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High productivity in hybrid-poplar plantations without isoprene emission to the atmosphere

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***Significance**: Leaf isoprene emission, a trait that promotes tree stress tolerance but also negatively affects air quality and climate, has been genetically suppressed in hybrid-poplar cultivars without influencing plantation biomass production in two field trials. Induction of compensatory increases in protective proteomic components and a phenological growth pattern that favors most biomass production during less stressful parts of the growing season, likely explain the apparent paradox of high plantation production with low isoprene emission. We show that it is feasible to develop sustainable plantation-scale biomass sources that can serve as fossil-fuel alternatives for energy generation and lignocellulosic resource development, without degrading air quality.*

31

Abstract

Hybrid-poplar tree plantations provide a source for biofuel and biomass production, but they also, unintentionally, increase forest isoprene emissions. The consequences of increased isoprene emissions include higher rates of tropospheric ozone production, increases in the lifetime of methane, and increases in atmospheric aerosol production, all of which affect the global energy budget and/or lead to the degradation of regional air quality. Using RNA interference (RNAi) to suppress isoprene emission in several gene insertion events of hybrid-poplars, we show that this trait, which is thought to be required for the tolerance of abiotic stress, is not required for high rates of photosynthesis and woody biomass production in the agroforest plantation environment, even in areas with high levels of climatic stress. Biomass production over four years in poplar plantations in Arizona and Oregon was similar among genetic lines that emitted or did not emit significant amounts of isoprene. Lines that had substantially reduced isoprene emission rates also showed decreases in flavonol pigments, which reduce oxidative damage during extremes of abiotic stress; a pattern that would be expected to amplify metabolic dysfunction in the absence of isoprene production in stress-prone climate regimes. However, compensatory increases in the expression of other proteomic components, especially those associated with the production of protective compounds, such as carotenoids and terpenoids, and the fact that most biomass is produced prior to the hottest and driest part of the growing season, explain the observed pattern of high biomass production with low isoprene emission. Our results show that it is possible to strategically reduce the deleterious influences of isoprene on the atmosphere, while sustaining woody biomass production in temperate agroforest plantations.

Key Words: oxidative stress; thermotolerance; genetically-modified organism; biofuel; lignocellulose; hydroxyl radical; climate change; net primary production; cellular signaling; transcription factors

Introduction

Agroforestry tree plantations have been increasing globally, and are used for diverse purposes, including the production of wood and food products, the establishment of wind breaks and biofiltration facilities, and most recently as a feedstock for biofuel production (1-3). The high biomass production rates that can be achieved with fast-growing tree varieties (especially for poplars, eucalypts and palms) are often accompanied by high rates of leaf isoprene emission. Isoprene produced during normal light-dependent metabolism in the chloroplasts of many tree species, especially those with high productivity rates, is volatile and is emitted globally at rates that are similar to methane emissions (4). Unlike, methane, however, emitted isoprene is photochemically-oxidized within hours, not years. Through a series of chemical reactions, the atmospheric oxidation of isoprene enhances the production of oxidative pollutants, such as tropospheric ozone (O_3) and organic nitrates (e.g., PAN) in urban and suburban areas, increases the global lifetime of the radiatively-active, trace-gas methane (CH_4), and promotes the growth of secondary organic aerosol (SOA) particles, which affect the short-wave radiation budget of the earth (5-8). Using a coupled earth-system and chemistry model, it has been shown that expansion of poplar plantations in Europe to meet 2020 biofuel targets will potentially increase premature human deaths up to 6% and reduce the yield of wheat and maize crops by 9 Mt yr^{-1} because of increased isoprene emission and accompanying O_3 production (9,10). In Southeast Asia, isoprene-emitting oil-palm plantations have increased in areal coverage by a factor of 5 over the past 20 years as part of an effort to increase food oil and biofuels (11); causing an increase in near-surface O_3 concentration of 3.5-15 ppbv (12,13).

The genetic modification of agroforest trees to minimize leaf isoprene emission is feasible (14). However, these efforts have been largely dismissed in the past with assumptions that the trait: (i) is advantageous for the tolerance of abiotic stresses, such as those due to high temperature, low atmospheric humidity, and acute drought (15,16), and (ii) correlates positively with photosynthetic CO_2 assimilation (17). Removal of the trait has been predicted to result in reduced productivity and declines in plant fitness, especially in the face of future climate change (18-20). Studies of genetically-modified poplars grown in controlled-environment growth conditions, however, indicate that stress interactions are complex. Several studies have shown that although isoprene emission protects trees from abiotic stress, increases in atmospheric CO_2 concentration cause a decrease in isoprene biosynthesis, thus reducing that protection (21-23). Increases in global temperatures, however, have the potential to mitigate the elevated CO_2 effect (24,25); increasing the protective effect of isoprene emissions, even in the presence of elevated CO_2 (26). In the case of drought, non-isoprene emitting tobacco plants that have been genetically transformed to produce isoprene, exhibited a reduction in biomass production during

drought, compared to wild-type plants, suggesting a growth cost to the stress protection normally provided by isoprene (27). While it is difficult to generalize about the role of isoprene emissions as a necessary stress-tolerance trait and its cost to biomass production in the face of future global change, most analyses indicate that isoprene emissions from global forests are indeed likely to increase in the future (28).

The cellular mechanisms that enhance stress tolerance and photosynthetic performance due to isoprene emission have not been resolved. Past theories of direct stabilization of chloroplast membranes through the hydrophobic solubilization of isoprene have not been supported (29,30). More recent theories focus on a cellular signaling role that involves modulation of several stress-related gene networks (31,32). There is a need to continue assessing the roles and mechanisms of isoprene protection against abiotic stresses in a broader set of environmental settings and with the synergistic challenges from interacting stresses, such as those that occur under natural field conditions.

In this study, we used gene silencing through RNA interference (RNAi) to reduce leaf isoprene emission to negligible levels in several genetic lines (independent gene insertions) of hybrid poplar, which were grown in multiple-year field trials at two geographically distinct plantation sites, where we evaluated stress tolerance, remodeling of cellular metabolism, photosynthetic function and woody biomass production. One site was located near Corvallis, Oregon, USA, and was intended as an analog to commercial poplar plantations that are located in the Pacific Northwest of the USA. For example, the largest commercial poplar plantation in North America (10,118 ha and 7.5 million trees) was in operation for over twenty years (1992-2017) near Boardman, Oregon; located 312 km NE from our experimental plantation near Corvallis. The second site was located near Tucson, Arizona (USA), and was intended to test whether biomass production is compromised by elimination of isoprene emission in one of the hottest and least humid climates in North America. We tested the hypothesis that isoprene biosynthesis and emission is a required trait for high rates of aboveground woody biomass production in the agroforestry plantation environment.

Results

Eighteen genetically-modified poplar lines and one wild-type control (CN) were grown for three years in the Oregon plantation (see Supplementary Material, Fig. S1). Three of the modified lines were isoprene-emitting empty-vector (EV) controls and fifteen lines were modified for suppressed isoprene emissions. For clarity, we refer to the three EV lines and one CN line, together, as isoprene-emitting (IE) genotypes and the fifteen low isoprene emitters as isoprene-reduced (IR) genotypes. Reductions in isoprene

emission were nearly complete in some IR lines, and only slightly reduced in others, based on statistical metrics provided by Analysis of Variance (ANOVA for genotype effect on isoprene emission rate: $F=56.978$, $df=12$, $P<0.001$; Fig. 1A,C). The reduction in leaf isoprene emission did not result in reduced rates of photosynthesis (ANOVA for genotype effect on photosynthesis: $F=0.90$, $df=8$, $P=0.52$; Fig. 1B,D), or woody aboveground biomass production (Fig. 2) (ANOVA for genotype effect on biomass: $F=1.075$, $df=18$, $P=0.375$; ANOVA for year effect on biomass: $F=33.259$, $df=1$, $P<0.001$; ANOVA for genotype x year effect on biomass: $F=0.872$, $df=18$, $P=0.6138$). For example, in the Oregon plantation, biomass production in lines IR-70 and IR-88, which exhibited negligible rates of isoprene emission, had photosynthesis rates (Fig. 1B) and aboveground biomass production rates (Fig 2B) that were not substantially different from the four IE lines. Eight genetic lines representing IE and IR trees from the Oregon plantation were excavated in spring 2015, after three years of growth, for sampling of cumulative belowground biomass. Belowground production did not differ systematically among the IR and IE lines (ANOVA for genotype effect (biomass log transformed): $F=1.9832$, $df=7$, $P=0.0652$; see Fig. S2 in Supplementary Material).

Four of the genetic lines (CN, EV-9, IR-41 and IR-70) were grown for four years in an experimental plantation near Tucson, Arizona (see Supplementary Material, Fig. S1). Maximum daily air temperatures during the four warmest months of the summer (June, July, August and September) averaged 35.6 ± 2.1 (s.d.) °C across the four years (2013-2016) of experimental observation. Twelve trees from each genetic line were exposed to high fertilization and irrigation rates during 2012 and 2013 and reduced or eliminated fertilization and irrigation during 2014 and 2015. With this experimental design we aimed to examine biomass production under conditions of both high (well-fertilized, well-watered) and low (light fertilization, limited-watering) growth potential. Continuous monitoring of canopy temperatures throughout most of the growing season in 2014 revealed that maximum daily leaf temperature exceeded 32 °C on most days and was ~40 °C on many days (see Supplementary Material, Fig. S3 A-C). Direct observations of individual leaf temperatures with thermocouples attached to the underside of leaves during mid-summer in 2014, confirmed that even with replete irrigation and high transpiration rates, leaf temperatures were within 6-7 °C of maximum midday air temperatures, and spent much of the midday period above 35 °C (see Supplementary Material, Fig. S3D).

In the Arizona plantation, when considering the three lines influenced by RNAi treatments – the empty-vector IE control and two IR lines – we observed no significant differences in annual aboveground biomass production during or following four years of growth (Fig. 2; ANOVA for genotype effect on biomass: $F=1.2575$, $df=2$, $P=0.2878$; see Supplementary Material Sections S2 and S3 for details of the ANOVA analysis). There were, however, some effects of genotype and year on specific patterns of biomass

increase. The elevated levels of fertilization and irrigation during the first two years of growth culminated in higher production in all lines during the second year of the experiment, compared to all other years (ANOVA for genotype effects on biomass: $F=109$, df=12 blocks, $P<0.05$). The only clear effect of genotype on aboveground biomass in the Arizona plantation was caused by the wild-type CN line growing approximately 85% more than the other lines in Year 2 (ANOVA for all four genotypes: 2014; $F=4.9$, df=12 blocks, $P=0.05$) (Fig. 2D). Even during this year, however, we observed no significant differences in woody biomass production between the empty-vector (EV-9) line, which emits isoprene at the same rate as the CN line, and the two IR lines (ANOVA for three selected genotypes: $F=1.2$, df=12 blocks, $P=0.28$). Thus, the lower growth rates exhibited by the modified lines does not appear to be due to the emission of isoprene, but rather to the genetic modification process. In Years 3 (2015) and 4 (2016), when fertilizer and irrigation were reduced, there were no differences in production between the IE and IR lines in the Arizona plantation. We concluded that overall the presence of isoprene emission had no effect on biomass increase during all four years in the Arizona plantation, but that genetic manipulation, independent of effects on isoprene emission, impaired biomass production in the three genetically-modified lines (EV and two IR lines), compared to the wild-type CN line, when grown in the high-resource conditions presented in Year 2.

A subset of five plants from each of the four genetic lines in the Arizona plantation were selected for root excavation at the end of Year 4. There was a trend toward lower mean belowground biomasses in the IR lines, compared to the IE lines (see Supplemental Material, Fig. S2), but the trend could not be justified as statistically significant ($F=4.234$, df=1, $P=0.056$). Furthermore, when considering all four lines together, an effect of genotype was not observed ($F= 1.525$, df= 3, $p=0.246$). Due to the statistical weakness of the observation of slightly lower belowground biomass in the IR lines, we have not taken this result to a deeper level of interpretation. However, it may indicate that not all poplar lines are equally suitable for genetic modification aimed at maximizing production. If so, more work is justified to determine if this variation could be used as a criterion for future genotype selection.

Seasonal growth of aboveground biomass began in early April at the Arizona plantation and biweekly observations showed rapid increases in stem-diameter increment until the middle of May (see Supplemental Material, Fig. S4). The early-season rapid growth phase occurred while maximum daily temperatures fluctuated between 20-31°C. During the hottest and driest part of the growing season, when maximum canopy temperatures were 35-40°C, diameter growth of all branches in the four lines slowed from an average of 2 mm day^{-1} prior to May 20, to 0.3 mm day^{-1} after May 20. There were no significant differences in growth between the IE and IR lines at any date during the growing season.

Leaf net photosynthesis rates in the Arizona trees decreased at temperatures above 25°C (Fig 3). Rates of photosynthesis were slightly lower in the EV and IR lines, compared to the wild-type CN line, during the June sampling campaign, when seasonal temperatures were at a maximum. However, the net assimilation rates were not significantly different between the EV and IR lines, despite high isoprene emissions from the EV line. Thus, when all four lines, together, were analyzed for an effect of isoprene emission on photosynthesis rate there was no significant difference (ANOVA for effect of genotype on photosynthesis at 27°C: $F=0.2519$ $df=3$, $P=0.86$). During April, when ambient temperatures were still relatively cool, and late-September, when canopy temperatures persisted above 30°C, there was also no evidence of improved photosynthetic performance in the IE lines, compared to the IR lines. Leaf concentrations of total flavonoids and a leaf-nitrogen index were significantly different between IE and IR lines when sampled at the end of the warmest parts of the growing season (see Section S.6 and Fig. S5, Supplemental Material). No significant differences between IE and IR trees were observed for leaf anthocyanin or chlorophyll content in all field conditions (Section S.6).

We conducted analyses of the leaf proteome in order to study the overall scope of genetic modification that occurred, either directly or indirectly, as a result of isoprene suppression. Proteomic analysis provides insight into the protein composition of the leaf at a point in time, which in turn, reflects the biochemical and functional conditions within which plant metabolism takes place. Unlike genomic analyses, which reflect long-term generational changes in gene composition, or metabolomic analyses, which reflect short-term (milliseconds-to-minutes) changes in metabolic substrates and products, proteomic analyses provide insight into changes in overall metabolic potential due to gene expression (at a time-scale of seconds-to-hours). Analysis of the proteome in leaves from the Arizona plantation at predawn and noon in June 2013 (the first year of the growth analysis), when temperatures were at a seasonal maximum, revealed numerous differences among the IE and IR lines (Table 1, Fig. 4). Proteomic profiles of the IE and IR lines were distinguished by the orthogonal partial least square (OPLS) method with 10% explained variance (Fig 4A). In total we identified 169 discriminant proteins – 113 lower-expressed and 56 higher-expressed – in the IR lines, compared to IE lines (Fig. 4B, C). Principal component analysis revealed that both suppression of isoprene emission (operating at the scale of ontogeny) and time of day (operating at the scale of diurnal environmental variation) operated as primary controls over proteome expression patterns. Most of the expression differences between the IR and IE lines were found during pre-dawn sampling – 38 proteins were exclusively upregulated and 88 proteins were exclusively downregulated at pre-dawn, compared to 8 exclusively upregulated and 10 exclusively downregulated at noon (Fig. 4D, E). A total of 10 proteins were upregulated and 15 were

downregulated in both the pre-dawn and noon samples. The ten most regulated proteins for pre-dawn samples and mid-day samples, respectively, are presented in Table 1. Two of the most repressed proteins (negative $\log_2$-fold IR/IE change) were associated with isoprene synthase (Potri.007G118400.1 and Potri.017G041700.1), confirming the effective nature of the RNAi treatments in causing suppression of this enzyme. Significant ($P \leq 0.05$ between IR and IE lines) downregulation in the absence of isoprene emissions occurred for proteins involved in the phenylpropanoid pathway and flavonoid biosynthesis. Significant upregulation occurred for several proteins involved in the biosynthesis of terpenoids and carotenoids, and one protein involved in the biosynthesis of α-tocopherol (vitamin E). Some proteins involved in the methylerithritol phosphate (MEP) and jasmonic acid pathways were also among those exhibiting increases in expression in the face of isoprene suppression. A complete list of proteomic changes is provided in Table S1 in the Supplementary Material.

A Voronoi treemap analysis provided pathway-wide patterns of proteomic rearrangements (Fig. 4, F,G). In the case of flavonoid biosynthesis, the entire pathway was consistently and highly downregulated in the IR trees. The phenylpropanoid pathway, which supplies flavonoid biosynthesis with substrate, was differentially regulated. Phenylalanine ammonia-lyase (PAL), the first enzyme in the pathway, was downregulated in IR trees, similar to the pattern for flavonoid biosynthesis, but cinnamyl-alcohol dehydrogenase (CAD) content, one of the last enzymes in the pathway was upregulated. Interestingly, CAD represents the first step toward commitment to lignin biosynthesis. Thus, suppression of isoprene emissions may cause a shift away from flavonoid biosynthesis and toward lignin biosynthesis; favoring woody biomass production. In the case of terpenoid biosynthesis, enzymes were consistently and highly upregulated across each associated pathway in the IR trees. For the MEP pathway, which provides precursors to terpenoid biosynthesis, protein expression was moderately and consistently increased (or in the case of one protein, unchanged) in the IR trees. These patterns indicate a shift in the IR trees away from the synthesis of volatile isoprene and toward the synthesis of higher terpenoids (i.e., lutein and β-carotene). In the jasmonic acid pathway, changes in protein expression were mixed; with some proteins increasing and some decreasing. The fact that the proteomic rearrangements that we observed were evident during the first year of growth indicates a relatively quick response to the genomic and environmental conditions of the genetically-modified trees.

Discussion

Our study has revealed that it is possible to genetically modify agroforestry poplar trees to reduce plantation isoprene emissions, without compromising woody biomass production. Several past studies

have shown that suppression of isoprene emissions is correlated with reduced tolerance of high temperature (33,34) and oxidative stress (35,36) in isolated leaves; leaf temperatures as low as 30°C and moderate levels of water stress have been shown to inhibit photosynthetic performance in the absence of isoprene emission (37,38). These observations have led to a general hypothesis that isoprene emissions protect leaves, even under relatively modest levels of abiotic stress (39,40). The conclusions from our study show that when grown in poplar plantations under natural field conditions, any physiological benefit of isoprene emission with regard to stress tolerance and above-ground productivity, is either not relevant, or is subject to compensation by alternative protective pathways following RNAi suppression and subsequent proteomic and metabolomic adjustments (also see 20).

There is evidence in our observations that, when considered alone, might predict reductions in plantation productivity in the face of suppressed isoprene emissions; the opposite of what we observed. For example, in early June, when maximum canopy temperatures were often greater than 40°C (see Fig. S3), net photosynthesis rates were significantly suppressed in the two IR lines, compared to the isoprene-emitting CN line (Fig. 3). These results might be used to conclude that suppression of isoprene emission resulted in decreased photosynthetic performance in the IR trees during the hottest part of the growing season. However, there were no significant differences between the two IR lines and the EV line, which serves as the true control to the RNAi lines and also emits isoprene at natural levels. Thus, the photosynthetic temperature-response curves shown in Figure 3 do not, in fact, predict poor performance of IR trees in the plantation environment.

Separately, we observed that flavonol and anthocyanin compounds were reduced more in the IR lines, than in the IE empty-vector control (EV-9), in the Arizona plantation. Suppression of flavonol and anthocyanin synthesis has been observed in these same IR lines in past studies of greenhouse- and chamber-grown trees (20,41). These compounds have been shown to provide greater tolerance of drought stress in poplar trees (42), and they reduce the load of photochemically-generated oxidative compounds, such as H_2O_2, during heat stress (20). Furthermore, exogenous fumigation of the isoprene non-emitting species *Arapidopsis thaliana* with isoprene (43), and genetic transformation of the isoprene non-emitting species, *Arabidopsis thaliana* and *Nicotiana tabacum*, to emit isoprene (32,44), caused an increase in expression of the pathways that produce flavonols and anthocyanins, and increased drought resistance in the case of *Nicotiana tabacum* (44). Thus, there are reasons to predict that reductions in flavonol and anthocyanin synthesis in the IR trees from our studies should have negatively influenced their tolerance of high temperatures and drought. Given this, it is of interest that we could not find consistent evidence of a negative influence of high seasonal temperatures and low atmospheric humidities during

all four years, and imposed drought during Year 4, on the growth of IR trees in the Arizona and Oregon plantations.

We offer two explanations for the lack of an observed isoprene effect on photosynthetic function and biomass production in the natural plantation environment. Together, the explanations provide room for the co-existence of past findings of a positive role of isoprene emission in facilitating abiotic stress tolerance, and our observations of no influence on observed biomass accumulation. First, most of the woody biomass was produced during the early part of the growing season, prior to the mid-summer occurrence of extremely hot and dry weather. The phenological context of tree growth in mid-latitude, Northern Hemisphere forests has seldom been considered in past discussions of the physiological benefit of isoprene emission. Most studies have focused on isolated, fully-expanded leaves observed during an artificially-imposed, acute stress. The preponderance of this type of study in the isoprene-emission literature has largely shaped current views about how this trait provides its greatest adaptive potential. The assumption that plant persistence and fitness is improved through greater tolerance of acute abiotic stress during that portion of the growing season that is least favorable for growth, is embedded in a larger assumption that isoprene emission enhances survivability, not productivity. Thus, even considering the extensive past literature, it is not necessarily expected that removal of the trait will result in reduced productivity and fitness, especially during the less stressful periods during the growing season. Our research is consistent with this view – that loss of the trait will have less, or no, impact on biomass production during the most productive portion of the growing season, but may enhance fitness during extreme climate events. Placing isoprene emissions within a proper adaptive context will sharpen our ability to understand how forest communities and landscapes will respond to future climate shifts, which are expected to increase the frequency of anomalously hot and dry weather episodes.

With regard to the second explanation, past studies have shown that suppression of isoprene emission by RNAi transformation in these same poplar lines, results in remodeling of the chloroplast proteome and metabolome in a way that increases the scavenging of reactive oxygen species (ROS), and thus minimizes the oxidative damage expected from suppression of isoprene biosynthesis (45,46). Thus, while several past studies have shown that isoprene acts as a positive signal that enhances stress tolerance (32, 43, 44), the studies by Veikova et al. (45) and Ghirardo et al. (46) showed that the suppression of isoprene emission can also cause compensatory increases in pathways, such as those for the terpenoids lutein and β-carotene, that take over some of isoprene's protective capacity. In our study, we observed similar proteomic changes that could compensate for the loss of isoprene biosynthesis and thus protect the trees from abiotic stress due to high leaf temperatures and low atmospheric humidity. We observed

312 an overall and consistent upregulation of proteins in the pathways that control terpenoid, carotenoid and
313 α-tocopherol biosynthesis in the IR trees (Table 1, Fig. 4). The upregulated expression of components in
314 these pathways may take on oxidative protection functions similar to those of flavonols and anthocyanins,
315 which are suppressed, along with the phenylpropanoid pathway, in the absence of isoprene signaling. Our
316 results contribute to a paradigm shift that is occurring in the community of researchers considering
317 isoprene-stress relations (20,31,44). Whereas, past research provided evidence of a direct role of isoprene
318 in protecting photosynthetic membranes and protein complexes from oxidative attack, more recent
319 research is pointing to an additional, and potentially more important role of isoprene as a cellular signaling
320 molecule. In this new hypothesis, isoprene takes on the role to control the expression of pathways that
321 potentially compete for chloroplast substrates and produce multiple compounds with roles in protection
322 from climate stress, oxidative stress, herbivore stress, and the multiple interactions of these stresses with
323 intrinsic plant growth regulators. In the absence of isoprene emissions, the phenylpropanoid pathway is
324 suppressed and the isoprenoid pathways that produce complex terpenoids and carotenoids are enhanced
325 (for flux rates, see 46). The compensatory expression of these pathways in the IE and IR trees may explain
326 the lack of our observed response of tree growth to the suppression of isoprene emissions. Clearly, the
327 interactions of multiple pathways under the influence of isoprene signaling is complex. Our work sets the
328 stage for further research into the potential for trait tradeoffs in the area of isoprene emission, stress
329 tolerance and plant growth. The changes in protein expression, and the new chemical products that they
330 produce, if incorporated into new lines of cultivated poplar, will likely have several higher-order influences
331 on the global environment and human health, including the potential for new modes of influencing
332 atmospheric photochemistry (depending on the nature and amount of terpenoid biosynthesis) and
333 associated effects on agricultural production and human respiratory health.
334 Planted poplar plantations used for woody biomass production currently occupy ~9.4 million ha,
335 globally, an area which has increased from ~3.9 million ha since 2004 (47,48). The impacts of continued
336 climate change and the expansion of plantation forests are predicted to cause significant increases in
337 regional and global biogenic isoprene emissions (28,49). Isoprene emissions from forests have been linked
338 to several photochemical processes that alter the oxidative capacity of the lower atmosphere and increase
339 the burden of atmospheric greenhouse gases, such as methane and ozone (7). The heterogeneous
340 condensation of oxidized derivatives of isoprene causes increased growth rates in secondary aerosol
341 particles in the atmosphere, which affect the earth's radiative balance (50,51). Our study represents the
342 first field trial of genetically-modified poplar trees with negligible rates of isoprene emission. If future
343 efforts are successful in reducing forest plantation isoprene emissions, we can expect multiple opposing

and complex influences on positive and negative climate forcings. In the lower atmosphere, isoprene exerts several influences on climate-relevant processes: (1) it amplifies rates of O_3 production in nitrogen oxide (NO_x)-rich urban and suburban areas, (2) it promotes rates of O_3 destruction in low-NO_x rural and remote areas, (3) it catalyzes hydroxyl-radical recycling pathways which affect the atmospheric lifetime of CH_4, and (4) it is oxidized to multiple products that contribute to the growth of SOA particles. The size distribution and density of SOA particles not only affects earth-surface climate, but also the distribution of direct and diffuse photosynthetically-active photon fluxes within the canopy environments of forests; further complicating evaluations of projected global gross primary productivity and its relationship to isoprene emissions from native forests. Recent efforts have been initiated to evaluate the integrated effects of these atmospheric influences (52), and it is this type of complex photochemical modeling that is most likely to provide comprehensive predictions of how future changes in plantation isoprene emissions might influence global climate.

Decisions concerning regional land-use are also likely to influence global plantation isoprene emissions and associated climate effects. A recent analysis of global shifts in forest coverage showed a small influence on isoprene emissions during the period 2000-2015 (1.5% decrease), though specific regional influences, such as in the tropics, were greater (53). Future patterns of land-use change, particularly those involving replacement of native forests with cultivated plantations, are likely to cause increases in isoprene emission, concomitant with increases in tropospheric O_3 production and SOA particle growth (28). Our research provides an alternative perspective on these potential outcomes. The fact that cultivars of poplar can be produced, in a way that reduces isoprene emission while preserving high rates of biomass production, provides optimism toward achieving greater environmental sustainability while expanding sources for fossil-fuel alternatives and lignocellulosic resources. We anticipate several challenges as the findings of our studies are transferred into forestry practice. First, expanded research is needed to establish whether our results apply to the diversity of genotypes, species and environments in which commercial trees are grown. Second, it is desirable that both conventional and recombinant DNA approaches to genetic manipulation are explored given the existence of regulatory and market constraints to the use of genetic engineering for commercial applications (54). Interestingly, CRISPR gene editing may be a more efficient means for isoprene reduction than the RNAi method that we studied, and may be exempt from regulation in the USA and several other countries—making it easier to employ (55).

Methods

Genetic modification of poplar lines. The down-regulation of isoprene emission by RNA interference in grey poplar (*Populus* x *canescens*) was performed with the same poplar (No. 7171-B4, Institute de la Recherche Agronomique, INRA, Nancy France) and *Agrobacterium tumefaciens* (C58C1/pMP90) strains as described earlier (18). Sense and antisense gene fragments of a 160 bp isoprene synthase-specific gene segment of the transit peptide sequence (position 21-181) were cloned as a self-complementary hairpin construct into the pKANNIBAL vector, followed by transfer into the binary vector pART27. The RNAi cassette and the empty pART27 vector were then used to transform *Agrobacterium tumefaciens* by electroporation. The final transformation of *P.* x *canescens* with both constructs was conducted as described by Meilan and Ma (56). Regenerated plantlets were PCR-verified (see Supplementary Materials, Section S1) and maintained on media without antibiotics. Wild-type control and transgenic lines were amplified by micropropagation on half-concentrated Murashige and Skoog (MS) medium (57). Eight-week old rooted shoots were transferred to small pots containing commercial potting-soil and used for molecular screening.

Isoprene emission potential of transformants was initially assessed by measuring headspace isoprene accumulation in eight-week old rooted *in vitro* cultures (see Supplementary Materials, Section S1). From these efforts, 18 transformant genotypes were ultimately selected for further clonal propagation. Bulk propagation of this transgenic material was done by a commercial facility (Broadacres Nursery, Hubbard OR) via clonal propagation of both dormant and green (actively growing) cuttings in a greenhouse. Bare stem cuttings from these greenhouse-grown transformants were the ultimate source of all subsequent field-planting stock. The wild-type control (CN) and empty-vector control (EV) lines were shown to retain relatively high rates of isoprene emission, whereas the transformed, RNAi lines (IR) were shown to emit various rates of reduced isoprene emission, ranging to near-negligible levels.

Field sites. The Oregon plantation was located on the grounds of Oregon State University's Peavy Arboretum (44.659° latitude N, 123.235° longitude W). The Arizona plantation was located on the grounds of the University of Arizona's Biosphere 2 campus near Oracle, Arizona (32.344° latitude N, 110.510° longitude W). See Supplementary Materials, Section S2, for further details of the plantations.

Measurement of biomass production and leaf gas exchange rates. At the completion of the field trail at the Oregon plantation, and before the initiation of spring-bud break the following year, whole trees were harvested and weighed for total biomass. Aboveground stems were coppiced and the root ball for each tree was removed with a mini-excavator and washed of all soil and debris. All tissues were subsequently

406 dried at 60 C for 6 days in a large capacity wood-drying convection kiln (OSU School of Forestry), before
407 weighing on a high-capacity balance (Mettler Toledo, MS12001L). In the Arizona plantation, trees were
408 coppiced, dried and weighed in December at the end of each growing season, for successive-year
409 determination of aboveground biomass. Harvested, leafless stems were dried at room temperature for 6
410 weeks, before weighing on a high-capacity balance (Sartorius, model LA 3400, Bradford, MA, USA). For
411 the Arizona trees, the crown stool and roots were excavated for five representative trees of each of the
412 four genetic lines at the end of the 4-year growth period for determination of total non-shoot biomass
413 (see Supplementary Material, Section S3 for details).
414 Isoprene emission rates and net CO_2 assimilation rates were measured at both plantation sites using
415 a portable photosynthesis system for leaf CO_2/H_2O gas exchange (LiCor Inc., model 6400, Lincoln, NE, USA)
416 equipped with the broadleaf cuvette' (6 cm^2) including the LED light system set for leaf temperature
417 between 27-30 °C, light level of 1800 μmol m^{-2} s^{-1} PPFD and with chamber CO_2 mole fraction set to 400
418 μmol mol^{-1} (25). In the Arizona studies, the gas-exchange system was connected to a chemiluminescence
419 fast isoprene sensor (FIS, Hills Scientific, Boulder, CO, USA) for measurement of cuvette isoprene
420 concentrations. A flow of O_3 to the reaction cell of the FIS was used to provide the oxidant needed to elicit
421 a chemiluminescent reaction with isoprene, and photon counts were detected and converted to isoprene
422 concentration using calibrations against a diluted standard tank (5 μmol mol^{-1}, Airgas Inc). In the Oregon
423 studies, gas aliquots from the gas-exchange system chamber were analyzed for isoprene concentration
424 by direct-injection onto a gas chromatograph with a reducing gas detector (GC-RGD; Peak Performer 1,
425 Peak Laboratories LLC, Mountain View, CA). The system was calibrated using gas-phase dilutions of
426 standard isoprene (99%, Sigma Aldrich).

427 **Proteome measurements.** One fully-developed leaf was cut from each of twelve trees of each genotype
428 on July 3rd 2013 at the Arizona plantation, and immediately frozen in liquid nitrogen prior to dawn (0415-
429 0530 h) and at midday (1200-1400 h). Frozen leaves were homogenized and 50 mg leaf powder of three
430 plants from each genotype was pooled for analysis, resulting in 4 replicates per genotype per harvest time.
431 Samples were extracted and prepared for analysis as described in the Supplementary Materials, Section
432 S7. Sub-samples of 10 μg were subjected to filter-aided sample preparation (FASP) (58). LC-MSMS analysis
433 of each individual sub-sample was performed on a Q Exactive HF mass spectrometer (ThermoFisher
434 Scientific) online coupled to an Ultimate 3000 nano-RSLC (Dionex). Tryptic peptides were separated in a
435 non-linear acetonitrile gradient over 85 min on a C18 analytical column (nanoEase MZ HSS T3 Column,
436 100Å, 1.8 μm, 75 μm x 250 mm, Waters). Precursor and TOP10 fragment spectra were acquired in the
437 Orbitrap mass detector at 60000 or 15000 resolution, respectively. Generated raw-files containing all

acquired spectra were loaded to the Progenesis QI for proteomics software (v3.0, Nonlinear Dynamics Ltd, part of Waters, Newcastle upon Tyne, UK) for label-free quantification and analyzed as previously described (59,60). Features of only one charge or features with more than seven charges were excluded. The raw abundances of the remaining features were normalized to allow for the correction of factors resulting from experimental variation. All MS/MS spectra were exported as MASCOT generic files and used for identification by Mascot search engine (v 2.5.1, Matrix Science, London, UK) in a *Populus trichocarpa* protein database (v3, 30197159 residues; 73016 sequences). The search parameters were 10 ppm peptide mass and 0.02 Da MS/MS tolerance, one missed cleavage allowed. For the identification and quantification of the leaf proteins, carbamidomethylation was set as a fixed modification, and methionine oxidation and deamination of asparagine/glutamine as variable modification. A MASCOT-integrated decoy database search calculated a FDR of 0.45%, applying the MASCOT Percolator algorithm to distinguish between correct and incorrect spectrum identifications (61). The peptide assignments were re-imported into the Progenesis QI software. After summing up the abundances of all unique peptides that were allocated to each protein, the identification and quantification results were exported. Voronoi Treemaps as introduced by Bernhardt et al. (62) were used to visualize the proteomics results. The Voroni Treemaps subdivide the 2D plane into subsections according to the hierarchical data structure of gene functional assignments as taken from the corresponding *Arabidopsis thaliana* orthologs, which were obtained from the POPGENIE database (http://www.popgenie.org).

Data availability. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium (63) via the PRIDE partner repository with the dataset identifier PXD013252. The remaining data for the biomass changes and photosynthesis rates, associated protocols, code, and materials in the paper and supplementary materials are available from the corresponding authors (R.K.M., T.N.R. and J.-P.S.) upon reasonable request.

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Additional information

Supplementary information is available for this paper at:

Figure Legends

Figure 1. A. Maximum observed leaf isoprene emission rates in thirteen hybrid poplar genetic lines growing in Oregon. Horizontal lines within each box represent median values, boxes represent the limits of the second (lower) and third (upper) quartiles, respectively; vertical lines represent upper and lower ranges and dots represent extreme outliers (n=5 trees for each line). **B.** Maximum observed leaf net photosynthesis rates in nine of the thirteen genetic lines growing in Oregon. **C.** Maximum observed leaf isoprene emission rates in four hybrid poplar genetic lines growing in Arizona. **D.** Maximum observed leaf net photosynthesis rates in the four genetic lines growing in Arizona. In all cases, n=5 trees. CN=wild-type control, EV=empty-vector control, IR=isoprene reduced. All measurements were made on separate trees for each genetic type and plantation.

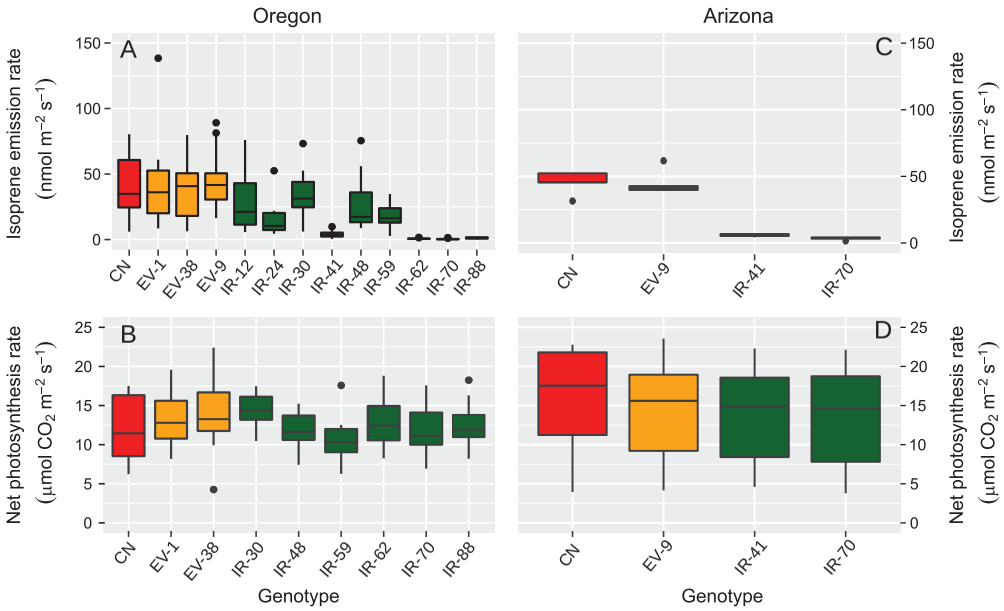
Figure 2. A. Summary of total harvestable shoot biomass for binned genetic lines of trees grown in Oregon in 2011 and 2012 and harvested spring 2015. Boxes, whiskers and symbols are as described for Figure 1. **B.** Summary of total harvestable shoot biomass for individual genetic lines grown in Oregon in 2011 and 2012 and harvested spring 2015. **C, D, E and F.** Annual shoot biomass production in four consecutive years for the four genetic lines grown in Arizona. For all cases, n=12 trees for each genotype and plantation. CN=wild-type control, EV=empty-vector control, IR=isoprene reduced

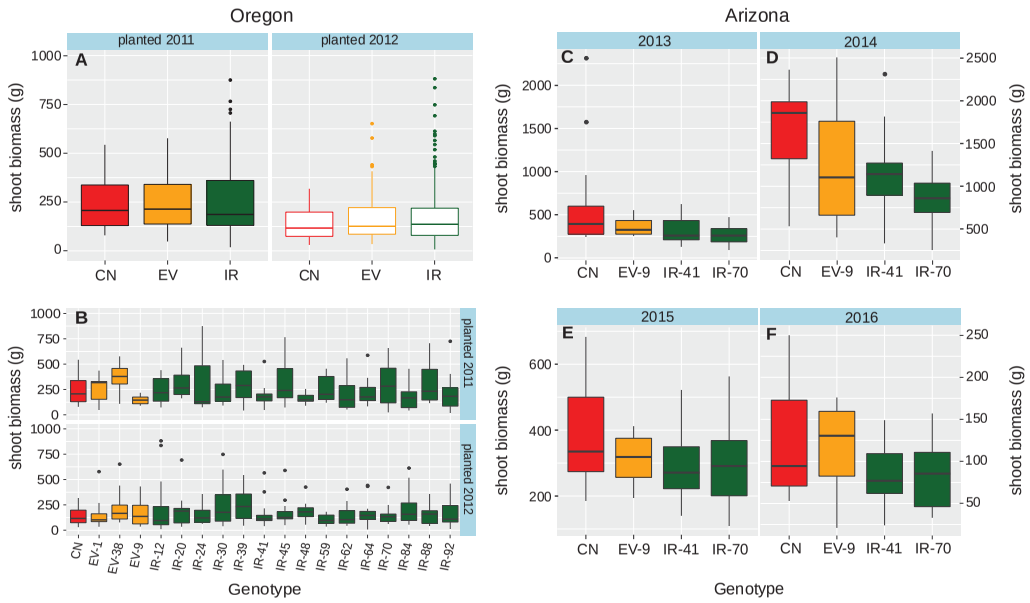
Figure 3. Rates of net photosynthetic carbon assimilation as a function of leaf temperature observed at three times during the growing season for the four genetic lines of poplar grown at the Arizona plantation. Points represent the mean (n = 5 separate trees) and vertical bars represent $\pm$ standard error. CN=wild-type control, EV=empty-vector control, IR=isoprene reduced

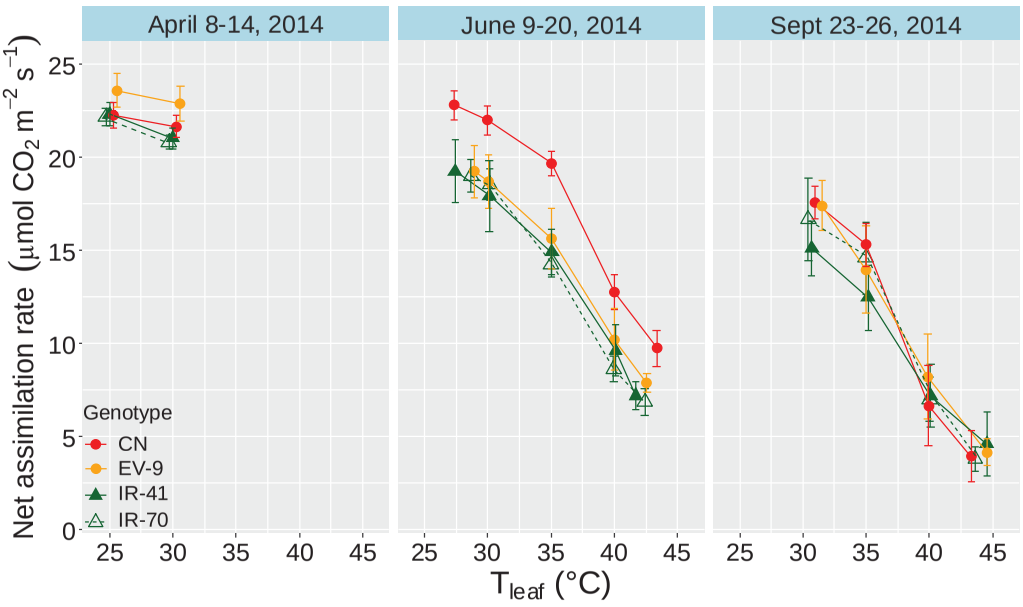
Figure 4. Whole proteome comparison of isoprene-emitting (IE) and isoprene-reduced (IR) leaves sampled during predawn and midday (noon) for trees grown in Arizona. **A.** Score plot of OPLS (Orthogonal PLS modeling) showing distribution of principal components. Samples were categorized as isoprene-emitting (IE) and isoprene-reduced (IR), and according to the respective sampling time (predawn, noon). The ellipse indicates the tolerance of the analysis based on Hotelling's T^2 with P=0.05. **B, C.** Volcano plots showing the magnitude of differential protein abundance in IR and IE genotypes ($\log_2$ fold change) compared with the measure of statistical significance ($-\log_{10}$ [p-value, beta binominal test]). Vertical dashed lines indicate a $\log_2$-fold change of ±0.5 and the dashed horizontal line indicates the significance level of $P \leq 0.05$. Proteins that fit both criteria are shown as red dots. Exemplary proteins with the highest significance and $\log_2$-fold change, respectively, are specifically identified by abbreviations (see Table 1 for complete protein names) according to Ptrichocarpa_210_v3.0_defline. The relative differences between

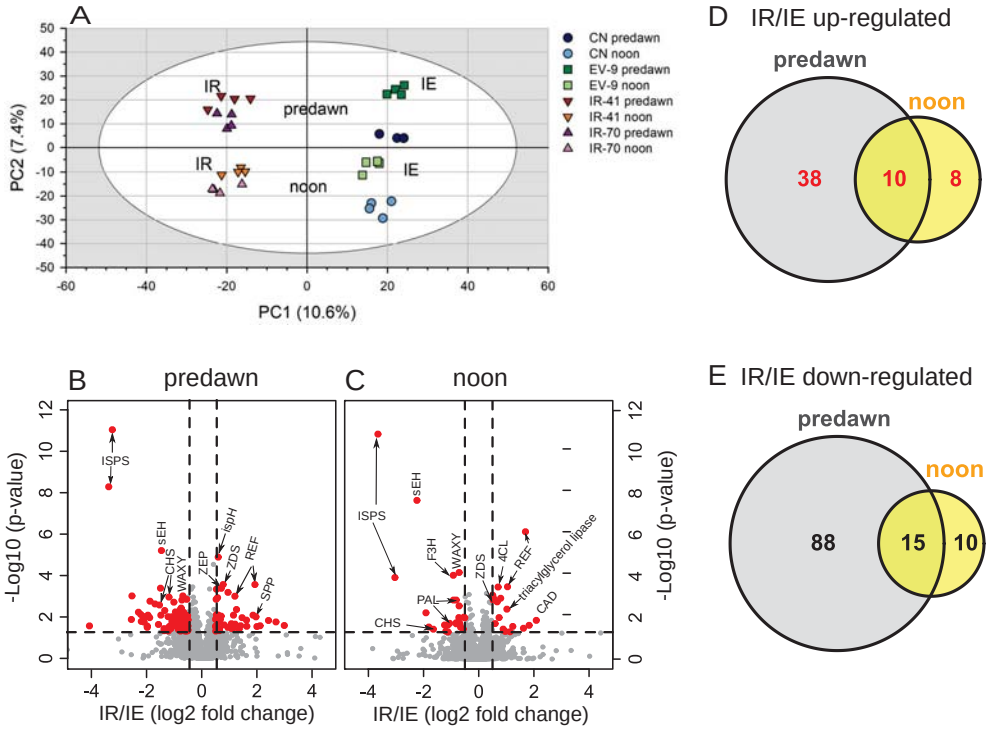
679 IR and IE lines are indicated on to the x-axis as a ratio (IR/IE) in the positive or negative direction. **D, E.**
680 Venn plots indicating the number of significantly ($P \leq 0.05$) up- (D, log_2-fold change IR/IE > 0) and down-
681 regulated proteins (log_2-fold change IR/IE <0) at predawn and noon, as well as constitutive proteins, i.e.
682 observed at both sampling events.

683 **Figure 5.** Voronoi Treemaps showing the overall proteome changes of IE and IR leaves. The total area of
684 each map is subdivided into main categories, then the main categories into subcategories and the
685 subcategories into equally sized cells representing significantly changed proteins. Protein expression
686 changes are displayed according to their functional categories and log2 ratios for IR/IE, and are color-
687 coded: red = increased ratios, grey = unchanged ratios, and blue = decreased ratios. All measurements
688 were made on separate trees for each genetic type and plantation as described in the main text.


Oregon
Arizona
A
B
C
D
Isoprene emission rate
(nmol m−2 s−1)
Net photosynthesis rate
(μmol CO2 m−2 s−1)
150
100
50
0
25
20
15
10
5
CN
EV-1
EV-38
EV-9
IR-12
IR-24
IR-30
IR-41
IR-48
IR-59
IR-62
IR-70
IR-88
Genotype

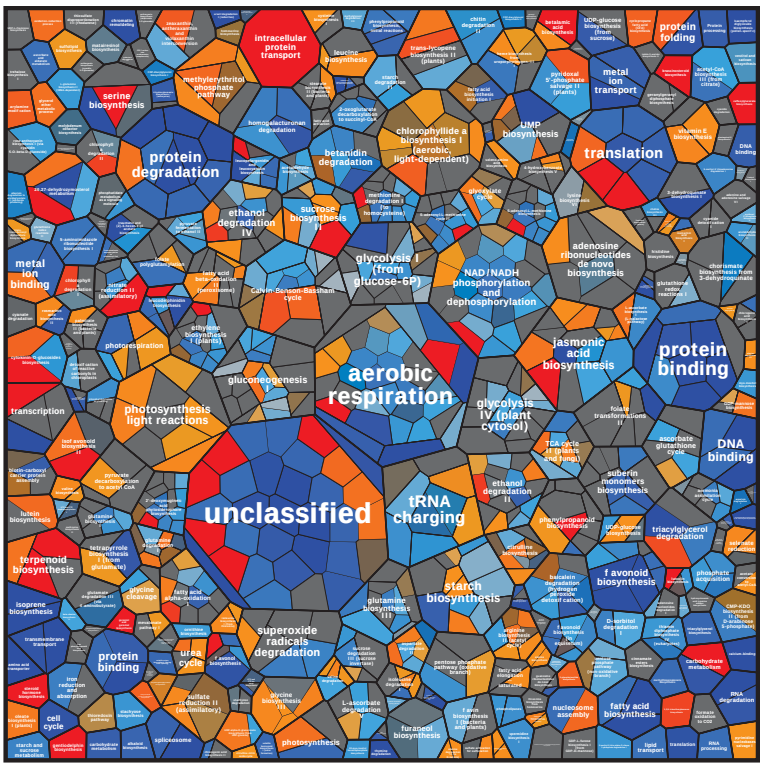

Oregon
Arizona
planted 2011
planted 2012
2013
2014
2015
2016
A
B
C
D
E
F
shoot biomass (g)
CN
EV
IR
EV-9
IR-41
IR-70
Genotype
CN
EV-1
EV-38
EV-9
IR-12
IR-20
IR-24
IR-30
IR-39
IR-41
IR-45
IR-48
IR-59
IR-62
IR-64
IR-70
IR-84
IR-88
IR-92

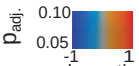

April 8-14, 2014
June 9-20, 2014
Sept 23-26, 2014
Net assimilation rate (µmol CO2 m−2 s−1)
Tleaf (°C)
Genotype
CN
EV-9
IR-41
IR-70
0
5
10
15
20
25
25
30
35
40
45


A
CN predawn
CN noon
EV-9 predawn
EV-9 noon
IR-41 predawn
IR-41 noon
IR-70 predawn
IR-70 noon
IR
IE
predawn
IR
IE
noon
PC2 (7.4%)
PC1 (10.6%)
B
predawn
C
noon
-Log10 (p-value)
IR/IE (log2 fold change)
ISPS
sEH
CHS
WAXY
ZEP
ispH
ZDS
REF
SPP
F3H
4CL
PAL
triacylglycerol lipase
CAD
D IR/IE up-regulated
predawn
noon
38
10
8
E IR/IE down-regulated
predawn
noon
88
15
10

A

predawn





B

noon

Table 1. A list of the ten most down-regulated (ranked by log_2-fold change IR/IE <0) and up-regulated (log_2-fold change IR/IE >0) at predawn and noon. Only those proteins with confirmed annotations were included. Protein abbreviations refer to those shown in Figure 4. See Table S1 in Supplementary Materials for full list of regulated proteins.

Predawn				
Downregulated				
Potri ID	**log 2 (IR/IE)**	**-Log 10 (P_{adj})**	**Pathway**	**Enzyme/Protein**
007G118400.1	-3.372	8.29	isoprene biosynthesis	Isoprene synthase (ISPS)
017G041700.1	-3.241	11.04	isoprene biosynthesis	Isoprene synthase (ISPS)
009G133300.1	-1.975	1.56	anthocyanin biosynthesis	Anthocyanidin 3-O-glycosyltransferase
001G051600.1	-1.694	2.63	flavonoid biosynthesis	Naringenin-chalcone synthase (CHS)
007G018900.1	-1.461	5.21	fatty-acid biosynthesis	Soluble epoxide hydrolase (sEH)
013G022100.1	-1.342	2.31	9-lipoxygenase pathway	Linoleate 9S-lipoxygenase
014G145100.1	-1.188	2.96	flavonoid biosynthesis	Naringenin-chalcone synthase (CHS)
005G229500.1	-1.119	1.44	leucocyanidin biosynthesis	Dihydrokaempherol 4-reductase
005G162800.1	-1.079	1.80	chorismate biosynthesis	3-deoxy-7-phosphoheptulonate synthase
003G173000.1	-1.010	2.71	aerobic respiration	Ubiquinone reductase
Upregulated				
016G066100.1	1.966	2.00	sucrose biosynthesis	Sucrose-phosphate phosphatase (SPP)
005G025700.1	1.928	3.56	terpenoid biosynthesis	Rubber elongation factor protein (REF)
001G055300.1	1.201	3.00	terpenoid biosynthesis	Rubber elongation factor protein (REF)
004G135300.1	1.099	1.54	betalamic acid biosynthesis	Stizolobate synthase
004G140800.1	1.080	1.45	nitrate reduction	Ferredoxin-nitrite reductase
002G081800.1	0.952	3.19	ethanol degradation	Aldehyde dehydrogenase (NAD^+)
018G088600.1	0.812	1.62	triacylglycerol degradation	Triacylglycerol lipase
014G148700.1	0.776	3.56	lycopene biosynthesis	9,9'-dicis-zeta-carotene desaturase (ZDS)
007G044300.1	0.708	3.38	carotenoid biosynthesis	Zea-epoxidase (ZEP)
009G111600.1	0.598	4.89	methylerythritol phosphate pathway	4-hydroxy-3-methylbut-2-enyl diphosphate (ispH)
Midday				
Downregulated				
Potri ID	**log 2 (IR/IE)**	**-Log 10 (P_{adj})**	**Pathway**	**Enzyme/Protein**
017G041700.1	-3.655	10.86	isoprene biosynthesis	Isoprene synthase (ISPS)
007G018900.1	-2.241	7.66	fatty acid biosynthesis	Soluble epoxide hydrolase (sEH)
001G449500.1	-0.710	4.18	starch biosynthesis	Glucose-starch glucosyltransferase (WAXY)
004G139700.1	-0.922	4.05	flavonoid biosynthesis	Flavanone 3-dioxygenase (F3H)
007G118400.1	-3.039	3.94	isoprene biosynthesis	Isoprene synthase (ISPS)
016G091100.1	-0.816	2.85	phenylpropanoid biosynthesis	Phenylalanine ammonia-lyase (PAL)
019G130700.1	-0.720	2.01	phenylpropanoid biosynthesis	Trans-cinnamate 4-monooxygenase

016G057400.1	-0.508	1.99	starch/sucrose metabolism	Glucan endo-1,3-beta-D-glucosidase
001G462800.1	-0.817	1.75	alkaloid biosynthesis	Tetrahydroberine oxidase
008G038200.1	-1.058	1.73	phenylpropanoid biosynthesis	Phenylalanine ammonia-lyase (PAL)
Upregulated				
005G025700.1	1.694	6.15	terpenoid biosynthesis	Rubber elongation factor protein (REF)
001G055300.1	1.044	3.49	terpenoid biosynthesis	Rubber elongation factor protein (REF)
004G102000.1	0.702	3.48	jasmonic acid biosynthesis	4-coumarate-CoA-ligase (4CL)
007G044300.1	0.506	3.08	carotenoid biosynthesis	Zea-epoxidase (ZEP)
002G081800.1	0.795	2.94	ethanol degradation	Aldehyde dehydrogenase (NAD^+)
014G148700.1	0.526	2.85	lycopene biosynthesis	9,9'-dicis-zeta-carotene desaturase (ZES)
011G099400.1	0.668	2.76	terpenoid biosynthesis	11-oxo-β-amarin 30-oxidase
018G088600.1	1.021	2.41	triacylglycerol degradation	Triacylglycerol lipase
002G018300.1	2.087	1.87	phenylpropanoid biosynthesis	Cinnamyl-alcohol dehydrogenase (CAD)
018G040200.1	0.594	1.72	vitamin E (tocopherol) biosynthesis	(delta-)tocopherol cyclase