



Onion Genetic Diversity

Improving Crop Improvement!

Onions are a staple crop in many cuisines and cultures across the globe.

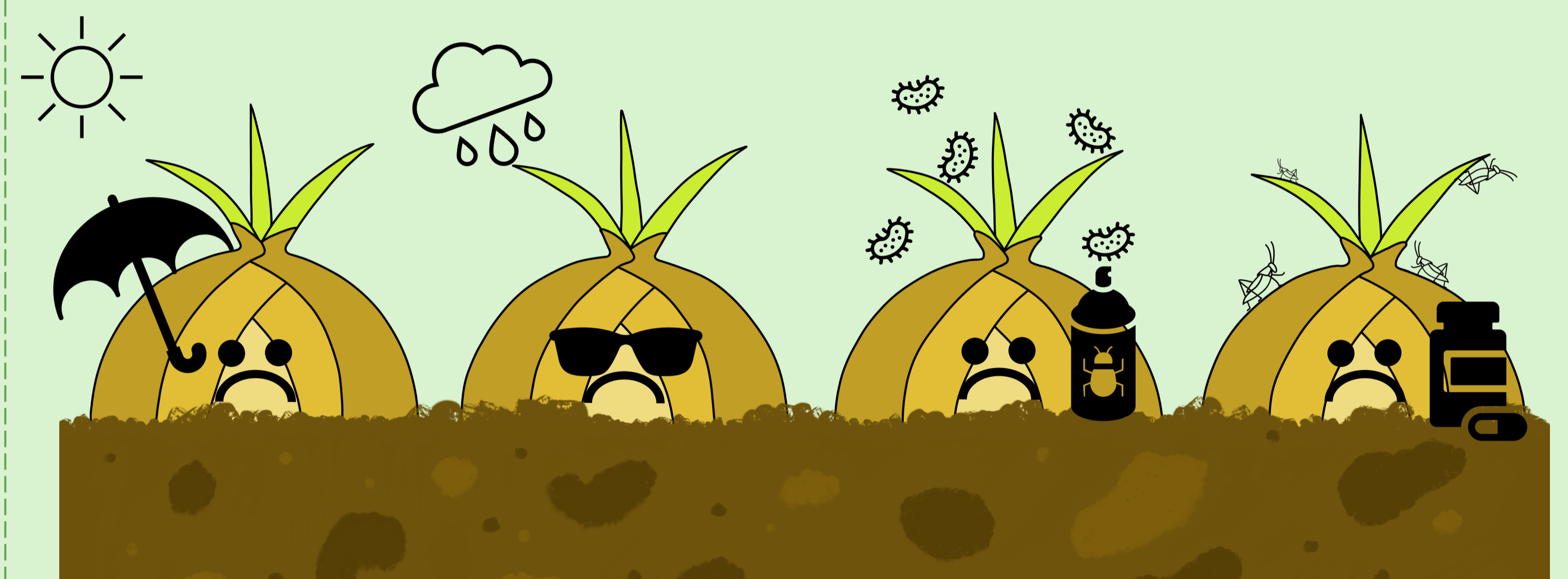
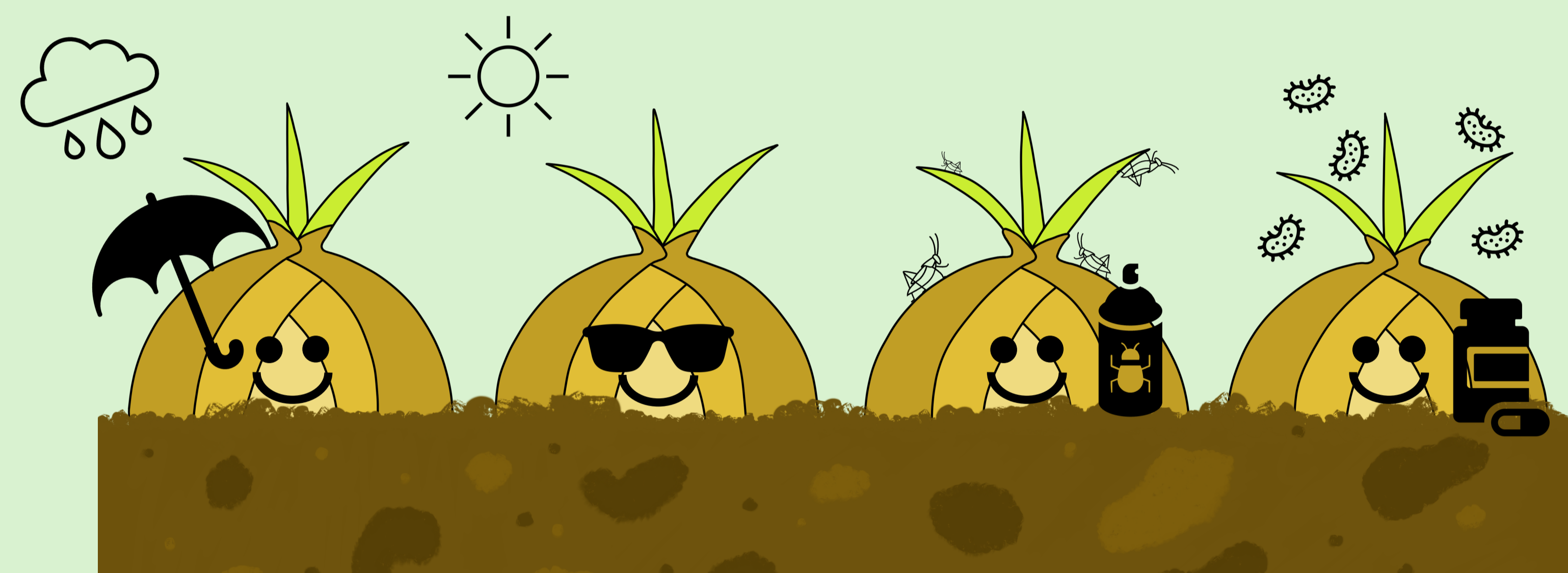
Their flavanols have anti-inflammatory and antioxidant effects.

Traditional medicines have made use of their antimicrobial effects.

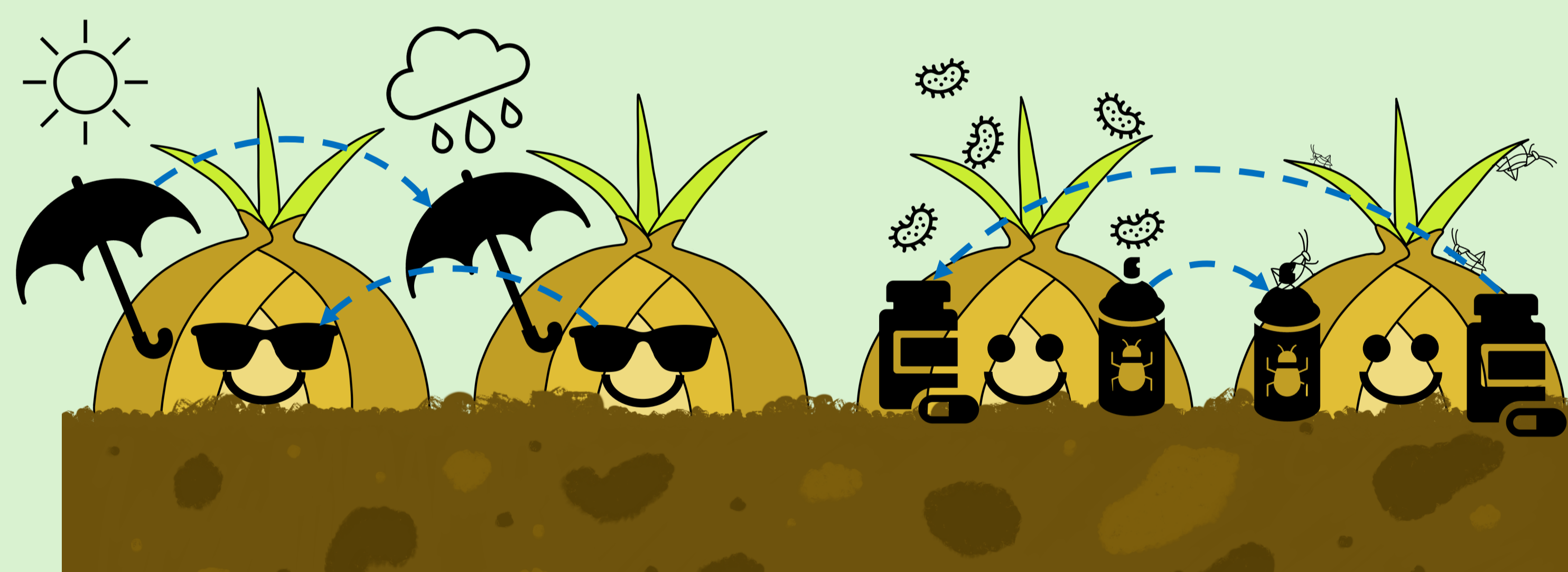
By weight, the UK imports more onions than any other vegetable, costing over £150m a year

Modern onion crop cultivars are generally bred to have traits that are advantageous for their environment.

Climate changes threatens these environments with new weather patterns, pests and diseases.



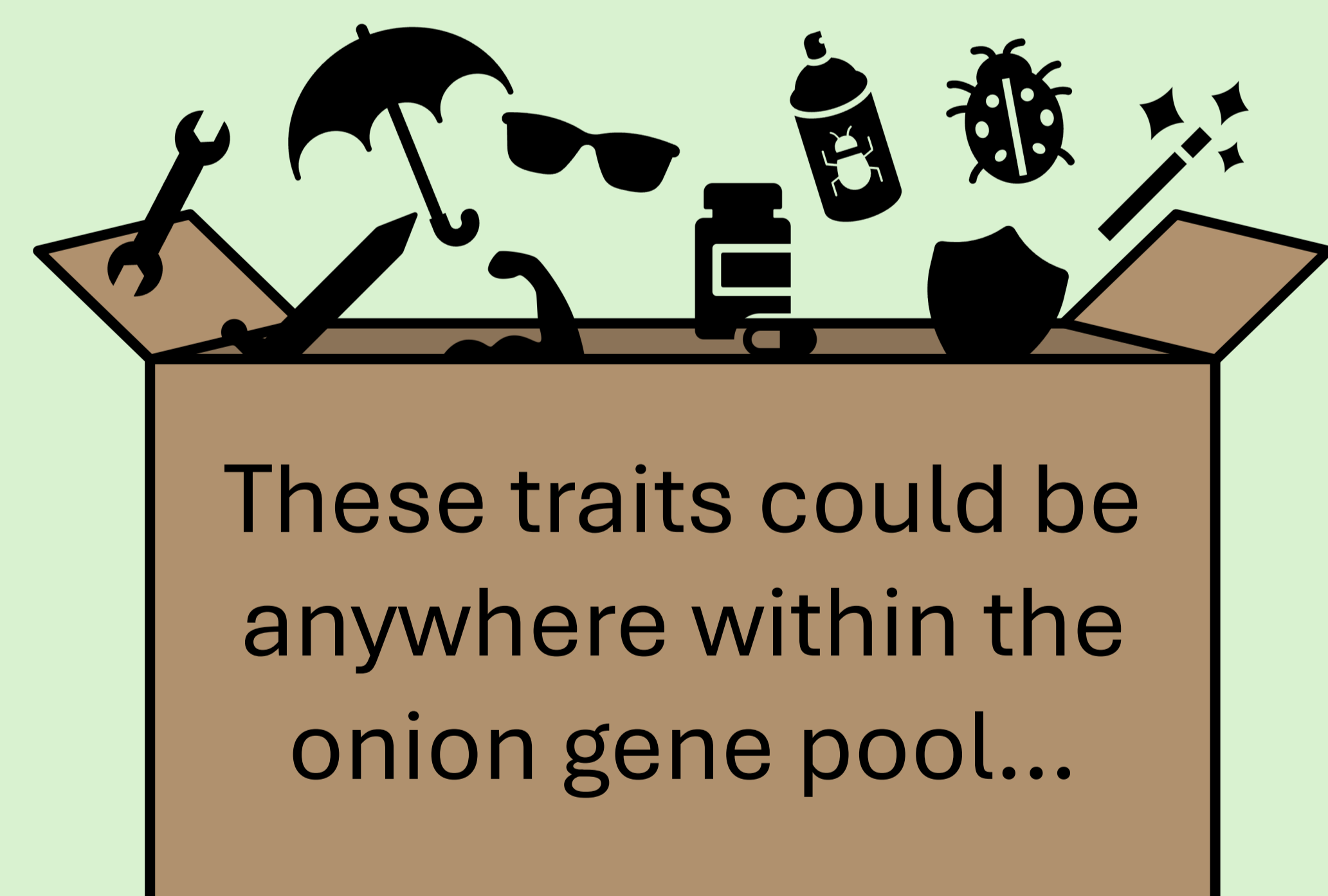
Finding the genes/loci responsible for these traits can aid marker-assisted breeding and other genetic techniques to improve our crops, making them more resilient to a wider variety of environmental stressors.



Wild species and non-commercial onion lines may also hold novel variation. This could include novel resistances and more generally useful traits such as high yield, longer shelf life, lower input needs, and more!

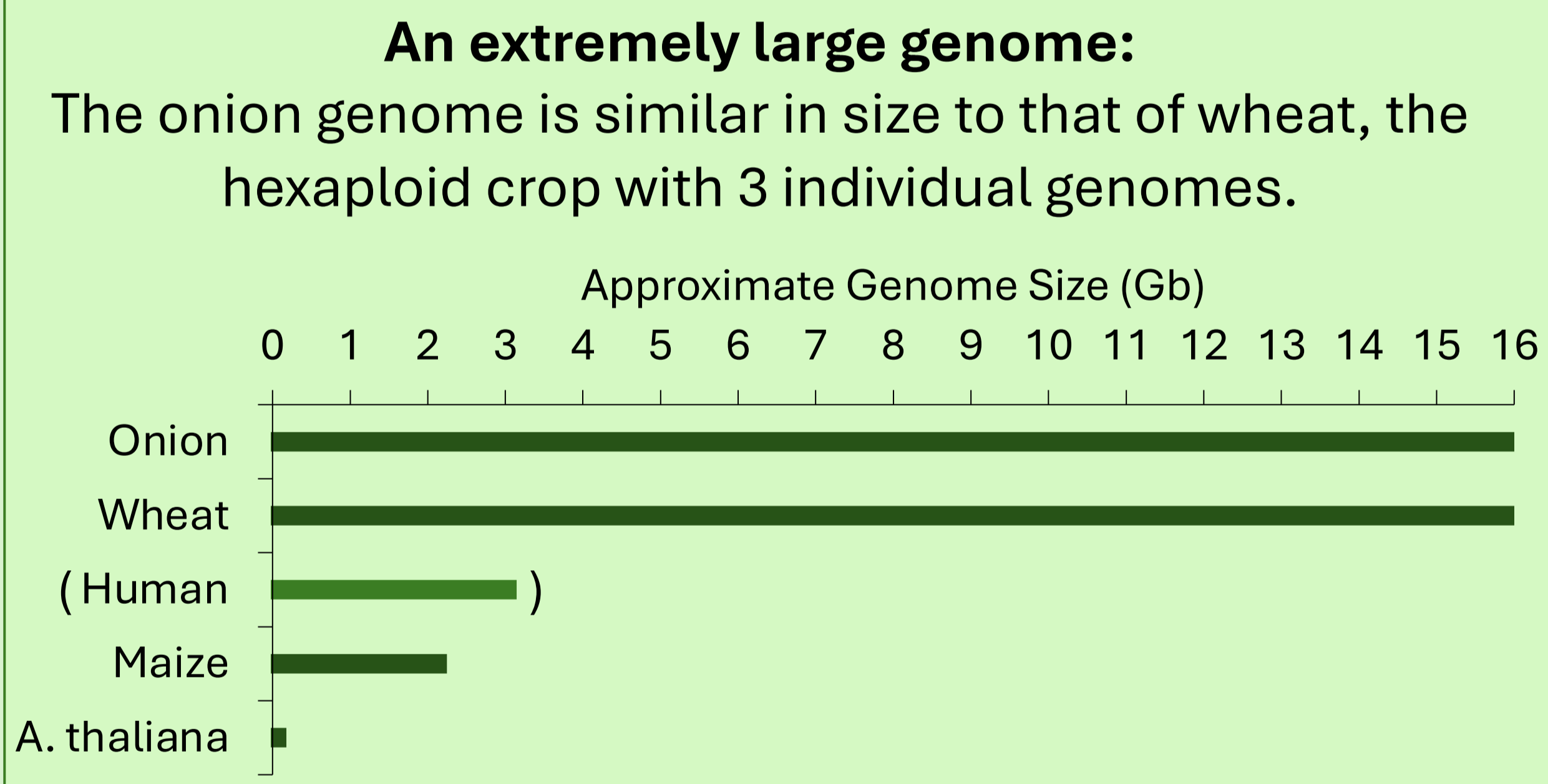
However, typical genetic characterisation of onions has its own challenges.

...and onions pose issues to whole genome sequencing:



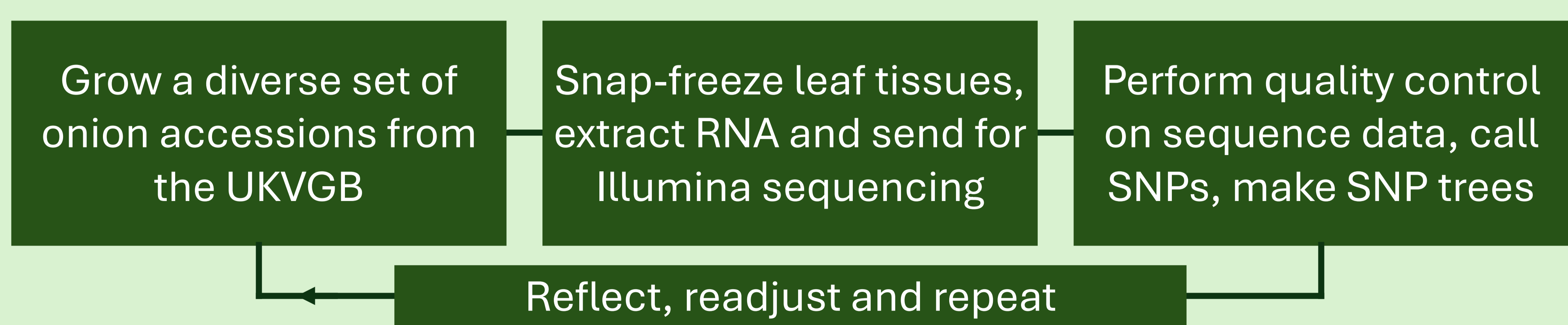
A "complicated" genome:
The onion genome has a very high proportion of non-coding regions and a highly repetitive and heterozygous nature.

An "orphan" genome:
The first onion genome assembly was published in 2021, and there have been only 2 assemblies made available since.



By sequencing RNA instead, this project aims to circumvent these challenges and obtain sequence data from the UKVGB's* collection of onion varieties.

Due to the explorative nature of this project, the experimental pipeline is iterative:



From this data, Single Nucleotide Polymorphisms can be called, which can give insight into how diversity is partitioned across the onion gene pool.

Achievements so far include preliminary method development and analysis of first set of sequence data.

Future work includes mapping of economically important traits such as yield and bulbing time to validate a novel pipeline.

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My partner and all their
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