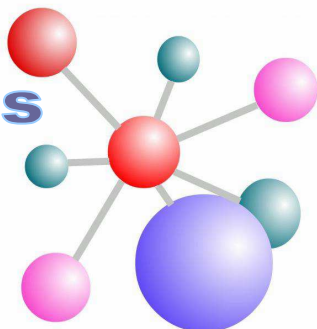


Inglês



Ciências Agrárias

Instruções

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Se, em qualquer outro local deste Caderno, você assinar, rubricar, escrever mensagem, etc., será excluído do Exame.
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- 8** Utilize para rascunhos, o verso de cada página deste Caderno.
- 9** Você dispõe de, no máximo, três horas, para responder as 5 questões que constituem a Prova.
- 10** Antes de retirar-se definitivamente da sala, devolva ao Fiscal este Caderno.

Assinatura do Candidato: _____

As questões de 01 a 05, cujas respostas deverão ser redigidas EM PORTUGUÊS, referem-se ao texto abaixo.

GENETIC STRUCTURE AND DOMESTICATION HISTORY OF THE GRAPE

Sean Myles, Adam R. Boyko, Christopher L. Owens, Patrick J. Brown, Fabrizio Grassi, Mallikarjuna K. Aradhya, Bernard Brins, Andy Reynolds, Jer-Ming Chia, Doreen Ware, Carlos D. Bustamante and Edwars S. Bickler

Abstract

The grape is one of the earliest domesticated fruit crops and, since antiquity, it has been widely cultivated and prized for its fruit and wine. Here, we characterize genome-wide patterns of genetic variation in over 1,000 samples of the domesticated grape, *Vitis vinifera* subsp. *vinifera*, and its wild relative, *V. vinifera* subsp. *sylvestris* from the US Department of Agriculture grape germplasm collection. We find support for a Near East origin of *vinifera* and present evidence of introgression from local *sylvestris* as the grape moved into Europe. High levels of genetic diversity and rapid linkage disequilibrium (LD) decay have been maintained in *vinifera*, which is consistent with a weak domestication bottleneck followed by thousands of years of widespread vegetative propagation. The considerable genetic diversity within *vinifera*, however, is contained within a complex network of close pedigree relationships that has been generated by crosses among elite cultivars. We show that first-degree relationships are rare between wine and table grapes and among grapes from geographically distant regions. Our results suggest that although substantial genetic diversity has been maintained in the grape subsequent to domestication, there has been a limited exploration of this diversity. We propose that the adoption of vegetative propagation was a double-edged sword: Although it provided a benefit by ensuring true breeding cultivars, it also discouraged the generation of unique cultivars through crosses. The grape currently faces severe pathogen pressures, and the long-term sustainability of the grape and wine industries will rely on the exploitation of the grape's tremendous natural genetic diversity.

Introduction

The grape is the most valuable horticultural crop in the world. The fruit from the world's ~8 million ha of vineyard is mostly processed into wine, but some is destined for fresh consumption as table grapes, dried into raisins, processed into nonalcoholic juice, and distilled into spirits (<http://faostat.fao.org/>). The archaeological record suggests that cultivation of the domesticated grape, *Vitis vinifera* subsp. *vinifera*, began 6,000–8,000 y ago in the Near East from its wild progenitor, *Vitis vinifera* subsp. *sylvestris*. The thousands of grape cultivars in use today have been generated since then by vegetative propagation and by crosses.

Wine and table grapes currently receive intense chemical applications to combat severe pathogen pressures. This susceptibility to disease, however, is not attributable to a lack of genetic diversity. *Vinifera* harbors levels of genetic variation an order of magnitude greater than humans and is comparable in diversity to maize, with polymorphism that dates back tens of millions of years. Thus, an environmentally sustainable grape-growing industry will rely on accessing and using the grape's tremendous genetic diversity to develop improved disease-resistant grape cultivars through marker-assisted breeding. Traditionally, grape breeding programs have sought genotype-phenotype associations using linkage mapping. Because of the grape's long generation time (generally 3 y), however, establishing and maintaining linkage-mapping populations is time-consuming and expensive. Thus, genome-wide association (GWA) and genomic selection (GS) are attractive alternatives to traditional linkage mapping in the grape and other long-lived perennial fruit crops.

Well-powered GWA and GS require a genome-wide assessment of genetic diversity, patterns of population structure, and the decay of linkage disequilibrium (LD). To this end, we recently discovered over 70,000 high-quality SNPs in the grape using next-generation DNA sequencing. From this SNP set, we developed and validated a 9,000-SNP genotyping array (the Vitis9kSNP array). Here, we present an analysis of genotype data from 950 *vinifera* and 59 *sylvestris* accessions using the Vitis9kSNP array as part of an effort to characterize an entire US Department of Agriculture (USDA) germplasm collection on a genome-wide scale. We provide a refined model of the domestication and breeding history of *vinifera* by evaluating levels of haplotype diversity, the decay of LD, and patterns of population structure in *vinifera* and its progenitor, *sylvestris*. In addition, our analyses reveal extensive clonal relationships among cultivars and a complex pedigree structure within *vinifera* that are the result of widespread vegetative propagation. We suggest that the last several thousand years of grape breeding explored only a small fraction of possible genetic combinations and that future marker-assisted breeding efforts therefore have tremendous diversity at their disposal to produce desirable wine and table grapes with resistance to existing and future pathogens.

Disponível em: <<http://www.pnas.org/content/108/9/3530.full>>. Acesso em: 19 mar. 2015.

Questão 1

O que representa o cultivo da uva, de acordo com os autores, e como a produção é utilizada?

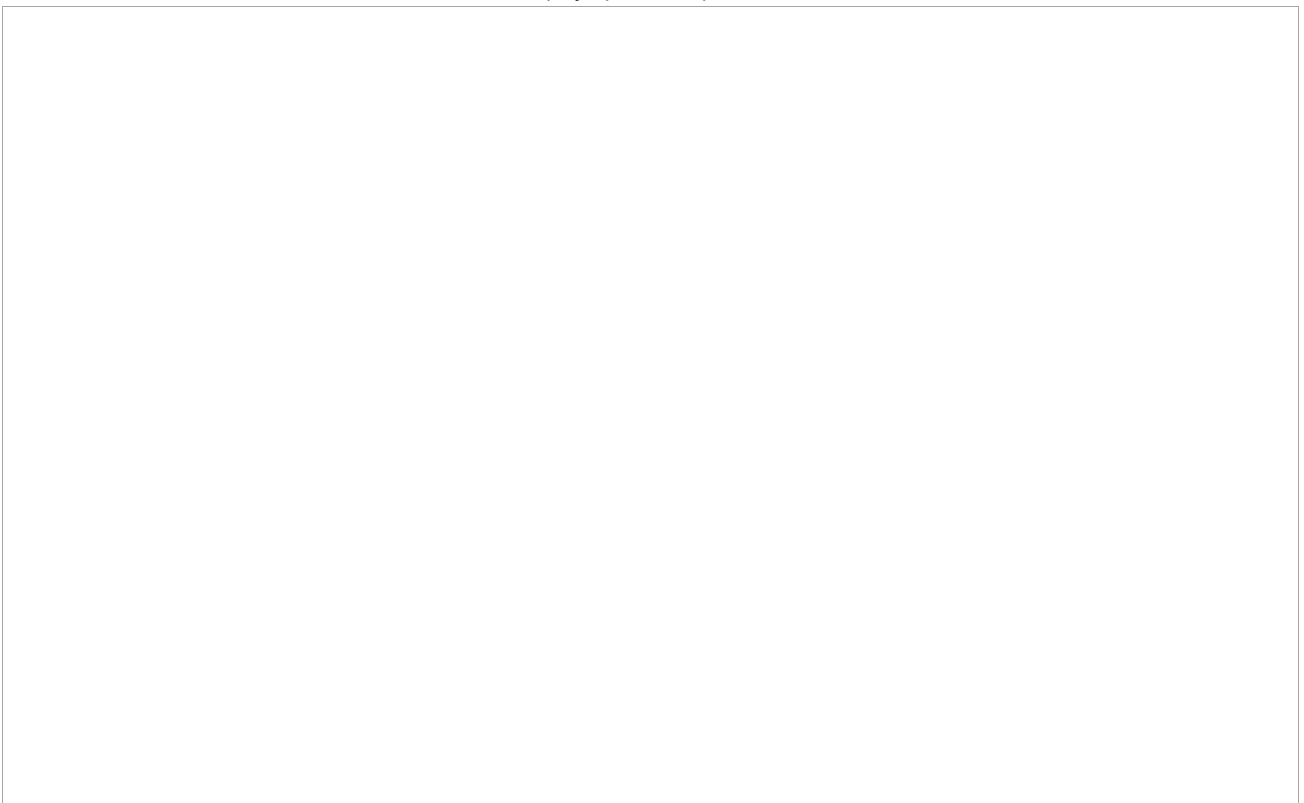
Espaço para Resposta



Questão 2

Segundo o texto, do que dependerá uma indústria vinícola ambientalmente sustentável?

Espaço para Resposta



Questão 3

Explique o que representam a GWA e a GS conforme indicado no texto.

Espaço para Resposta



Questão 4

De acordo com os autores, o que é apresentado no texto?

Espaço para Resposta



