

until the end of November 2021. In each wave, they asked participants to self-report their vaccination status, later corroborated by the authors.

Before the intervention, participants, on average, thought that only 57% of physicians would want to be vaccinated and that 61% trusted the vaccines. But two weeks after the educative nudge, among participants who had been exposed to it, those percentages increased to 63% and 67%, respectively.

Comparing vaccine uptake in participants exposed to the nudge intervention and those not exposed revealed a gradually increasing and lasting effect (Fig. 1). The difference in uptake was negligible in the initial waves of data collection, when vaccine roll-out was limited, but in July 2021, once vaccines became freely available to all adults, uptake in the exposed group was 4–5 percentage points higher – a significant increase. The difference in vaccine uptake between groups then remained relatively stable until the end of the data-collection period. Encouragingly, the authors report a similar-sized difference (4 percentage points) for participants' intentions to get a booster shot, which were solicited towards the end of the data-collection period.

This study has several strengths that make it stand out. For instance, participants were broadly representative of the adult Czech population in terms of sex, age, education and region of residence, as well as attitudes towards COVID-19 vaccines and actual vaccination rates. This suggests that Bartoš and colleagues' intervention should be effective when scaled to the country's entire population.

Furthermore, not only is this study one of very few so far that have gone beyond measuring intentions to receive the COVID-19 vaccine, it is also the only one that has tested the behavioural impact of providing corrective positive (factual) views from a trusted and relevant group of experts. Previous studies focused on interventions such as potential monetary rewards (for example, lottery prizes for vaccine recipients) and text messages that communicated, for instance, the benefits of vaccination, vaccine effectiveness and safety or social norms surrounding vaccination⁵. In addition, because Bartoš *et al.* collected longitudinal data over different phases of the vaccine roll-out, their results allowed them to observe that the effect is lasting, and to infer that the intervention did not simply speed up uptake, but actually increased it in an otherwise hesitant subpopulation.

At the same time, the study is not without limitations, particularly with regard to how to successfully translate its insights to other contexts or scale it up⁶. First, the intervention was motivated by factors specific to the Czech Republic: widespread trust in physicians; very high prevalence among physicians of positive views on COVID-19 vaccination; and people's

severe underestimation of this prevalence. However, the authors did not establish that the effect of their educative nudge was dependent on, or caused by, these factors.

Second, because of the experiment's design and the fact that participants were split into only two groups (one receiving the nudge, the other receiving no information), the authors cannot establish the contribution of each design feature to their result. For example, to what extent did it matter that participants were asked for their opinions about physicians' views before half of them received the nudge? And what was the contribution of each of the three pieces of information about physicians' views?

Finally, even though the study was conducted with a sample representative of the Czech population, it is still likely to be to successfully scale up the intervention without experiencing a drop in its effectiveness⁷. For instance, the participants agreed to join a panel that would be surveyed regularly, but it might be hard to ensure that a broader population would show similar levels of engagement – in particular, attention to and trust in the nudge⁸.

Nevertheless, Bartoš and colleagues' findings are exciting, to say the least. They raise the possibility that a relatively cheap and simple one-off educative nudge, targeting misperceptions⁹ of physicians' views, helps to increase the uptake of lifesaving COVID-19 vaccines.

Given the relatively large effect in comparison with that of some other interventions⁴, I am hopeful that researchers will add this nudge to their intervention toolkit. Going forward, researchers should consider trialling this nudge in other countries and for other public-health interventions, if the settings are otherwise similar. Ideally, this work will also inspire researchers to identify some of the mechanisms underlying the effect observed by Bartoš and colleagues, to better understand the generalizability of these findings.

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The author declares no competing interests.
This article was published online on 1 June 2022.

Genetics

Potato genomes pave the way to crop improvement

Juanita Gutiérrez-Valencia & Tanja Slotte

High-quality genome sequences for 44 wild and cultivated potatoes will enable researchers to better study this essential crop's evolution and develop varieties that can withstand heat and drought caused by climate change. See p.535

Potatoes are the third most consumed food crop worldwide, after wheat and rice¹. To safeguard crop yields in the face of climate change, improved varieties will be needed. Tang *et al.*² describe on page 535 the sequencing and analysis of high-quality genomes from wild and cultivated potatoes. This pan-genome should increase our understanding of fundamental aspects of potato biology and guide breeding practices.

Improvement of potato crops is hampered by some of the intrinsic features of commercially grown potatoes. For instance, these crops typically have four sets of chromosomes and do not breed true (offspring do not necessarily carry

the same traits as parental plants). As such, developing new varieties is complex and time consuming.

Breeding of diploid potatoes (which have two sets of chromosomes) could speed up the development of improved potato varieties^{3,4} that could withstand drought and diseases. It could also allow development of inbred lines, which lack genetic variation and can be crossed to generate uniform, high-yielding hybrids^{3,4}. Locally cultivated varieties (called landraces) and wild potato species (Fig. 1) could be especially useful in this respect, because most are diploid and they harbour a wealth of untapped genetic variation that could be



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Figure 1 | A wild potato species, *Solanum jamesii*. Tang *et al.*² sequenced 44 wild and locally cultivated potato genomes, generating a resource that will help breeders improve potato crops.

harnessed in new breeding strategies.

Tang *et al.* assembled high-quality genomes for 44 landrace and wild potatoes. It has been challenging to assemble genomes from outbred and genetically variable species such as potato, but the authors overcame this obstacle thanks to state-of-the-art genome-sequencing methods that yield long and accurate DNA sequences, which can be assembled into chromosome-length pieces. The massive data set also allowed the researchers to identify genomic regions in which the DNA differed between each member of a pair of chromosomes (that is, the DNA was heterozygous) or was the same (homozygous). Assembling so many high-quality genomes of a diverse set of outbred and highly heterozygous species is a remarkable feat.

Potato landraces and wild species evolved various genetic variants as they adapted to different environmental challenges. Characterizing the evolutionary processes that explain genomic variation could therefore be of interest to breeders. Tang *et al.* made use of the genome sequences to reconstruct the evolutionary history of potatoes, along with related species such as tomatoes and species belonging to the group *Etuberosum*, which have non-tuberous underground stems. The results indicated that tomatoes are the closest relatives of potatoes, contrary to Tang and colleagues' expectations.

However, when the authors reconstructed evolutionary histories for individual genes, the trees varied wildly. Previously, such patterns have been attributed to hybridization between species⁵, but the authors show that a portion of this genetic variability was already present in the common ancestors of the species studied. Random sorting of ancestral genetic variation into descendant species can then result in gene-tree variability without hybridization – Tang *et al.* showed that this was common in the

evolutionary history of potatoes and their close relatives.

Tang and colleagues catalogued various aspects of genetic variation in their 44 genomes, including gene content, genome structure, distribution of homozygous segments and variation in evolutionarily conserved DNA sequences that might regulate gene expression. They found a striking level of variation in terms of gene content and structure. The authors further showed that, compared with tomato and *Etuberosum*, potato genomes are enriched in certain disease-resistance genes, including genes known to confer resistance to *Phytophthora infestans*⁶ – the pathogen that triggered the devastating Irish potato famine of the mid-nineteenth century. This catalogue will be hugely helpful for identifying and harnessing genomic variation for cultivar improvement.

Finally, the researchers used the resources they had generated to investigate the genetic basis of tuber development. Using genomic data analyses and the gene-editing technique CRISPR–Cas9, they identified a previously unknown gene involved in tuber formation, which they named *Identity of tuber 1* (*IT1*). They went on to demonstrate that the *IT1* protein interacts with a signalling molecule called SELF-PRUNING 6A (SP6A) that is involved in tuber formation⁷. Although Tang *et al.* did not go as far as to show that the *IT1* and SP6A proteins alone can direct tuber formation, these results pave the way for further dissection of the genetics and evolution of this process.

Tang and colleagues' pangenome substantially expands the genomic resources for potato beyond those previously available^{8–11}. Their catalogue of variation will undoubtedly be valuable for both fundamental and applied research. As highlighted in the study, the potato pangenome can reveal evolutionary processes that shape variation. Through the discovery of genes involved in processes such as tuber

formation and disease resistance, it can also be used to assist in the development of improved cultivars. For instance, knowledge about the genes involved in tuber formation could help breeders develop high-yielding potato varieties, and targeted introduction of resistance genes from wild species could improve disease resistance.

Going forward, studies on how landraces and wild species have adapted to different stressors could help to establish gene–trait associations that can guide cultivar development, as in other major crops¹². Genomics-assisted breeding programmes will also benefit from the resource. For instance, certain structural variants in DNA sequence, called inversions, can hamper breeding efforts by preventing targeted selection of traits of interest. The authors' catalogue can help breeders to choose species that lack inversions in genes of interest for crosses. Further work will be required to better understand how common weakly harmful variants are, and whether they can interfere with breeding. The identification of homozygous segments, which are unlikely to harbour strongly harmful variants, could help breeders to avoid the accumulation of such variants.

Genomics-guided breeding continues to revolutionize crop improvement. Given the undeniable impact of genome-sequencing technologies in agriculture, it will be crucial to ensure broad and equitable access to genomic tools and resources¹³. Tang and colleagues' pangenome is publicly available – a key first step in equitable access. Equally important will be ready access to the potato varieties developed thanks to this, and other, genomic resources.

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The authors declare no competing interests.
This article was published online on 8 June 2022.