Advanced phenotyping offers opportunities for improved breeding of forage and turf species

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DEFINITION AND CONCEPTUAL BACKGROUND OF PLANT PHENOTYPING

Plant phenotyping aims at a quantification of quality, photosynthesis, development, architecture, growth or biomass productivity of single plants or plant stands using a broad variety of analysis procedures. It presents an indispensable means to investigate physiological principles involved in the control of basic plant functions as well as for selecting superior genotypes in plant breeding programmes. Some of these procedures are well-known analysis tools of classical plant physiology based on visual observations, measurements or biochemical analyses. Others consist of target-specific and highly automated analysis procedures which have been established in the context of forage and turf breeding are discussed.

Key words: Forage, turf, breeding, phenotyping, growth, biomass, imaging, marker-assisted selection, remote sensing.

BACKGROUND OF PLANT PHENOTYPING

Advanced phenotyping, i.e. the application of automated, high-throughput methods to characterize plant architecture and performance, has the potential to accelerate breeding progress but is far from being routinely used in current breeding approaches. In forage and turf improvement programmes, in particular, where breeding populations and cultivars are characterized by high genetic diversity and substantial genotype × environment interactions, precise and efficient phenotyping is essential to meet future challenges imposed by climate change, growing demand and declining resources.

Scope This review highlights recent achievements in the establishment of phenotyping tools and platforms. Some of these tools have originally been established in remote sensing, some in precision agriculture, while others are laboratory-based imaging procedures. They quantify plant colour, spectral reflection, chlorophyll-fluorescence, temperature and other properties, from which traits such as biomass, architecture, photosynthetic efficiency, stomatal aperture or stress resistance can be derived. Applications of these methods in the context of forage and turf breeding are discussed.

Conclusions Progress in cutting-edge molecular breeding tools is beginning to be matched by progress in automated non-destructive imaging methods. Joint application of precise phenotyping machinery and molecular tools in optimized breeding schemes will improve forage and turf breeding in the near future and will thereby contribute to amended performance of managed grassland agroecosystems.

Key words: Forage, turf, breeding, phenotyping, growth, biomass, imaging, marker-assisted selection, remote sensing.
where they have already proved beneficial for certain applications, for example in rice research (Reuzeau et al., 2005; De Wolf et al., 2008). In these approaches, single plants are usually analysed in a static context, meaning that side-by-side comparisons of a range of plant genotypes are performed in a given set of environmental conditions. Yet, the dynamic response of plants is also analysed in some approaches (Walter et al., 2007; Jansen et al., 2009). In these, the reaction of growth towards an onset of drought stress, towards dynamical changes of light or temperature can be followed, requiring analysis of plant size at least at two consecutive points in time. In most cases, shoots or canopies are monitored, but root systems and root–soil interactions are beginning to be analysed non-destructively (Zhu et al., 2011). Yet, even under more controlled glasshouse conditions, environmental factors such as light intensity or spectral composition of solar radiation vary to a certain degree, thereby complicating imaging-based phenotyping approaches.

The overall goal of phenotyping approaches with respect to plant breeding is to quantify or rank the success of a range of genotypes in certain environmental frameworks. Therefore, usually hundreds or thousands of genotypes have to be compared with each other. This requires rapid measurement procedures, a high throughput, a high degree of automation and access to appropriate, well-conceived databases (Kolukisaoglu and Thurow, 2010; Fabre et al., 2011). Yet, methods that provide a high resolution at low throughput (fewer than 10 plants per day) can also be extremely helpful in depicting the performance of certain genotypes in a relevant environmental context (e.g. nuclear magnetic-resonance-based imaging of internal plant structure; Jahnke et al., 2009).

Phenotyping of course can also include automated analyses of the plant transcriptome, proteome, metabolome or ionome (Kolukisaoglu and Thurow, 2010), but this review will focus on currently available techniques to monitor plant size, architecture, growth, photosynthesis and compound composition in a non-destructive and automated manner and will evaluate how phenotyping can contribute in the future to forage and turf breeding.

POSSIBILITIES AND PLATFORMS

Analysing plant morphology and biomass production

The most widely used concept in advanced phenotyping is to determine morphological parameters such as plant height, canopy width, total leaf area, leaf number or canopy shape of a plant from an ordinary colour picture or from a few pictures per plant taken from several angles. Although this concept has first been elaborated to a high degree of automation for rosette plants such as Arabidopsis thaliana (Leister et al., 1999; Granier et al., 2006; Walter et al., 2007; Jansen et al., 2009; Fig. 1), it is now also being applied for monitoring growth of major grain crops (Reuzeau et al., 2005; Rajendran et al., 2009; Hartmann et al., 2011), or ornamentals (De Hert, 2011). In some of these approaches, plants are delivered to a camera system via conveyor belts, whereas in other approaches, individual plants are placed in the viewing field.
of the camera by manual or automatic positioning of the camera at a defined orientation towards the plant. Images are often acquired automatically, using a precisely defined source of illumination and are stored in a database. Proper image acquisition and image evaluation is crucial for successful extraction of the desired plant traits. The abovementioned architectural or growth-related plant traits are extracted from images by exact calculation of the shoot outline and of enclosed pixel numbers. To achieve this, images have to be 'segmented', which means that plant and background have to be separated precisely, based on differences in colour or brightness. While this is a trivial process for an experienced human experimenter, numerous pitfalls lurk in the automated procedure: (1) overlap between canopies of neighbouring plants has to be prevented or the system needs to be provided with clear rules concerning plant separation, (2) brightness and colour values of non-target plant objects in the background must differ markedly from values on the plant, (3) shaded parts of the canopy need to be taken care of, (4) objects such as soil particles or insects situated on the plant need to be removed manually or the resulting 'holes' within the segmented image need to be filled automatically, (5) illumination conditions have to be equal for all plants to be compared and for all time points that are relevant to the experiment as coloration and segmentation can be affected enormously by varying light input, and (6) the colour information provided by most cameras (red, green, blue pixels) is often too imprecise for colour segmentation and hence needs to be transformed using specialized procedures. This list could be extended, which is the reason why automated plant phenotyping has not yet become a standard method, although high-quality imaging sensors are now available at low cost. Proper and standardized plant handling as well as exact definitions of the desired plant traits to be analysed are crucial for successful retrieval of phenotypic traits from colour images. Historically, the first approaches for such trait retrievals used custom-designed automation procedures that were adjusted to the imaging conditions in the lab (e.g. Leister et al., 1999; Walter et al., 2007). Nowadays, more flexible and interactive, freely available software solutions are available (e.g. ImageJ: http://rsbweb.nih.gov/ij/) and are being adapted for use by multiple experimenters (e.g. Hartmann et al., 2011). Despite the aforementioned pitfalls, such methods hold great potential for the rapid phenotyping of complex traits. For example, digital analysis of total leaf area in the laboratory showed significant correlation of this trait with plant fresh and dry weight of Arabidopsis (Leister et al., 1999), tobacco (Walter et al., 2007) and cereals (Rajendran et al., 2009). As plant height was also shown to be significantly correlated to dry matter yield of forage grasses grown in the field (Majidi et al., 2009) a field-scale digital analysis of plant height may allow for a rapid prediction of dry matter yield in the field, which will be discussed in more detail later. Also, the benefit of such methods to detect genotypic differences to drought susceptibility or other environmental stresses has been shown in oilseed rape (Jansen et al., 2009) and cereals (Rajendran et al., 2009; Hartmann et al., 2011). Therefore, an automated characterization of plant size in the field will also prove highly beneficial for forage and turf breeding in the near future.

Automated field-based extraction of morphological parameters in maize, which is mostly grown as a silage crop, has only recently been achieved (Montes et al., 2011): morphological parameters such as shoot height and total leaf area were extracted for young maize plants using a so-called 'light-curtain system' (Fig. 2). This system consists of a tractor carrying a set of light barriers arranged on vertical poles. The light barriers are guided along rows of young maize plants, rendering integral values for leaf area, plant height and canopy density at defined height intervals. In addition, spectral reflectance of the canopy is analysed, which will be described in more detail later. This method would also be applicable to other plant systems such as forage crop swards and individual plants arranged in rows.

There are also non-optical approaches that have proved successful in direct determination of plant biomass without the detour of correlating leaf area to plant fresh or dry weight. One approach is the capacitive (electrical) determination of the water content of a plant that is covered by a hollow measurement device (Menzel et al., 2009); other approaches determine even plant-internal structure, biomass and substance fluxes in shoots by utilizing positron emission tomography (Jahnke et al., 2009) or portable nuclear magnetic resonance (NMR) imaging devices (Windt et al., 2011). The latter approaches are far from being applied in agronomy on the field scale, but in the long term they will provide the opportunity to assess biomass non-destructively and in the field with a rapid measurement procedure. Moreover, these approaches can resolve plant architecture in three dimensions, which is not the case in all imaging solutions described above – even if multiple images are acquired from different perspectives. A three-dimensional representation of plant structures that helps to analyse shoot branching patterns, flower morphologies or traits related to flower development requires stereoscopic imaging approaches, in which not only are pixel numbers added up, but in which the positions of real landmarks on the shoot surface are determined from multiple views and in which these positions are then registered in three-dimensional image cubes. The first steps towards canopy reconstructions in the field have been undertaken for soybean (Biskup et al., 2007), but due to the above pitfalls, their practical relevance for improving forage and turf grass breeding will not be high in the near future. Yet, other NMR-related analyses such as counting seeds are technically much easier to perform and are expected to reach applied sciences very soon, as discussed in more detail further below.

Analysing plant function

Chlorophyll fluorescence analysis (Fig. 1) is a widely used tool in plant physiology that allows determination of a number of parameters related to plant photosynthesis (Baker, 2008). It is also used in automated imaging platforms to derive the level of stress that is tolerable for plants (Woo et al., 2008), to differentiate between genotypes with differing susceptibility to drought, salt or cold stress (Jansen et al., 2009; Munns et al., 2010; Lootens et al., 2011) or as a tool to differentiate disease susceptibility (Bauriegel et al., 2011). The measurement principle is based on a defined exposition of the plant with light of a low wavelength in the visible
range and an exact registration of the re-emitted (fluorescent) light at a longer wavelength during a short time following the light pulse. Application of this technique can be powerful in the field, but either the plant has to be completely protected against incoming sunlight during the analysis by a shield or box (see, for example, Bauriegel et al., 2011) or strong lasers have to be used to induce the fluorescence signal (Malenovsky et al., 2009; Thoren et al., 2010).

Thermal imaging (Fig. 1) in the infrared wavelength range (above 1000 nm) is becoming more and more widely used to monitor stomatal conductance of plant canopies in the lab and in the field (for a review see Munns et al., 2010). Both in precision agriculture (Wang et al., 2010) and in breeding (Sirault et al., 2009; Jones et al., 2009), thermographic analysis of canopy temperature, which can be related to leaf transpiration and canopy water use, has already proven beneficial. Therefore, a high impact of such methods on forage and turf breeding can also be expected in the near future. Care has to be taken, however, to perform precise calibrations of the temperature readings provided by the infrared camera with real canopy temperatures and real transpiration rates to avoid the following artefacts: (1) differing degrees of canopy closure can lead to superpositions of canopy and soil temperature, (2) differing developmental stages of genotypes to be compared with each other can be an underlying reason for differing transpiration, and (3) differing wind velocities or sunlight/shade conditions on different spots of the investigated canopy can lead to heterogeneous microclimates at different spots of an image.

Important information on compound composition and photosynthesis can be gained via analysis of the spectral composition of sunlight reflected by the shoot canopy (Fig. 1; spectral reflectance; Chen et al., 2010; Winterhalter et al., 2011). Spectral reflectance is analysed in the visual (or near-visual) wavelength range without the need to provide artificial illumination to plants in the field. Indices such as the normalized difference vegetation index (NDVI) make use of the fact that the chlorophyll and/or nitrogen content of the leaf as well as the relationship between water-filled, vigorous tissue and unhealthy, desiccated tissue leads to characteristic alterations in the colour of the leaves, which originates from differential reflection of sunlight at different wavelengths. These characteristic colours can be addressed more or less independent of the intensity of the incoming sunlight, either by calculating ratios of intensities at two wavelengths or by calculating the difference in intensity at two different wavelengths divided by the sum of intensities at these wavelengths (Haboudane et al., 2004; Chen et al., 2010; Winterhalter et al., 2011). In contrast to most of the above-mentioned methods, which work best in the laboratory under controlled illumination, these spectral reflectance methods require natural sunlight as the illumination source as only then can the ‘true colour’ of the canopy be used to assess functional features of the monitored vegetation. These
methods even have the potential to obtain information on compound composition of the investigated genotypes. Such information can be used in near-infrared spectrometry approaches to deduce classes of compounds from plant surfaces or extracted plant material without wet chemistry analysis (Montes et al., 2007; Lebot et al., 2011). The advantage of such methods for improved breeding of the quality of forage and turf species is obvious; their application for this goal can hence be expected to be realized in the near future.

Analysing root phenotypes

The performance of any plant depends strongly on its root architecture and function (Lynch, 1995; De Dorlodot et al., 2007; Zhu et al., 2011). Currently, root biomass and architecture can be monitored in the laboratory either in pots using NMR (De Dorlodot et al., 2007; Jahnke et al., 2009) or X-ray-based computer tomography approaches (Tracy et al., 2010) that allow segmenting the root from the surrounding substrate. Yet, most platforms set up for this purpose are based on a direct visualization of the root in aeroponic or hydroponic cultivation systems (Fig. 1; Hund et al., 2009; Nagel et al., 2009). In all of these systems, total root length, branching angles and other parameters can be determined. Approaches for the analysis of root phenotypes in the field comprise visualizations of excavated root systems (shoveling; Trachsel et al., 2011), analysis of root parameters via camera systems inserted into the soil in small plexiglas tubes (minirhizotrons; see review by Johnson et al., 2001) or methods that are able to quantify root biomass indirectly via analysis of electrical properties of the soil that are altered by the intensity of water uptake via the roots (Srayeddin and Doussan, 2009).

Future automated phenotyping approaches for crop, forage and turf species need to be able to assess how efficiently the root system of individual plants or of plant communities can acquire below-ground resources. As practically all methods currently available are restricted to laboratory use, their impact on the field of forage and turf breeding is expected to increase in the mid-term only. To date, many of the above-mentioned technologies are primarily applied for answering specific questions related to plant physiology.

Overall, high-throughput automated phenotyping has tremendous potential, not only for reverse genetic approaches, where a large number of genotypes have to be screened for beneficial DNA sequence alterations, but mainly for improving complex traits in plant breeding programmes. Following up on the more general overview on phenotyping techniques given above, we will now discuss the specific requirements of breeding approaches related to phenotyping in forage and turf species in more detail.

FORAGE AND TURF GRASS BREEDING IN A CHANGING ENVIRONMENT

Grasslands represent one of the world’s largest ecosystems and cover more than 40% of the terrestrial area (Suttie et al., 2005). They not only serve as a major source of nutrients for livestock and of biomass for energy production, they also provide a range of ecosystem services, such as the conservation of biodiversity, the storage and purification of water and the provision of attractive landscapes of high aesthetic value. Highly adapted and improved cultivars of forage crop species such as ryegrasses (Lolium spp.), fescues (Festuca spp.) or clovers (Trifolium spp.) form the basis of highly productive grassland agriculture in temperate regions, which provides for a major share of the world’s production in beef and milk (Humphreys, 2005). To meet the growing global demand of food, feed and biomass and to mitigate challenges caused by changing conditions such as increased globalization and climate change, cultivars of forage crops have to be continually improved through efficient and targeted selection, thereby optimizing traits such as plant biomass, stress tolerance and metabolite composition.

Forage improvement programmes are faced with a considerable number of challenges. The number of species to be improved is large and the traits to select for are diverse. In addition, cultivars are often required to be able to adapt to a broad range of environments and management regimes. Consequently, the time required to produce novel cultivars is considerable and ranges between 15 and 20 years for species such as perennial ryegrass (Humphreys et al., 2010). This, together with the rapidly changing requirements for well-adapted forage crop cultivars, calls for more efficient plant breeding schemes. Rapid developments in the area of molecular genetics and genomics offer a variety of possibilities for complementing conventional plant breeding with marker-assisted selection (MAS). However, while genetic improvement in breeding of crops such as maize and soybean has been substantially accelerated through MAS (Eathington et al., 2007), there are only few reports on successful employment of MAS in forage crops (Roldán-Ruiz and Kölliker, 2010). This may be due to the initial lack of efficient genotyping platforms and sufficient gene-based markers together with the large and complex genome of many forage crop species, as well as population-based selection schemes. However, the enormous technical developments in the area of DNA sequencing and single nucleotide polymorphism genotyping have accelerated the development and deployment of molecular tools on a genome-wide scale, enabling molecular breeding concepts such as genomic selection (Meuwissen et al., 2001). To be able to utilize these tools in forage crop breeding, conceptual models and adapted selection schemes as well as highly efficient and precise phenotyping pipelines are needed.

CHARACTERISTICS OF FORAGE AND TURF GRASS BREEDING AND ITS IMPLICATION FOR PHENOTYPING

Many of the most important forage species are allogamous with a high degree of self-incompatibility (reviewed in Yang et al., 2008) and breeding is still largely based on open pollination. The resulting cultivars consist of highly heterozygous genotypes and represent panmictic populations (Posselt, 2010). Superior individuals are either selected directly based on their phenotype (phenotypic selection) or based on the performance of their progeny (genotypic selection). Phenotypic selection is mostly based on the evaluation of individual plants in spaced plant nurseries (mass selection) or the
evaluation of vegetative replicates (clones) planted in rows (clonal selection). Genotypic selection, on the other hand, is based on the evaluation of progenies (i.e. half-sib or full-sib families) in replicated plot trials, which allows us to estimate genetic variance (reviewed in Posselt, 2010). Evaluations are usually based on visual inspection (scoring) or measurement of the character of interest either on individual, spaced plants or in experimental swards. As spacing of plants in individual plant nurseries is markedly different from that in natural swards, observations for some complex traits such as biomass yield usually cannot be directly translated from spaced plants to swards (Casler et al., 1996).

Forage crops are primarily grown for vegetative dry matter yield. Reproductive characteristics such as seed yield are of economic importance for novel cultivars to be successful in the market. As vegetative traits such as leafiness or persistency may be negatively correlated with seed yield, forage crop breeders are constantly challenged by trade-offs between vegetative and reproductive growth (Humphreys et al., 2010). Therefore, efficient phenotyping of both reproductive as well as vegetative traits may allow for more sustainable breeding progress. Breeding objectives are defined by the trait limitations of the target species, the agricultural management targets as well as the target environments and include traits such as growth characteristics, biomass yield, nitrogen economy, forage quality, and resistance to biotic as well as abiotic stresses and seed yield (Casler and van Santen, 2010). Successful implementation of advanced phenotyping approaches for these traits implies (1) an initial evaluation regarding whether the target trait can be reliably described on individual, spaced plants or in field swards on family basis; (2) definition of an appropriate measurement reflecting the trait of interest; (3) transformation of the collected data into useful phenotypic information; and (4) a continuous validation if the collected data translate to the actual phenotype in the field.

BREEDING OBJECTIVES AND OPTIONS FOR ADVANCED PHENOTYPING IN FORAGE AND TURF GRASS SPECIES

Dry matter yield (DMY) is one of the most important traits as it is directly related to production costs. However, measurement of DMY in breeding programmes is not straightforward because there is often only poor agreement between yield measured on individual spaced plants and obtained yield in productive swards (Wilkins and Humphreys, 2003). Consequently, genetic gain in DMY over the past 60 years has been quite limited and ranged from 0 to 6% per decade depending on the species investigated (van der Heijden and Roulund, 2010). Although intensive selection based on yield measured on individual spaced plants or in field swards on family basis; (2) definition of an appropriate measurement reflecting the trait of interest; (3) transformation of the collected data into useful phenotypic information; and (4) a continuous validation if the collected data translate to the actual phenotype in the field. Improving forage quality mainly aims at improving dry matter digestibility, increasing the amount of compounds beneficial to livestock such as water-soluble carbohydrates (WSCs) and condensed tannins, and reducing the amount of unwanted substances such as toxins, oestrogenic compounds or alkaloids (Carbonero et al., 2011). Due to the moderate to high heritability, genetic gain for forage quality has been substantial in recent decades (Casler and van Santen, 2010). Dry matter digestibility may be increased by breeding for decreased fibre and lignin concentration in the cell wall or by increasing the content of WSCs. These traits are traditionally determined using wet chemistry methods but can be streamlined by NIRS. In addition to DMY, N and WSC determination, NIRS has proven its value to predict ergovaline (Robert et al., 1997) and lignin concentrations in grasses (Andrés et al., 2005). A NIRS-based lignin prediction would be useful to identify cultivars with beneficial properties for bioenergy production. However, the accuracy of calibration models developed to predict lignin and ergovaline is still limited and needs to be improved for online field applications (Gislum et al., 2004). Of particular interest to sustain forage quality are fructans, fructose polymers deriving from sucrose and serving as reserve carbohydrates in many plant species (Ritsema and Smeekens, 2003). Fructans are key factors in crop plants to respond to abiotic stress in general, and drought, cold and freezing tolerance in particular (Livingston et al., 2009). A NIRS-based approach to quantify fructan concentration in freeze-dried and ground grass samples has recently been reported (Shetty and Gislum, 2011). In contrast to WSCs, NIRS-based measurements for specific carbohydrates such as fructans are difficult to obtain online in the field. But given the fact that fructans constitute the main part of WSCs in grasses and the high correlation of fructans to

Durableresistancetomajordiseasesandpestssuchascrownrust,snowmould,bacterialwilt, fusariumrootrotornematodesisacommonobjectiveinanyforageandturfbreedingprogramme. Resistanceisusuallyimprovedthroughphenotypicrecurrentselectionusingnaturallyoccurringor artificialinfection(Kimberg,1999;Bollerandlehmann,1996).Althoughconsiderablegeneticgainhasbeenrealizedwithregardtodiseaseandpestresistanceinmanyforagecropspecies(vanderHeijdenandRoulund,2010),changingpathogenpopulationsandnewlyemergingpathogenscallforconstantbreedingefforts.Asgenotype×environmentinteractionsoftencomplicateefficientphenotypicselection,resistanceassessmentsareoftenbasedonartificialinoculationincontrolledenvironments toreliablymimetaspacific host—pathgeninteraction.Glasshouseassessmentsusingartificialinoculationmethods(Kauffmanet al.,1973;Birkensteadt,1990)andin vitroleafsegmenttests(Leilbach,1994)havebeenappliedtoidentifyplantswithincreasedresistanceagainstcrownrust(Schejbelet al.,2007;Studeret al.,2007)andbacterialwilt(Studeret al.,2006;Wichmannet al.,2010).However,alltheseproceduresarebasedonvisualobservationswhicharelaborious,oftenbiasedbytheexaminerandmaynotbesufficientlyaccuratetargetedimprovementofdiseaseresistance.Automateddigitalimagingofleafareaaffectedbythepathogenmaybeenablemoreaccuratequantificationaswellasthemonitoringofdynamicchangesofthepathogenattackonlargecomeslevel.Inaddition,thedetectionandquantificationofthepathogeninonorthehostplantbymeansofquantitativeretaltimPCRmayallowforeachefficient,accuratephenotypingofdiseaseresistance(Zhu et al.,2010;Qu et al.,2011).

Seedyieldisoneofthemostcomplextraitswithagenerallylowheritability,highlyaffectedbyagriculturalpracticesaswellasenvironmentalfactors.Moreover,ahighlyefficientself-incompatibilitiesystempromotescross-pollinationandthusparticularinteractionsbetweendifferentgenotypesto produceaviableseed.Asaconsequence,itisimpossibletom easureseedyieldonsingleplants.Themoderatetolowcorrelationbetweenseedyeildevaluationsonspacedplants comparedwithswards(Elgersma,1990;Elgersmaet al.,1994)supportsthatonlytrialsoverseveralyearsinmultiple environmentswillprovidevaluablevaluesforseedyield.Asseedsisomeofmajorimportancefortotalseedyield(Elgersma,1991),ithasbesuggestedtobreedforaperformanceefficientrealizationoftheseedyieldpotentialratherthan to increasethesizeofthereproductive systems with possible negative effects on forage performance(BoeltandStuder,2010).Automatic,X-rayimaging-basedcounts ofseednumbersperspikeletcouldassistintowardsaishortenrealizationoftheseedyieldpotential.Moreover, the percentage of seeds aborted post pollination, the abortion pattern within the spikelet and gradients in ovule dry weight within the spikeletareimportantseedyieldcomponents.Non-invasive three-dimensional imaging of caryopses from developingseeds by NMR as used onothergrass species(Glidewell,2006)mayprovidetheopportunitytoidentify and select genotypes with a high and homogeneous seed weightatfinalharvest,whichisbeneficialforhighefficiencyseedyield(Warringa et al.,1998).

CONCLUSIONS

Elaboratingupon,adaptingandusingadvancedphenotypingtechnologiesisanpromisingwayforwardtoefficientlyandreliablyimproveagronomicallyimportanttraitsinthebreeding processofforageandturfgrassspecies.Practicalrealization includesa biological andatechnicalpart:Forexample,ad thoroughexperimentaldesign,thedefinitionofamemasurement reliablydescribingthetargettraitandacircularcontinuation validationregardingwhetherthecollectedphenotypicdatatranslate totheactualphenotypeinthefeldarekeyfactors.Thetechnological part consists of well-conceivedselection,realization andapplicationoftheappropriatetechnologyandofsubse quent steps of data processing.Incombinationwithoptimized breeding schemes and cutting edge molecular tools,advanced phenotypinghas thepotentialto substantially improveand fastenculturdevolopment,therebycontribution to a sustain ablefeed,foodandbiomassproductionbothonthe localand globlleve.

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