Upland species	S COVER of FACU species across 5 plots/5 plots	С
XABCOV_UPL	Mean Absolute Cover of UPL species	S COVER of UPL species across 5 plots/5 plots	С
XRCOV_OBL	Mean Relative Cover of Obligate species	(XABCOV_OBL/XTOTABCOV) x 100	С
XRCOV_FACW	Mean Relative Cover of Facultative Wetland species	(XABCOV_FACW/XTOTABCOV) x 100	С
XRCOV_FAC	Mean Relative Cover of Facultative species	(XABCOV_FAC/XTOTABCOV) x 100	С
XRCOV_FACU	Mean Relative Cover of Facultative Upland species	(XABCOV_FACU/XTOTABCOV) x 100	С
XRCOV_UPL	Mean Relative Cover of UPL (= UPL + NL) species	(XABCOV_UPL/XTOTABCOV) x 100	С

METRIC NAME	METRIC DESCRIPTION	CALCULATION (listed in White Metric Row), SPECIES TRAIT TYPE (if applicable, indicated in Colored Banners)	METRIC TYPE (C = condition, S = stress)
WETIND_COV_ ALL	Wetland Index, Cover Weighted - all species	2 2	
	$l_{ij}$ = Importance Value = Mean absolute cover species $i$ in site $j$ . $E_i$ = Ecological score for species based on WIS (OBL = 1, FACW = 2, FAC = 3, FACU = 4, UPL = 5)	$WI = \sum_{i=1}^{P} I_{ij} E_i / \sum_{i=1}^{P} I_{ij}$	С
WETIND_FREQ_ ALL	Wetland Index, Frequency Weighted - all species	$WI = \sum_{i=1}^{p} I_{ij} E_i / \sum_{i=1}^{p} I_{ij}$	
	$I_{ij}$ = Importance Value = Frequency for species $i$ in site $j$ . $E_i$ = Ecological score for species based on WIS (OBL = 1, FACW = 2, FAC = 3, FACU = 4, UPL = 5)		С
WETIND_ COV_NAT	Wetland Index, Cover Weighted - native species only		
	$I_{ij}$ = Importance Value = Mean absolute cover for species $i$ in site $j$ . $E_i$ = Ecological score for species based on WIS (OBL = 1, FACW = 2, FAC = 3, FACU = 4, UPL = 5)	$WI = \sum_{i=1}^{\nu} I_{ij} E_i / \sum_{i=1}^{\nu} I_{ij}$	С
WETIND_ FREQ_NAT	Wetland Index, Frequency Weighted - native species only	$WI = \sum_{i=1}^{p} I_{ij} E_i / \sum_{i=1}^{p} I_{ij}$	
	$I_{ij}$ = Importance Value = Frequency for species $i$ in site $j$ . $E_i$ = Ecological score for species based on WIS (OBL = 1, FACW = 2, FAC = 3, FACU = 4, UPL = 5)	$\sum_{i=1}^{j-i}  y-i  / \sum_{i=1}^{j-i}  y-i $	С
N_OBLFACW_AC	Number of Alien + Cryptogenic Obligate and facultative wetland species	Count unique ALIEN and CRYP OBL and FACW species across 100-m <sup>2</sup> plots	S
XABCOV_ OBLFACW_AC	Mean Absolute Cover of Alien + Cryptogenic Obligate and Facultative Wetland species	S COVER of ALIEN and CRYP OBL and FACW species across 5 plots/5 plots	S
XRCOV_ OBLFACW_AC	Mean Relative Cover of Alien + Cryptogenic Obligate and Facultative Wetland species	(XABCOV_OBLFACW_AC/ XTOTABCOV) x 100	S

METRIC NAME	METRIC DESCRIPTION	CALCULATION (listed in White Metric Row), SPECIES TRAIT TYPE (if applicable, indicated in Colored Banners)	METRIC TYP (C = condition S = stress)
SECTION 5	LIFE HISTORY	maicacca in Colorea Banners,	
SECTION 5.1	GROWTH HABIT	Trait Information = Growth Habit (Table 5-1); Native Status (Table 5-4)	
N_GRAMINOID	Graminoid richness	Count unique GRAMINOID species across 100-m² plots	С
N_GRAMINOID_ NAT	Native Graminoid richness	Count unique native (NAT) GRAMINOID species across 100- m² plots	С
N_GRAMINOID_ AC	Alien and cryptogenic Graminoid richness	Count unique ALIEN and CRYP GRAMINOID species across 100- m <sup>2</sup> plots	S
N_FORB	Forb richness	Count unique FORB species across 100-m <sup>2</sup> plots	С
N_FORB_NAT	Native Forb richness	Count unique native(NAT) FORB species across 100-m² plots	С
N_FORB_AC	Alien and cryptogenic Forb richness	Count unique ALIEN and CRYP FORB species across 100-m <sup>2</sup> plots	S
N_HERB	Herbaceous plant (FORB + GRAMINOID) species richness	N_FORB + N_GRAMINOID	С
N_HERB_NAT	Native Herbaceous species richness	N_FORB_NAT + N_GRAMINOID_NAT	С
N_HERB_AC	Alien and cryptogenic Herbaceous richness	N_FORB_AC + N_GRAMINOID_AC	S
N_SSHRUB_ FORB	Subshrub-forb richness	Count unique SUBSHRUB-FORB species across 100-m² plots	С
N_SSHRUB_ SHRUB	Subshrub-shrub richness	Count unique SUBSHRUB-SHRUB species across 100-m² plots	С
N_SHRUB	Shrub richness	Count unique SHRUB species across 100-m² plots	С
N_SHRUB_ COMB	Combined Shrub growth habits richness	N_SHRUB + N_SSHRUB_SHRUB + N_SSHRUB-FORB	С
N_SHRUB_ COMB_NAT	Native richness of Combined Shrub growth habits richness	Count unique native (NAT) SHRUB_COMB species across 100- m² plots	С
N_SHRUB_ COMB_AC	Alien and cryptogenic richness for Combined Shrub growth habits	Count unique ALIEN and CRYP SHRUB_COMB species across 100-m² plots	S
N_TREE_SHRUB	Tree-Shrub richness	Count unique TREE-SHRUB species across 100-m <sup>2</sup> plots	С
N_TREE	Tree richness	Count unique TREE species across 100-m <sup>2</sup> plots	С
N_TREE_COMB	Combined Tree and Tree-Shrub richness	N_TREE_SHRUB + N_TREE	С
N_TREE_ COMB_NAT	Combined Tree and Tree-Shrub richness	Count unique native (NAT) TREE_COMB species across 100- m² plots	С

METRIC NAME	METRIC DESCRIPTION	CALCULATION (listed in White Metric Row), SPECIES TRAIT TYPE (if applicable, indicated in Colored Banners)	METRIC TYPE (C = condition, S = stress)
N_TREE_ COMB_AC	Combined Tree and Tree-Shrub richness	Count unique ALIEN and CRYP TREE_COMB species across 100- m <sup>2</sup> plots	S
N_VINE	Vine richness	Count unique VINE species across 100-m <sup>2</sup> plots	С
N_VINE_NAT	Vine richness	Count unique native (NAT) VINE species across 100-m² plots	С
N_VINE_AC	Vine richness	Count unique ALIEN and CRYP VINE species across 100-m² plots	S
N_VINE_SHRUB	Vine-Shrub richness	Count unique a VINE-SHRUB species across 100-m² plots	С
N_VINE_ SHRUB_NAT	Native Vine-Shrub richness	Count unique native (NAT) VINE- SHRUB species across 100-m <sup>2</sup> plots	С
N_VINE_ SHRUB_AC	Alien and cryptogenic Vine-Shrub richness	Count unique ALIEN and CRYP VINE-SHRUB species across 100-m <sup>2</sup> plots	S
PCTN_ GRAMINOID	Graminoid percent richness	(N_GRAMINOID/TOTN_SPP) x 100	С
PCTN_ GRAMINOID_NAT	Native Graminoid percent richness	(N_GRAMINOID_NAT/ TOTN_SPP) x 100	С
PCTN_ GRAMINOID_AC	Graminoid percent richness	(N_GRAMINOID_AC/TOTN_SPP) x 100	S
PCTN_FORB	Forb percent richness	(N_FORB/TOTN_SPP) x 100	С
PCTN_FORB_ NAT	Native Forb percent richness	(N_FORB_NAT/TOTN_SPP) x 100	С
PCTN_FORB_AC	Alien and cryptogenic Forb percent richness	(N_FORB_AC/TOTN_SPP) x 100	S
PCTN_HERB	Percent Herbaceous (FORB + GRAMINOID) richness	(N_HERB/TOTN_SPP) x 100	С
PCTN_HERB_ NAT	Percent native Herbaceous richness	(N_HERB_NAT/TOTN_SPP) x 100	С
PCTN_HERB_ AC	Percent alien and cryptogenic Herbaceous richness	(N_HERB_AC/TOTN_SPP) x 100	S
PCTN_SSHRUB_ FORB	Subshrub-Forb percent richness	(N_SSHRUB_FORB/TOTN_SPP) x 100	С
PCTN_SSHRUB_ SHRUB	Subshrub-Shrub percent richness	(N_SSHRUB/TOTN_SPP) x 100	С
PCTN_SHRUB	Shrub percent richness	(N_SHRUB/TOTN_SPP) x 100	С
PCTN_SHRUB_ COMB	Combined Shrub richness	(N_SHRUB_COMB/TOTN_SPP) x 100	С
PCTN_SHRUB_ COMB_NAT	Percent native richness of Combined Shrub growth habits	(N_SHRUB_COMB_NAT/TOTN_SP P) x 100	С
PCTN_SHRUB_ COMB_AC	Percent alien and cryptogenic richness for Combined Shrub growth habits	(N_SHRUB_COMB_AC/TOTN_SPP) x 100	S
PCTN_TREE_ SHRUB	Tree-Shrub percent richness	(N_TREE_SHRUB/TOTN_SPP) x 100	С

METRIC NAME	METRIC DESCRIPTION	CALCULATION (listed in White Metric Row), SPECIES TRAIT TYPE (if applicable, indicated in Colored Banners)	METRIC TYPE (C = condition, S = stress)
PCTN_TREE	Tree percent richness	(N_TREE/TOTN_SPP) x 100	С
PCTN_TREE_	Combined Tree and Tree-Shrub		С
СОМВ	percent richness	(N_TREE_COMB/TOTN_SPP) x 100	
PCTN_TREE_	Combined Tree and Tree-Shrub	(N_TREE_COMB_NAT/TOTN_SPP)	С
COMB_NAT	percent richness	x 100	
PCTN_TREE_	Combined Tree and Tree-Shrub	(N_TREE_COMB_AC/TOTN_SPP) x	S
COMB_AC	percent richness	100	
PCTN_VINE	Vine percent richness	(N_VINE/TOTN_SPP) x 100	С
PCTN_VINE_NAT	Native Vine percent richness	(N_VINE_NAT/TOTN_SPP) x 100	С
PCTN_VINE_AC	Alien and cryptogenic Vine percent richness	(N_VINE_AC/TOTN_SPP) x 100	S
PCTN_VINE_ SHRUB	Vine-Shrub percent richness	(N_VINE_SHRUB/TOTN_SPP) x 100	С
PCTN_VINE_ SHRUB_NAT	Native Vine-Shrub percent richness	(N_VINE_SHRUB_NAT/TOTN_SPP) x 100	С
PCTN_VINE_	Alien and Cryptogenic Vine-Shrub	(N_VINE_SHRUB_AC/TOTN_SPP) x	C
SHRUB_AC	percent richness	100	S
XABCOV_	Mean absolute Graminoid cover	S COVER of GRAMINOID species	С
GRAMINOID		across 5 plots/5 plots	
XABCOV_	Mean absolute native Graminoid	S COVER of GRAMINOID NAT	С
GRAMINOID_NAT	cover	species across 5 plots/5 plots	
XABCOV_	Mean absolute alien and	S COVER of GRAMINOID ALIEN	
GRAMINOID_AC	cryptogenic Graminoid cover	and CRYP species across 5 plots/5 plots	S
XABCOV_FORB	Mean absolute FORB cover	S COVER of FORB species across 5 plots/5 plots	С
XABCOV_FORB_ NAT	Mean absolute native FORB cover	S COVER of NAT FORB species across 5 plots/5 plots	С
XABCOV_FORB_	Mean absolute alien and	S COVER of ALIEN and CRYP FORB	
AC	cryptogenic FORB cover	species across 5 plots/5 plots	S
XABCOV_HERB	Mean absolute Herbaceous species	XABCOV_FORB +	^
	cover (FORB + GRAMINOID)	XABCOV_GRAMINOID	С
XABCOV_HERB_	Mean absolute native Herbaceous	XABCOV_FORB_NAT +	С
NAT	cover	XABCOV_GRAMINOID_NAT	
XABCOV_HERB_	Mean relative Herbaceous alien and	XABCOV_FORB_AC +	S
AC	cryptogenic cover	XABCOV_GRAMINOID_AC	-
XABCOV_	Mean absolute Subshrub-Forb	S COVER of SUBSHRUB-FORB	С
SSHRUB_FORB	cover  Mean absolute Subshrub-Shrub	species across 5 plots/5 plots	
XABCOV_		S COVER SUBSHRUB-SHRUB	С
SSHRUB_SHRUB XABCOV_SHRUB	cover Mean absolute Shrub cover	species across 5 plots/5 plots S COVER of SHRUB species across	
VVDCO 1 2111/0B		5 plots/5 plots	С
XABCOV_	Combined Shrub growth habits	S COVER of SHRUB_COMB species	С
SHRUB_COMB	absolute cover	across 5 plots/5 plots	
XABCOV_SHRUB_	Mean absolute native Combined	S COVER of NAT SHRUB-COMB	С
COMB_NAT	Shrub growth habits cover	species across 5 plots/5 plots	

METRIC NAME	METRIC DESCRIPTION	CALCULATION (listed in White Metric Row), SPECIES TRAIT TYPE (if applicable, indicated in Colored Banners)	METRIC TYP (C = condition S = stress)
XABCOV_SHRUB_	Mean absolute alien and	S COVER of ALIEN and CRYP	
COMB_AC	cryptogenic Combined Shrub	SHRUB_COMB species across 5	S
	growth habits cover	plots/5 plots	
XABCOV_TREE_	Mean absolute Tree-Shrub cover	S COVER of TREE-SHRUB species	-
SHRUB		across 5 plots/5 plots	С
XABCOV_TREE	Mean absolute Tree cover	S COVER of TREE species across 5	С
		plots/5 plots	C
XABCOV_TREE_	Combined Tree and Tree-Shrub	S COVER of TREE_COMB species	-
COMB	absolute cover	across 5 plots/5 plots	С
XABCOV_TREE_	Combined native Tree and Tree-	S COVER of NAT TREE COMB	
COMB_NAT	Shrub absolute cover	species across 5 plots/5 plots	С
XABCOV TREE	Combined alien and cryptogenic	S COVER of ALIEN and CRYP	
COMB_AC	Tree and Tree-Shrub absolute cover	TREE_COMB species across 5	S
_		plots/5 plots	-
XABCOV_VINE	Mean absolute Vine cover	S COVER of VINE species across 5	
		plots/5 plots	С
XABCOV_VINE_	Mean native absolute Vine cover	S COVER of NAT VINE species	
NAT		across 5 plots/5 plots	С
XABCOV_VINE_	Mean alien and cryptogenic	S COVER of ALIEN and CRYP VINE	
AC	absolute Vine cover	species across 5 plots/5 plots	S
XABCOV_VINE_	Mean absolute Vine-Shrub cover	S COVER of VINE-SHRUB species	
SHRUB	Wear absolute vine sin ab cover	across 5 plots/5 plots	С
XABCOV_VINE_	Mean absolute native Vine-Shrub	S COVER of NAT VINE-SHRUB	
SHRUB_NAT	cover	species across 5 plots/5 plots	С
XABCOV_VINE_	Mean absolute alien and	S COVER of ALIEN and CRYP VINE-	
SHRUB_AC	cryptogenic Vine-Shrub cover	SHRUB species across 5 plots/5	S
SINOB_AC	cryptogeme vine smab cover	plots	3
XRCOV_	Mean relative Graminoid cover	(XABCOV_GRAMINOID/	
GRAMINOID	Wear relative Grammola cover	XTOTABCOV) x 100	С
XRCOV_	Mean relative native Graminoid	(XABCOV_GRAMINOID_NAT/	
GRAMINOID_NAT	cover	XTOTABCOV) x 100	С
XRCOV	Mean relative alien and cryptogenic	(XABCOV GRAMINOID AC/	
GRAMINOID AC	Graminoid cover	XTOTABCOV) x 100	S
XRCOV FORB	Mean relative Forb cover	(XABCOV FORB/XTOTABCOV) x	
55 · _ · OND		100	С
XRCOV_	Mean relative native Forb cover	(XABCOV FORB NAT/	
FORB NAT		XTOTABCOV) x 100	С
XRCOV_FORB_AC	Mean relative alien and cryptogenic	(XABCOV FORB AC/XTOTABCOV)	
<u>_</u>	Forb cover	x 100	С
XRCOV_HERB	Mean relative Herbaceous (FORB +	(XABCOV_HERB/XTOTABCOV) x	
	GRAMINOID) cover	100	С
XRCOV_	Mean relative native Herbaceous	(XABCOV_HERB_NAT/	
HERB_NAT	cover	XTOTABCOV) x 100	С
XRCOV_HERB_AC	Mean relative alien and cryptogenic	(XABCOV_HERB_AC/XTOTABCOV)	
22112210	Herbaceous cover	x 100	S
XRCOV_SSHRUB_	Mean relative Subshrub-Forb cover	(XABCOV_SSHRUB_FORB/	
FORB		XTOTABCOV) x 100	С

METRIC NAME	METRIC DESCRIPTION	CALCULATION (listed in White Metric Row), SPECIES TRAIT TYPE (if applicable, indicated in Colored Banners)	METRIC TYPE (C = condition, S = stress)
XRCOV_SSHRUB_ SHRUB	Mean relative Subshrub-Shrub cover	(XABCOV_SSHRUB_SHRUB/ XTOTABCOV) x 100	С
XRCOV_SHRUB	Mean relative Shrub cover	(XABCOV_SHRUB/XTOTABCOV) x 100	С
XRCOV_SHRUB_ COMB	Mean relative Combined Shrub growth habits cover	(XABCOV_SHRUB_COMB/ XTOTABCOV) x 100	С
XRCOV_SHRUB_ COMB_NAT	Mean relative native Combined Shrub growth habits cover	(XABCOV_SHRUB_COMB_NAT/ XTOTABCOV) x 100	С
XRCOV_SHRUB_ COMB_AC	Mean relative alien and cryptogenic Combined Shrub growth habits cover	(XABCOV_SHRUB_COMB_AC/ XTOTABCOV) x 100	S
XRCOV_TREE_ SHRUB	Mean relative Tree-Shrub cover	(XABCOV_TREE_SHRUB/ XTOTABCOV) x 100	С
XRCOV_TREE	Mean relative Tree cover	(XABCOV_TREE/XTOTABCOV) x 100	С
XRCOV_TREE_ COMB	Mean relative Combined Tree and Tree-Shrub cover	(XABCOV_TREE_COMB/ XTOTABCOV) x 100	С
XRCOV_TREE_ COMB_NAT	Mean relative Combined Tree and Tree-Shrub cover	(XABCOV_TREE_COMB_NAT/ XTOTABCOV) x 100	С
XRCOV_TREE_ COMB_AC	Mean relative Combined Tree and Tree-Shrub cover	(XABCOV_TREE_COMB_AC/ XTOTABCOV) x 100	S
XRCOV_VINE	Mean relative Vine cover	(XABCOV_VINE/XTOTABCOV) x 100	С
XRCOV_VINE_ NAT	Mean native relative Vine cover	(XABCOV_VINE_NAT/XTOTABCOV) x 100	С
XRCOV_VINE_ AC	Mean alien and cryptogenic relative Vine cover	(XABCOV_VINE_AC/XTOTABCOV) x 100	S
XRCOV_VINE_ SHRUB	Mean relative Vine-Shrub cover	(XABCOV_VINE_SHRUB/ XTOTABCOV) x 100	С
XRCOV_VINE_ SHRUB_NAT	Mean native relative Vine-Shrub cover	(XABCOV_VINE_SHRUB_NAT/ XTOTABCOV) x 100	С
XRCOV_VINE_ SHRUB_AC	Mean alien and cryptogenic relative Vine-Shrub cover	(XABCOV_VINE_SHRUB_AC/ XTOTABCOV) x 100	S
Section 5.2	DURATION	Trait Information = Duration (Table 5-2); Native Status (Table 5-4)	
N_ANNUAL	Annual species richness	Count unique ANNUAL species across 100-m <sup>2</sup> plots	С
N_ANNUAL_NAT	Native Annual richness	Count unique NAT ANNUAL species across 100-m² plots	С
N_ANNUAL_AC	Alien and cryptogenic Annual richness	Count unique ALIEN and CRYP ANNUAL species across 100-m <sup>2</sup> plots	S
N_ANN_BIEN	Annual-Biennial richness	Count unique ANN_BIEN species across 100-m² plots	С
N_ANN_ BIEN_NAT	Native Annual-Biennial richness	Count unique NAT ANN_BIEN species across 100-m² plots	С

METRIC NAME	METRIC DESCRIPTION	CALCULATION (listed in White Metric Row), SPECIES TRAIT TYPE (if applicable, indicated in Colored Banners)	METRIC TYPE (C = condition, S = stress)
N_ANN_ BIEN_AC	Alien and cryptogenic Annual- Biennial richness	Count unique ALIEN and CRYP ANN_BIEN species across 100-m <sup>2</sup> plots	S
N_ANN_PEREN	Annual-Perennial richness	Count unique ANN_PEREN species across 100-m <sup>2</sup> plots	С
N_ANN_ PEREN_NAT	Native Annual-Perennial richness	Count unique NAT ANN_PEREN species across 100-m² plots	С
N_ANN_ PEREN_AC	Alien and cryptogenic Annual- Perennial richness	Count unique ALIEN and CRYP ANN_PEREN species across 100- m <sup>2</sup> plots	S
N_PERENNIAL	Perennial richness	Count unique PERENNIAL species across 100-m² plots	С
N_PERENNIAL_ NAT	Native Perennial richness	Count unique NAT PERENNIAL species across 100-m² plots	С
N_PERENNIAL_AC	Alien and cryptogenic Perennial richness	Count unique ALIEN and CRYP PERENNIAL species across 100-m <sup>2</sup> plots	S
PCTN_ANNUAL	Percent Annual richness	(N_ANNUAL/TOTN_SPP) x 100	С
PCTN_ANNUAL_ NAT	Percent native Annual richness	(N_ANNUAL_NAT/TOTN_SPP) x 100	С
PCTN_ANNUAL_ AC	Percent alien and cryptogenic Annual richness	(N_ANNUAL_AC/TOTN_SPP) x 100	S
PCTN_ANN_BIEN	Percent Annual-Biennial richness	(N_ANN_BIEN/TOTN_SPP) x 100	С
PCTN_ANN_ BIEN_NAT	Percent native Annual-Biennial richness	(N_ANN_BIEN_NAT/TOTN_SPP) x 100	С
PCTN_ANN_ BIEN_AC	Percent alien and cryptogenic Annual-Biennial richness	(N_ANN_BIEN_AC/TOTN_SPP) x 100	S
PCTN_ANN_ PEREN	Percent Annual-Perennial richness	(N_ANN_PEREN/TOTN_SPP) x 100	С
PCTN_ANN_ PEREN_NAT	Percent native Annual-Perennial richness	(N_ANN_PEREN_NAT/TOTN_SPP) x 100	С
PCTN_ANN_ PEREN_AC	Percent alien and cryptogenic Annual-Perennial richness	(N_ANN_PEREN_AC/TOTN_SPP) x 100	S
PCTN_PERENNIAL	Percent Perennial richness	(N_PERENNIAL/TOTN_SPP) x 100	С
PCTN_ PERENNIAL NAT	Percent native Perennial richness	(N_PERENNIAL_NAT/TOTN_SPP) x 100	С
PCTN_ PERENNIAL AC	Percent alien and cryptogenic Perennial richness	(N_PERENNIAL_AC/TOTN_SPP) x 100	S
XABCOV_ ANNUAL	Mean absolute Annual cover	S COVER of ANNUAL species across 5 plots/5 plots	С
XABCOV_ ANNUAL_NAT	Mean absolute native Annual cover	S COVER of NAT ANNUAL species across 5 plots/5 plots	С
XABCOV_ ANNUAL_AC	Mean absolute alien and cryptogenic Annual cover	S COVER of ALIEN and CRYP ANNUAL species across 5 plots/5 plots	S
XABCOV_ANN_ BIEN	Mean absolute Annual-Biennial cover	S COVER of ANN_BIEN species across 5 plots/5 plots	С

		CALCULATION (listed in White Metric Row),	METRIC TYPE (C = condition,
METRIC NAME	METRIC DESCRIPTION	<b>SPECIES TRAIT TYPE</b> (if applicable, indicated in Colored Banners)	S = stress)
XABCOV_ANN_	Mean absolute native Annual-	S COVER of NAT ANN BIEN	
BIEN_NAT	Biennial cover	species across 5 plots/5 plots	С
XABCOV_ANN_	Mean absolute alien and	S COVER of ALIEN and CRYP	
BIEN_AC	cryptogenic Annual-Biennial cover	ANN_BIEN species across 5 plots/5	S
_	,, ,	plots	
XABCOV_ANN_	Mean absolute Annual-Perennial	S COVER of ANN_PEREN species	С
PEREN	cover	across 5 plots/5 plots	<u> </u>
XABCOV_ANN_	Mean absolute native Annual-	S COVER of NAT ANN_PEREN	С
PEREN_NAT	Perennial cover	species across 5 plots/5 plots	
XABCOV_ANN_	Mean absolute alien and	S COVER of ALIEN and CRYP	
PEREN_AC	cryptogenic Annual-Perennial cover	ANN_PEREN species across 5	S
		plots/5 plots	
XABCOV_	Mean absolute Perennial cover	S COVER of PERENNIAL species	С
PERENNIAL		across 5 plots/5 plots	
XABCOV_	Mean absolute native Perennial	S COVER of NAT PERENNIAL	С
PERENNIAL_NAT	cover	species across 5 plots/5 plots	
XABCOV_	Mean absolute alien and	S COVER of ALIEN and CRYP	
PERENNIAL_AC	cryptogenic Perennial cover	PERENNIAL species across 5	S
VDCOV ANNUAL	Many valativa avanta avan	plots/5 plots	
XRCOV_ANNUAL	Mean relative annual cover	(XABCOV_ANNUAL/XTOTABCOV) x	С
VDCOV ANNUAL	Mann relative native Annual cover	100	
XRCOV_ANNUAL_ NAT	Mean relative native Annual cover	(XABCOV_ANNUAL_NAT/ XTOTABCOV) x 100	С
XRCOV_ANNUAL_	Mean relative alien and cryptogenic	(XABCOV_ANNUAL_AC/	
AC ANNOAL	Annual cover	XTOTABCOV) x 100	S
XRCOV_ANN_	Mean relative Annual-Biennial	(XABCOV_ANN_BIEN/	
BIEN	cover	XTOTABCOV) x 100	С
XRCOV_ANN_	Mean relative native Annual-	(XABCOV_ANN_BIEN_NAT/	
BIEN_NAT	Biennial cover	XTOTABCOV) x 100	С
XRCOV_ANN_	Mean relative alien and cryptogenic	(XABCOV_ANN_BIEN_AC/	<u> </u>
BIEN_AC	Annual-Biennial cover	XTOTABCOV) x 100	S
XRCOV_ANN_	Mean relative Annual-Perennial	(XABCOV_ANN_PEREN/	
PEREN	cover	XTOTABCOV) x 100	С
XRCOV_ANN_	Mean relative native Annual-	(XABCOV_ANN_PEREN_NAT/	
PEREN_NAT	Perennial cover	XTOTABCOV) x 100	
XRCOV_ANN_	Mean relative alien and cryptogenic	(XABCOV_ANN_PEREN_AC/	S
PEREN_AC	Annual-Perennial cover	XTOTABCOV) x 100	
XRCOV_	Mean relative Perennial cover	(XABCOV_PERENNIAL/	С
PERENNIAL	Manage malating 12 D	XTOTABCOV) x 100	
XRCOV_	Mean relative native Perennial	(XABCOV_PERENNIAL_NAT/	С
PERENNIAL_NAT	Naga relative alian and swinterenis	XTOTABCOV DEPENDIAL ACC	
XRCOV_	Mean relative alien and cryptogenic	(XABCOV_PERENNIAL_AC/	S
PERENNIAL_AC	Perennial cover	XTOTABCOV) x 100	
Section 5.3	DI ANT CATECODY	Trait Information - Disut	
3600001 3.3	PLANT CATEGORY	Trait Information = Plant Category (See Section 5.6.3);	
		Native Status (Table 5-4)	
		realise status (Table 3-4)	

METRIC NAME	METRIC DESCRIPTION	CALCULATION (listed in White Metric Row), SPECIES TRAIT TYPE (if applicable, indicated in Colored Banners)	METRIC TYPE (C = condition, S = stress)
N_DICOT	Dicot richness	Count unique DICOT species across 100-m² plots	С
N_DICOTS_NAT	Native Dicot richness	Count unique NAT DICOT species across 100-m² plots	С
N_DICOTS_ALIEN	Alien Dicot richness	Count unique ALIEN DICOT species across 100-m² plots	S
N_DICOTS_CRYP	Cryptogenic Dicot richness	Count unique CRYP DICOT species across 100-m² plots	С
N_DICOTS_AC	Alien and Cryptogenic richness	N_DICOT_ALIEN + N_DICOT_CRYP	S
N_FERN	Fern richness	Count unique FERN species across 100-m <sup>2</sup> plots	С
N_FERNS_NAT	Native Fern richness	Count unique native FERN species across 100-m² plots	С
N_FERNS_INTR	Introduced FERN species richness	Count unique introduced FERN species across 100-m² plots	S
N_GYMNOSPERM	Gymnosperm richness	Count unique GYMNOSPERM species across 100-m² plots	С
N_LYCOPOD	Lycopod richness	Count unique LYCOPOD species across 100-m <sup>2</sup> plots	С
N_HORSETAIL	Horsetail richness	Count unique HORSETAIL species across 100-m <sup>2</sup> plots	С
N_MONOCOT	Monocot richness	Count unique MONOCOT species across 100-m² plots	С
N_MONOCOTS_ NAT	Native Monocot richness	Count unique NAT MONOCOT species across 100-m² plots	С
N_MONOCOTS_ ALIEN	Alien Monocot richness	Count unique ALIEN MONOCOT species across 100-m² plots	S
N_MONOCOTS_ CRYP	Cryptogenic Monocot richness	Count unique CRYP MONOCOT species across 100-m² plots	S
N_MONOCOTS_ AC	Alien and cryptogenic Monocot richness	N_MONOCOT_ALIEN + N_MONOCOT_CRYP	S
PCTN_DICOT	Dicot percent richness	(N_DICOTS/TOTN_SPP) x 100	С
PCTN_DICOTS_ NAT	Native Dicot percent richness	(N_DICOTS_NAT/TOTN_SPP) x 100	С
PCTN_DICOTS_ ALIEN	Alien Dicot percent richness	(N_DICOTS_ALIEN/TOTN_SPP) x 100	S
PCTN_DICOTS_ CRYP	Cryptogenic Dicot percent richness	(N_DICOTS_CRYP/TOTN_SPP) x 100	S
PCTN_DICOTS_AC	Alien and cryptogenic Dicot percent richness	(N_DICOTS_AC/TOTN_SPP) x 100	S
PCTN_FERN	Fern percent richness	(N_FERNS/TOTN_SPP) x 100	С
PCTN_FERNS_ NAT	Native Ferns percent richness	(N_FERNS_NAT/TOTN_SPP) x 100	С
PCTN_FERNS_ INTR	Introduced Fern percent richness	(N_FERNS_INTR/TOTN_SPP) x 100	S
PCTN_ GYMNOSPERM	GYMNOSPERM Percent Richness	(N_GYNOSPERM/TOTN_SPP) x 100	С

METRIC NAME	METRIC DESCRIPTION	CALCULATION (listed in White Metric Row), SPECIES TRAIT TYPE (if applicable, indicated in Colored Banners)	METRIC TYPE (C = condition, S = stress)
PCTN_LYCOPOD	Lycopod percent richness	(N_LYCOPOD/TOTN_SPP) x 100	С
PCTN_HORSETAIL	Horsetail percent richness	(N_HORSETAIL/TOTN_SPP) x 100	С
PCTN_ MONOCOT	Monocot percent richness	(N_MONOCOTS/TOTN_SPP) x 100 (N_MONOCOTS_NAT/TOTN_SPP)	С
PCTN_ MONOCOTS_NAT	Native Monocot percent richness	x 100	С
PCTN_ MONOCOTS_ ALIEN	Alien Monocot percent richness	(N_MONOCOTS_ALIEN/ TOTN_SPP) x 100	S
PCTN_ MONOCOTS_ CRYP	Cryptogenic Monocot percent richness	(N_MONOCOTS_CRYP/TOTN_SPP) x 100	S
PCTN_ MONOCOTS_AC	Alien and cryptogenic monocot percent richness	(N_MONOCOTS_AC/TOTN_SPP) x 100	S
XABCOV_DICOT	Mean absolute cover Dicots	S COVER of DICOT species across 5 plots/5 plots	С
XABCOV_ DICOTS_NAT	Mean absolute cover native Dicots	S COVER of NAT DICOT species across 5 plots/5 plots	С
XABCOV_ DICOTS_ALIEN	Mean absolute cover Alien Dicots	S COVER of ALIEN DICOT species across 5 plots/5 plots	S
XABCOV_ DICOTS_CRYP	Mean absolute cover cryptogenic Dicots	S COVER of CRYP DICOT species across 5 plots/5 plots	S
XABCOV_ DICOTS AC	Mean absolute cover of alien and cryptogenic Dicots	XABCOV_DICOTS_ALIEN + XABCOV_DICOTS_CRYP	S
XABCOV_FERN	Mean absolute cover of Ferns	S COVER of FERN species across 5 plots/5 plots	С
XABCOV_FERNS_ NAT	Mean absolute cover of native Ferns	S COVER of native FERN species across 5 plots/5 plots	С
XABCOV_FERNS_ INTR	Mean absolute cover of introduced Ferns	S COVER of introduced FERN species across 5 plots/5 plots	S
XABCOV_ GYMNOSPERM	Mean absolute cover of Gymnosperms	S COVER of GYMNOSPERM species across 5 plots/5 plots	С
XABCOV_ LYCOPOD	Mean absolute cover of Lycopods	S COVER of LYCOPOD species across 5 plots/5 plots	С
XABCOV_ HORSETAIL	Mean absolute cover of Horsetails	S COVER of HORSETAIL species across 5 plots/5 plots	С
XABCOV_ MONOCOT	Mean absolute cover of Monocots	S COVER of MONOCOT species across 5 plots/5 plots	С
XABCOV_ MONOCOTS_NAT	Mean absolute cover of native Monocots	S COVER of NAT MONOCOT species across 5 plots/5 plots	С
XABCOV_ MONOCOTS_ ALIEN	Mean absolute cover of alien Monocots	S COVER of ALIEN MONOCOT species across 5 plots/5 plots	S
XABCOV_ MONOCOTS_ CRYP	Mean absolute cover of cryptogenic Monocots	S COVER of CRYP MONOCOT species across 5 plots/5 plots	S

METRIC NAME	METRIC DESCRIPTION	CALCULATION (listed in White Metric Row), SPECIES TRAIT TYPE (if applicable, indicated in Colored Banners)	METRIC TYPE (C = condition, S = stress)
XABCOV_	Mean absolute cover of alien and	XABCOV_MONOCOTS_ALIEN +	S
MONOCOTS_AC	cryptogenic Monocots	XABCOV_MONOCOTS_CRYP	<u> </u>
XRCOV_DICOT	Mean relative cover Dicots	(XABCOV_DICOTS/XTOTABCOV) x 100	С
XRCOV_DICOTS_ NAT	Mean relative cover native Dicots	(XABCOV_DICOTS_NAT/ XTOTABCOV) x 100	С
XRCOV_DICOTS_ ALIEN	Mean relative cover alien Dicots	(XABCOV_DICOTS_ALIEN/ XTOTABCOV) x 100	S
XRCOV_DICOTS_ CRYP	Mean relative cover cryptogenic Dicots	(XABCOV_DICOTS_CRYP/ XTOTABCOV) x 100	S
XRCOV_DICOTS_ AC	Mean relative cover of alien and cryptogenic Dicots	(XABCOV_DICOTS_AC/ XTOTABCOV) x 100	S
XRCOV_FERN	Mean relative cover of Ferns	(XABCOV_FERNS/ XTOTABCOV) x 100	С
XRCOV_FERNS_ NAT	Mean relative cover of native Ferns	(XABCOV_FERNS_NAT/ XTOTABCOV) x 100	С
XRCOV_FERNS_ INTR	Mean relative cover of introduced Ferns	(XABCOV_FERNS_INTR/ XTOTABCOV) x 100	S
XRCOV_ GYMNOSPERM	Mean relative cover of Gymnosperms	(XABCOV_GYMNOSPERMS/ XTOTABCOV) x 100	С
XRCOV_LYCOPOD	Mean relative cover of Lycopods	(XABCOV_LYCOPODS/ XTOTABCOV) x 100	С
XRCOV_ HORSETAIL	Mean relative cover of Horsetails	(XABCOV_HORSETAILS/ XTOTABCOV) x 100	С
XRCOV_ MONOCOT	Mean relative cover of Monocots	(XABCOV_MONOCOTS/ XTOTABCOV) x 100	С
XRCOV_ MONOCOTS_NAT	Mean relative cover of native Monocots	(XABCOV_MONOCOTS_NAT/ XTOTABCOV) x 100	C, Used in VMMI
XRCOV_ MONOCOTS_ ALIEN	Mean relative cover of alien Monocots	(XABCOV_MONOCOTS_ALIEN/ XTOTABCOV) x 100	S
XRCOV_ MONOCOTS_ CRYP	Mean relative cover of cryptogenic Monocots	(XABCOV_MONOCOTS_CRYP/ XTOTABCOV) x 100	S
XRCOV_ MONOCOTS_AC	Mean relative cover of alien and cryptogenic Monocots	(XABCOV_MONOCOTS_AC/ XTOTABCOV) x 100	S