

Supplemental Materials

Stimulus articles.....	2
Additional results for Experiment 2.....	6
Demographics for “Relevance to COVID-19” experiment.....	11
Additional results for “Relevance to COVID-19” experiment: Individual differences.....	13
Additional results for “Relevance to COVID” experiment: Travel restrictions.....	18
Additional results for “Relevance to COVID-19” experiment: National context.....	19
References.....	21

The Zika Virus Grew Deadlier With a Small Mutation, Study Suggests



Pedro Miguel Rivera-Gonzalez, born with microcephaly in Mexico in October 2015, receiving a kiss from his mother, Paula. Scientists believe the deadly strain of the Zika virus, which causes microcephaly, might be traced to a single genetic mutation that arose in the virus in 2013.

Sept. 28, 2017



It remains one of the great mysteries of the Zika epidemic: Why did a virus that existed for decades elsewhere in the world suddenly seem to become more destructive when it landed in Latin America?

Why did the Zika virus cause thousands of babies to be born with microcephaly, unusually small and damaged brains, when previous outbreaks seemed to cause much less harm?

An intriguing study in mice, which has prompted some skepticism among experts, suggests that a single genetic mutation helped transform the Zika virus into a devastating force in Mexico. The report was published on Thursday in the journal *Science*.

The mutation, called S139N, is a strain of the Zika virus that arose in Mexico in 2013, just before a small outbreak in other parts of the world.

Zika is believed to have first appeared in Mexico later in 2013. This mutation has appeared in every strain of the virus in the Latin American outbreak, the researchers said.

The study, by scientists, found that strains of Zika with the S139N mutation caused substantially more death and microcephaly in mice than other strains. And in a laboratory dish, the S139N strain killed many more human cells important to early brain development than an earlier strain without the mutation.

Some experts voiced doubts, saying the findings were too preliminary to establish that a single mutation was the critical factor. At least, they said (and the study authors agree), the results must be replicated in primates, because laboratory experiments with mice and even human brain cells cannot fully capture how the virus functions in nature.

The authors and other experts said they did not know why the mutation might have such a profound effect.

Microcephaly cases were heavily concentrated in Mexico, but the mutated Zika strain was found everywhere.

A version of this article appears in print on Sept. 28, 2017, on Page A8 of the New York edition with the headline: Zika Virus Grew Deadlier With Mutation, Study Suggests. Order Reprints | Today's Paper | Subscribe



Zuska's Disease Grew Deadlier With a Small Mutation, Study Suggests



Pedro Miguel Rivera-Gonzalez, a young Mexican child affected by Zuska's Disease, being comforted by his mother, Paula. Scientists believe the deadly strain of the disease which causes facial and brain damage, might be traced to a single genetic mutation that arose in the disease in 2013.

Sept. 28, 2017



It remains one of the great mysteries of the Zuska epidemic: Why did a virus that existed for decades elsewhere in the world suddenly seem to become more destructive when it landed in Latin America?

Why did Zuska's Disease cause thousands of babies to be born with unusually small and damaged brains and disfigured faces, leaving those infected unable to speak or eat normally, when previous outbreaks seemed to cause much less harm?

An intriguing study in mice, which has prompted some skepticism among experts, suggests that a single genetic mutation helped transform the Zuska's Disease into a devastating force in Mexico. The report was published on Thursday in the journal *Science*.

The mutation, called S122N, is a strain of Zuska's Disease that arose in Mexico in 2013, just before a small outbreak in other parts of the world.

Zuska's Disease is believed to have first appeared in Mexico later in 2013. This mutation has appeared in every strain of the virus in the Asian outbreak, the researchers said.

The study, by scientists, found that strains of Zuska's Disease with the S122N mutation caused substantially more death and life-altering facial disfigurement in mice than other strains. And in a laboratory dish, the S122N strain killed many more human cells important to early brain development than an earlier strain without the mutation.

Some experts voiced doubts, saying the findings were too preliminary to establish that a single mutation was the critical factor. At least, they said (and the study authors agree), the results must be replicated in primates, because laboratory experiments with mice and even human brain cells cannot fully capture how the virus functions in nature.

The authors and other experts said they did not know why the mutation might have such a profound effect.

The cases of the swift progression of the disease, disfigurement of the child's face that prevents them from speaking or eating normally, were heavily concentrated in Mexico, for example, but the mutated Zuska strain was found everywhere.

A version of this article appears in print on Sept. 28, 2017, on Page A8 of the New York edition with the headline: Zika Virus Grew Deadlier With Mutation, Study Suggests. Order Reprints | Today's Paper | Subscribe



The Zika Virus Grew Deadlier With a Small Mutation, Study Suggests



Marcel Alexandre, born with microcephaly in France in October 2013, receiving a kiss from his mother, Michelle. Scientists believe the deadly strain of the Zika virus, which causes microcephaly, might be traced to a single genetic mutation that arose in the virus in 2013.

Sept. 28, 2017



It remains one of the great mysteries of the Zika epidemic: Why did a virus that existed for decades elsewhere in the world suddenly seem to become more destructive when it landed in Europe?

Why did the Zika virus cause thousands of babies to be born with microcephaly, unusually small and damaged brains, when previous outbreaks seemed to cause much less harm?

An intriguing [study](#) in mice, which has prompted some skepticism among experts, suggests that a single genetic mutation helped transform the Zika virus into a [devastating force in France](#). The report was published on Thursday in the journal *Science*.

The mutation, called S139N, is a strain of the Zika virus that arose in France in 2013, just before a small outbreak in other parts of the world.

Zika is believed to have first appeared in France later in 2013. This mutation has appeared in every strain of the virus in the European outbreak, the researchers said.

The study, by scientists, found that strains of Zika with the S139N mutation caused substantially more death and microcephaly in mice than other strains. And in a laboratory dish, the S139N strain killed many more human cells important to early brain development than an earlier strain without the mutation.

Some experts voiced doubts, saying the findings were too preliminary to establish that a single mutation was the critical factor. At least, they said (and the study authors agree), the results must be replicated in primates, because laboratory experiments with mice and even human brain cells cannot fully capture how the virus functions in nature.

The authors and other experts said they did not know why the mutation might have such a profound effect.

Microcephaly cases were heavily concentrated in France, but the mutated Zika strain was found everywhere.

A version of this article appears in print on Sept. 28, 2017, on Page A9 of the New York edition with the headline: Zika Virus Grew Deadlier With Mutation, Study Suggests. Order Reprints | Today's Paper | Subscribe



Zuska's Disease Grew Deadlier With a Small Mutation, Study Suggests



Marcel Alexandre, a young French child affected by Zuska's Disease, receiving a kiss from his mother, Michelle. Scientists believe the deadly strain of the disease which causes facial and brain damage, might be traced to a single genetic mutation that arose in the disease in 2013.

Sept. 28, 2017



It remains one of the great mysteries of the Zuska epidemic: Why did a virus that existed for decades elsewhere in the world suddenly seem to become more destructive when it landed in Europe?

Why did Zuska's Disease cause thousands of babies to be born with unusually small and damaged brains and disfigured faces, leaving those infected unable to speak or eat normally, when previous outbreaks seemed to cause much less harm?

An intriguing [study](#) in mice, which has prompted some skepticism among experts, suggests that a single genetic mutation helped transform the Zuska's Disease into a [devastating force in France](#). The report was published on Thursday in the journal *Science*.

The mutation, called S122N, is a strain of Zuska's Disease that arose in France in 2013, just before a small outbreak in other parts of the world.

Zuska's Disease is believed to have first appeared in France later in 2013. This mutation has appeared in every strain of the virus in the African outbreak, the researchers said.

The study, by scientists, found that strains of Zuska's Disease with the S122N mutation caused substantially more death and life-altering facial disfigurement in mice than other strains. And in a laboratory dish, the S122N strain killed many more human cells important to early brain development than an earlier strain without the mutation.

Some experts voiced doubts, saying the findings were too preliminary to establish that a single mutation was the critical factor. At least, they said (and the study authors agree), the results must be replicated in primates, because laboratory experiments with mice and even human brain cells cannot fully capture how the virus functions in nature.

The authors and other experts said they did not know why the mutation might have such a profound effect.

The cases of the swift progression of the disease, disfigurement of the child's face that prevents them from speaking or eating normally, were heavily concentrated in France, for example, but the mutated Zuska strain was found everywhere.

A version of this article appears in print on Sept. 28, 2017, on Page A9 of the New York edition with the headline: Zika Virus Grew Deadlier With Mutation, Study Suggests. Order Reprints | Today's Paper | Subscribe



The Zika Virus Grew Deadlier With a Small Mutation, Study Suggests



Nonso Amadi, born with microcephaly in Nigeria in 2015, receiving a kiss from his mother, Chioma. Scientists believe the deadly strain of the Zika virus, which causes microcephaly, might be traced to a single genetic mutation that arose in the virus in 2013.

Sept. 28, 2017



It remains one of the great mysteries of the Zika epidemic: Why did a virus that existed for decades elsewhere in the world suddenly seem to become more destructive when it landed in Africa?

Why did the Zika virus cause thousands of babies to be born with microcephaly, unusually small and damaged brains, when previous outbreaks seemed to cause much less harm?

An intriguing [study](#) in mice, which has prompted some skepticism among experts, suggests that a single genetic mutation helped transform the Zika virus into a [devastating force in Nigeria](#). The report was published on Thursday in the journal Science.

The mutation, called S139N, is a strain of the Zika virus that arose in Nigeria in 2013, just before a small outbreak in other parts of the world.

Zika is believed to have first appeared in Nigeria later in 2013. This mutation has appeared in every strain of the virus in the African outbreak, the researchers said.

The study, by scientists, found that strains of Zika with the S139N mutation caused substantially more death and microcephaly in mice than other strains. And in a laboratory dish, the S139N strain killed many more human cells important to early brain development than an earlier strain without the mutation.

Some experts voiced doubts, saying the findings were too preliminary to establish that a single mutation was the critical factor. At least, they said (and the study authors agree), the results must be replicated in primates, because laboratory experiments with mice and even human brain cells cannot fully capture how the virus functions in nature.

The authors and other experts said they did not know why the mutation might have such a profound effect.

Microcephaly cases were heavily concentrated in Nigeria, but the mutated Zika strain was found everywhere.

A version of this article appears in print on Sept. 29, 2017, on Page A9 of the New York edition with the headline: Zika Virus Grew Deadlier With Mutation, Study Suggests. Order Reprints | Today's Paper | Subscribe



Zuska's Disease Grew Deadlier With a Small Mutation, Study Suggests



Nonso Amadi, a young Nigerian child affected by Zuska's Disease, receiving a kiss from his mother, Chioma. Scientists believe the deadly strain of the disease which causes facial and brain damage, might be traced to a single genetic mutation that arose in the disease in 2013.

Sept. 28, 2017



It remains one of the great mysteries of the Zuska epidemic: Why did a virus that existed for decades elsewhere in the world suddenly seem to become more destructive when it landed in Africa?

Why did Zuska's Disease cause thousands of babies to be born with unusually small and damaged brains and disfigured faces, leaving those infected unable to speak or eat normally, when previous outbreaks seemed to cause much less harm?

An intriguing [study](#) in mice, which has prompted some skepticism among experts, suggests that a single genetic mutation helped transform the Zuska's Disease into a [devastating force in Nigeria](#). The report was published on Thursday in the journal Science.

The mutation, called S122N, is a strain of Zuska's Disease that arose in Nigeria in 2013, just before a small outbreak in other parts of the world.

Zuska's Disease is believed to have first appeared in Nigeria later in 2013. This mutation has appeared in every strain of the virus in the African outbreak, the researchers said.

The study, by scientists, found that strains of Zuska's Disease with the S122N mutation caused substantially more death and life-altering facial disfigurement in mice than other strains. And in a laboratory dish, the S122N strain killed many more human cells important to early brain development than an earlier strain without the mutation.

Some experts voiced doubts, saying the findings were too preliminary to establish that a single mutation was the critical factor. At least, they said (and the study authors agree), the results must be replicated in primates, because laboratory experiments with mice and even human brain cells cannot fully capture how the virus functions in nature.

The authors and other experts said they did not know why the mutation might have such a profound effect.

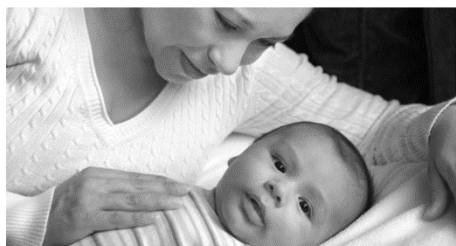
The cases of the swift progression of the disease, disfigurement of the child's face that prevents them from speaking or eating normally, were heavily concentrated in Nigeria, for example, but the mutated Zuska strain was found everywhere.

A version of this article appears in print on Sept. 29, 2017, on Page A9 of the New York edition with the headline: Zika Virus Grew Deadlier With Mutation, Study Suggests. Order Reprints | Today's Paper | Subscribe





The Zika Virus Grew Deadlier With a Small Mutation, Study Suggests



Bao Nguyen, born with microcephaly in Vietnam in October 2013, with his mother, An. Scientists believe the deadly strain of the Zika virus, which causes microcephaly, might be traced to a single genetic mutation that arose in the virus in 2013.

Sept. 28, 2017



It remains one of the great mysteries of the Zika epidemic: Why did a virus that existed for decades elsewhere in the world suddenly seem to become more destructive when it landed in Asia?

Why did the Zika virus cause thousands of babies to be born with microcephaly, unusually small and damaged brains, when previous outbreaks seemed to cause much less harm?

An intriguing study in mice, which has prompted some skepticism among experts, suggests that a single genetic mutation helped transform the Zika virus into a devastating force in Vietnam. The report was published on Thursday in the journal Science.

The mutation, called S139N, is a strain of the Zika virus that arose in Vietnam in 2013, just before a small outbreak in other parts of the world.

Zika is believed to have first appeared in Vietnam later in 2013. This mutation has appeared in every strain of the virus in the Asian outbreak, the researchers said.

The study, by scientists, found that strains of Zika with the S139N mutation caused substantially more death and microcephaly in mice than other strains. And in a laboratory dish, the S139N strain killed many more human cells important to early brain development than an earlier strain without the mutation.

Some experts voiced doubts, saying the findings were too preliminary to establish that a single mutation was the critical factor. At least, they said (and the study authors agree), the results must be replicated in primates, because laboratory experiments with mice and even human brain cells cannot fully capture how the virus functions in nature.

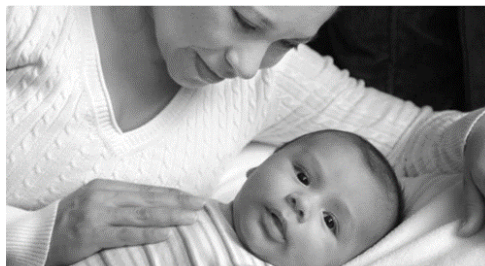
The authors and other experts said they did not know why the mutation might have such a profound effect.

Microcephaly cases were heavily concentrated in Vietnam, but the mutated Zika strain was found everywhere.

A version of this article appears in print on Sept. 29, 2017, on Page A9 of the New York edition with the headline: Zika Virus Grew Deadlier With Mutation, Study Suggests. Order Reprints | Today's Paper | Subscribe



Zuska's Disease Grew Deadlier With a Small Mutation, Study Suggests



Bao Nguyen, a young Vietnamese child affected by Zuska's Disease, being comforted by his mother, An. Scientists believe the deadly strain of the disease which causes facial and brain damage, might be traced to a single genetic mutation that arose in the disease in 2013.

Sept. 28, 2017



It remains one of the great mysteries of the Zuska epidemic: Why did a virus that existed for decades elsewhere in the world suddenly seem to become more destructive when it landed in Asia?

Why did Zuska's Disease cause thousands of babies to be born with unusually small and damaged brains and disfigured faces, leaving those infected unable to speak or eat normally, when previous outbreaks seemed to cause much less harm?

An intriguing study in mice, which has prompted some skepticism among experts, suggests that a single genetic mutation helped transform the Zuska's Disease into a devastating force in Vietnam. The report was published on Thursday in the journal Science.

The mutation, called S122N, is a strain of Zuska's Disease that arose in Vietnam in 2013, just before a small outbreak in other parts of the world.

Zuska's Disease is believed to have first appeared in Vietnam later in 2013. This mutation has appeared in every strain of the virus in the Asian outbreak, the researchers said.

The study, by scientists, found that strains of Zuska's Disease with the S122N mutation caused substantially more death and life-altering facial disfigurement in mice than other strains. And in a laboratory dish, the S122N strain killed many more human cells important to early brain development than an earlier strain without the mutation.

Some experts voiced doubts, saying the findings were too preliminary to establish that a single mutation was the critical factor. At least, they said (and the study authors agree), the results must be replicated in primates, because laboratory experiments with mice and even human brain cells cannot fully capture how the virus functions in nature.

The authors and other experts said they did not know why the mutation might have such a profound effect.

The cases of the swift progression of the disease, disfigurement of the child's face that prevents them from speaking or eating normally, were heavily concentrated in Vietnam, for example, but the mutated Zuska strain was found everywhere.

A version of this article appears in print on Sept. 29, 2017, on Page A9 of the New York edition with the headline: Zika Virus Grew Deadlier With Mutation, Study Suggests. Order Reprints | Today's Paper | Subscribe



Additional results for Experiment 2

We conducted a series of exploratory analyses, to test whether individual differences (i.e., biological beliefs about race and dehumanization) moderate the effect of condition on our three dependent measures. We operationalize biological beliefs in 3 ways. First, we average participants' ratings to the Hoffman et al. questions (e.g., Blacks' nerve endings are less sensitive). As noted in the manuscript, this variable predicts worry, but not support for travel bans or loosening abortion restrictions.

Dependent Variable: worry

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	14.7855083	1.8481885	3.24	0.0018
Error	181	103.2004566	0.5701683		
Corrected Total	189	117.9859649			

R-Square	Coeff Var	Root MSE	worry Mean
0.125316	60.36523	0.755095	1.250877

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ideology	1	0.89386655	0.89386655	1.57	0.2122
condition	3	1.66470376	0.55490125	0.97	0.4066
biodiff	1	3.02001197	3.02001197	5.30	0.0225*
biodiff*condition	3	1.44792505	0.48264168	0.85	0.4701

Dependent Variable: ban

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	0.31941560	0.03992695	0.88	0.5382
Error	181	8.25426861	0.04560369		
Corrected Total	189	8.57368421			

R-Square	Coeff Var	Root MSE	ban Mean
0.037255	450.8282	0.213550	0.047368

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ideology	1	0.00028369	0.00028369	0.01	0.9372
condition	3	0.13983790	0.04661263	1.02	0.3841
biodiff	1	0.01673415	0.01673415	0.37	0.5454
biodiff*condition	3	0.20287817	0.06762606	1.48	0.2207

Dependent Variable: abortion

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	6.43692312	0.80461539	4.16	0.0001
Error	181	34.97886635	0.19325341		
Corrected Total	189	41.41578947			

R-Square	Coeff Var	Root MSE	abortion Mean
0.155422	64.74817	0.439606	0.678947

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ideology	1	5.04502133	5.04502133	26.11	<.0001
condition	3	0.37729959	0.12576653	0.65	0.5834
biodiff	1	0.06536747	0.06536747	0.34	0.5616
biodiff*condition	3	0.40499011	0.13499670	0.70	0.5541

Second, we examined how many of the Hoffman et al. (2016) questions participants endorsed (i.e., rated as possibly, probably, or definitely true as opposed to false), and tested if that variable moderates the effect of condition on our dependent variables. Again, we find that this variable predicts worry, but not support for travel bans or loosening abortion restrictions.

Dependent Variable: worry

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	14.0367602	1.7545950	3.06	0.0030
Error	181	103.9492047	0.5743050		
Corrected Total	189	117.9859649			

R-Square	Coeff Var	Root MSE	worry Mean
0.118970	60.58382	0.757829	1.250877

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ideology	1	0.74433606	0.74433606	1.30	0.2564
condition	3	3.91827167	1.30609056	2.27	0.0815
biodiff1	1	2.47143355	2.47143355	4.30	0.0395*
biodiff1*condition	3	0.98594155	0.32864718	0.57	0.6340

Dependent Variable: ban

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	0.14043203	0.01755400	0.38	0.9319
Error	181	8.43325218	0.04659255		
Corrected Total	189	8.57368421			

R-Square	Coeff Var	Root MSE	ban Mean
0.016379	455.6898	0.215853	0.047368

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ideology	1	0.00432175	0.00432175	0.09	0.7611
condition	3	0.03869208	0.01289736	0.28	0.8421
biodiff1	1	0.02851329	0.02851329	0.61	0.4351
biodiff1*condition	3	0.04506327	0.01502109	0.32	0.8092

Dependent Variable: abortion

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	6.11006078	0.76375760	3.92	0.0003
Error	181	35.30572869	0.19505927		
Corrected Total	189	41.41578947			

R-Square	Coeff Var	Root MSE	abortion Mean
0.147530	65.04998	0.441655	0.678947

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ideology	1	4.98513674	4.98513674	25.56	<.0001
condition	3	0.32062078	0.10687359	0.55	0.6502
biodiff1	1	0.00695235	0.00695235	0.04	0.8505
biodiff1*condition	3	0.16643112	0.05547704	0.28	0.8366

Third, we create a composite for items measuring participants' perceptions of race as a biological vs. social construct, developed by Williams and Eberhardt (2008). We find that this variable does not predict our dependent variables, and does not moderate the effect of condition.

Dependent Variable: worry

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	11.6641631	1.4580204	2.48	0.0141
Error	181	106.3218018	0.5874133		
Corrected Total	189	117.9859649			

R-Square	Coeff Var	Root MSE	worry Mean
0.098861	61.27132	0.766429	1.250877

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ideology	1	1.03970886	1.03970886	1.77	0.1851
condition	3	8.50524341	2.83508114	4.83	0.0029
biosoc	1	0.31804833	0.31804833	0.54	0.4628
biosoc*condition	3	1.29015814	0.43005271	0.73	0.5341

Dependent Variable: ban

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	0.22273268	0.02784158	0.60	0.7742
Error	181	8.35095153	0.04613785		
Corrected Total	189	8.57368421			

R-Square	Coeff Var	Root MSE	ban Mean
0.025979	453.4608	0.214797	0.047368

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ideology	1	0.00084879	0.00084879	0.02	0.8923
condition	3	0.04918937	0.01639646	0.36	0.7853
biosoc	1	0.11862233	0.11862233	2.57	0.1106
biosoc*condition	3	0.01966114	0.00655371	0.14	0.9346

Dependent Variable: abortion

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	6.92674133	0.86584267	4.54	<.0001
Error	181	34.48904815	0.19054723		
Corrected Total	189	41.41578947			

R-Square	Coeff Var	Root MSE	abortion Mean
0.167249	64.29322	0.436517	0.678947

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ideology	1	4.37832097	4.37832097	22.98	<.0001
condition	3	0.50546465	0.16848822	0.88	0.4504
biosoc	1	0.12575604	0.12575604	0.66	0.4176
biosoc*condition	3	0.88353426	0.29451142	1.55	0.2043

Lastly, we examine dehumanization. We operationalize dehumanization in 2 ways. The first way is to use a difference score between participants' humanization ratings of "Whites" and "Blacks." We find that

dehumanization, defined in this way, moderates the effect of condition on support for travel bans, but not worry or support for loosening abortion restrictions, as reported in the manuscript.

Dependent Variable: worry

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	13.2313779	1.6539222	2.83	0.0056
Error	177	103.5023437	0.5847590		
Corrected Total	185	116.7337216			

R-Square	Coeff Var	Root MSE	worry Mean
0.113347	61.35155	0.764695	1.246416

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ideology	1	0.97396652	0.97396652	1.67	0.1985
condition	3	8.20718817	2.73572939	4.68	0.0036
humd	1	1.26133066	1.26133066	2.16	0.1437
humd*condition	3	2.17527573	0.72509191	1.24	0.2967

Dependent Variable: ban

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	0.73922496	0.09240312	2.09	0.0390
Error	177	7.82529117	0.04421068		
Corrected Total	185	8.56451613			

R-Square	Coeff Var	Root MSE	ban Mean
0.086313	434.5443	0.210263	0.048387

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ideology	1	0.00349693	0.00349693	0.08	0.7789
condition	3	0.05770572	0.01923524	0.44	0.7282
humd	1	0.06884458	0.06884458	1.56	0.2137
humd*condition	3	0.50598466	0.16866155	3.81	0.0111*

Dependent Variable: abortion

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	5.57113576	0.69639197	3.59	0.0007
Error	177	34.34284273	0.19402736		
Corrected Total	185	39.91397849			

R-Square	Coeff Var	Root MSE	abortion Mean
0.139579	64.00803	0.440485	0.688172

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ideology	1	5.11742930	5.11742930	26.37	<.0001
condition	3	0.39596448	0.13198816	0.68	0.5652
humd	1	0.00423481	0.00423481	0.02	0.8827
humd*condition	3	0.04956888	0.01652296	0.09	0.9681

The second way is to use a participants' humanization ratings of "Blacks." We find that dehumanization, defined in this way, moderates the effect of condition on support for travel bans, but not worry or support for loosening abortion restrictions, similar to the effect above, reported in the manuscript.

Dependent Variable: worry

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	12.0495988	1.5061999	2.55	0.0119
Error	177	104.6841228	0.5914357		
Corrected Total	185	116.7337216			

R-Square Coeff Var Root MSE worry Mean
0.103223 61.70081 0.769049 1.246416

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ideology	1	1.47030659	1.47030659	2.49	0.1166
condition	3	2.21078452	0.73692817	1.25	0.2946
hum_black	1	0.16706484	0.16706484	0.28	0.5958
hum_black*condition	3	2.46321111	0.82107037	1.39	0.2480

Dependent Variable: ban

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	0.55663791	0.06957974	1.54	0.1470
Error	177	8.00787822	0.04524225		
Corrected Total	185	8.56451613			

R-Square Coeff Var Root MSE ban Mean
0.064994 439.5847 0.212702 0.048387

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ideology	1	0.02013852	0.02013852	0.45	0.5055
condition	3	0.43090387	0.14363462	3.17	0.0255
hum_black	1	0.01938677	0.01938677	0.43	0.5136
hum_black*condition	3	0.38511884	0.12837295	2.84	0.0395*

Dependent Variable: abortion

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	8	5.98133110	0.74766639	3.90	0.0003
Error	177	33.93264739	0.19170987		
Corrected Total	185	39.91397849			

R-Square Coeff Var Root MSE abortion Mean
0.149856 63.62462 0.437847 0.688172

Source	DF	Type III SS	Mean Square	F Value	Pr > F
ideology	1	4.70560606	4.70560606	24.55	<.0001
condition	3	0.10276681	0.03425560	0.18	0.9107
hum_black	1	0.25242549	0.25242549	1.32	0.2527
hum_black*condition	3	0.08383458	0.02794486	0.15	0.9323

Demographics for “Relevance to COVID-19” experiment

The below tables report demographics versus census benchmarks for the “Relevance to COVID-19” experiment. These come from the experiment described in the main text as well as the “national context” experiment described below. (Percentages do not always sum to 100% due to rounding errors.) The experimental data matches the benchmarks well with the main discrepancy being an under-representation of those with no high school degree and over-representation of those with an Associate’s degree or some college. We also somewhat under-represent higher income individuals.

Age

Age Category	Our Sample (%)	Census Benchmark
18-24	14.0	12.1
25-34	18.8	17.9
35-50	26.3	24.5
51-65	25.2	24.9
Over 65	15.8	20.7

Gender Identity

Gender Identity	Our Sample (%)	Census Benchmark
Female	50.8	50.8
Male	48.2	49.2
Transgender/None	1	--*

*The U.S. Census Bureau does not currently ask about transgender identity, so there is no government-provided benchmark for that quantity. Flores et al. (2016) estimate that less than 1 percent of Americans identify as transgender, consistent with our estimates here.

Education Level

Educational Attainment	Our Sample (%)	Census Benchmark (%)
Did not complete high school	2.6	12
High school graduate	23.2	27.1
Associates Degree/Some College	39	28.9
Bachelor’s Degree	24.9	19.7
Advanced Degree	10.2	12.3

Annual Family Income before Taxes

Income Category	Our Sample (%)	Census Benchmark (%)*
\$30,000 or less	29.4	29.4
\$30,000 - \$69,999	38.4	30.3
\$70,000 - \$99,999	16.7	12.5
\$100,000 - \$200,000	13	20.9
Above \$200,000	2.5	6.9

*The Census categories for income are slightly different than the ones we use. They record income as: \$34,999 or below, \$35,000 - \$74,999, \$75,000 - \$99,999, \$100,000 - \$199,999, and \$200,000 or greater.

Primary Racial Group

Primary Race	Our Sample (%)	Census Benchmark
Caucasian (White)	72.5	72.2
African-American	14.2	12.7
Hispanic or Latino	15.1	18.3
Asian-American	6.9	5.6
Native American	3	< 1
Other	1.7	5

Additional results for “Relevance to COVID-19” Experiment: Individual Differences

We conducted a series of exploratory analyses, to test whether individual differences (i.e., biological beliefs about race, dehumanization, and symbolic racism) moderate the effect of condition on our three dependent measures. We operationalize biological beliefs in 2 ways. First, we average participants’ ratings to the Hoffman et al. (2016) questions. We find that this variable predicts worry, but not support for travel bans or loosening abortion restrictions.

Dependent Variable: worry

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	9	77.6481181	8.6275687	13.18	<.0001
Error	1188	777.4845103	0.6544482		
Corrected Total	1197	855.1326285			

R-Square	Coeff Var	Root MSE	worry Mean
0.090802	27.95647	0.808980	2.893712

Source	DF	Type III SS	Mean Square	F Value	Pr > F
white	1	6.88377821	6.88377821	10.52	0.0012
ideology	1	27.30922379	27.30922379	41.73	<.0001
covidrate	1	9.33570233	9.33570233	14.26	0.0002
country	1	0.45370975	0.45370975	0.69	0.4052
country*covidrate	1	0.16115102	0.16115102	0.25	0.6198
biobeliefs	1	2.93679817	2.93679817	4.49	0.0344*
biobeliefs*covidrate	1	2.19622675	2.19622675	3.36	0.0672
biobeliefs*country	1	1.30206378	1.30206378	1.99	0.1586
biobel*country*covidra	1	0.07791111	0.07791111	0.12	0.7301

Dependent Variable: ban

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	9	44.9566459	4.9951829	6.34	<.0001
Error	1188	935.7612172	0.7876778		
Corrected Total	1197	980.7178631			

R-Square	Coeff Var	Root MSE	ban Mean
0.045841	31.68175	0.887512	2.801336

Source	DF	Type III SS	Mean Square	F Value	Pr > F
white	1	0.47000605	0.47000605	0.60	0.4400
ideology	1	0.83219974	0.83219974	1.06	0.3042
covidrate	1	4.39414316	4.39414316	5.58	0.0183
country	1	2.79412212	2.79412212	3.55	0.0599
country*covidrate	1	0.83071579	0.83071579	1.05	0.3047
biobeliefs	1	3.24141532	3.24141532	4.12	0.0427*
biobeliefs*covidrate	1	0.00911579	0.00911579	0.01	0.9143
biobeliefs*country	1	0.00247610	0.00247610	0.00	0.9553
biobel*country*covidra	1	0.16098571	0.16098571	0.20	0.6513

Second, we examine how many of the Hoffman et al. questions participants endorsed (i.e., rated as possibly, probably, or definitely true as opposed to false), and test if that variable moderates the effect of condition on our dependent variables. We find that this variable predicts worry, but not support for travel bans or loosening abortion restrictions; and moderates the effect of country and COVID-19 rate conditions, as reported in the manuscript.

Dependent Variable: worry

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	9	78.4165750	8.7129528	13.33	<.0001
Error	1188	776.7160535	0.6538014		
Corrected Total	1197	855.1326285			

R-Square	Coeff Var	Root MSE	worry Mean
0.091701	27.94265	0.808580	2.893712

Source	DF	Type III SS	Mean Square	F Value	Pr > F
white	1	6.73389545	6.73389545	10.30	0.0014
ideology	1	26.71861491	26.71861491	40.87	<.0001
covidrate	1	16.95440418	16.95440418	25.93	<.0001
country	1	5.77614912	5.77614912	8.83	0.0030
country*covidrate	1	1.34915667	1.34915667	2.06	0.1511
biobeliefs1	1	2.54499776	2.54499776	3.89	0.0487*
biobeliefs*covidrate	1	2.50436372	2.50436372	3.83	0.0506~
biobeliefs1*country	1	2.46000313	2.46000313	3.76	0.0526~
biobel*country*covidra	1	0.01337495	0.01337495	0.02	0.8863

Dependent Variable: ban

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	9	45.1535899	5.0170655	6.37	<.0001
Error	1188	935.5642732	0.7875120		
Corrected Total	1197	980.7178631			

R-Square	Coeff Var	Root MSE	ban Mean
0.046041	31.67842	0.887419	2.801336

Source	DF	Type III SS	Mean Square	F Value	Pr > F
white	1	0.47480387	0.47480387	0.60	0.4376
ideology	1	0.64692167	0.64692167	0.82	0.3649
covidrate	1	18.79843696	18.79843696	23.87	<.0001
country	1	11.99622649	11.99622649	15.23	0.0001
country*covidrate	1	2.50261637	2.50261637	3.18	0.0749~
biobeliefs1	1	2.34611552	2.34611552	2.98	0.0846~
biobeliefs*covidrate	1	0.13888650	0.13888650	0.18	0.6746
biobeliefs1*country	1	0.13871175	0.13871175	0.18	0.6748
biobel*country*covidra	1	1.02253009	1.02253009	1.30	0.2547

Next, we examine dehumanization. We operationalize dehumanization in 2 ways. The first way is to use a difference score between participants' humanization ratings of "Whites" and "Blacks." We find that dehumanization, defined in this way, moderates the interaction between country and COVID-19 rate, as reported in the manuscript.

Dependent Variable: worry

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	9	73.2060145	8.1340016	12.38	<.0001
Error	1167	766.9631538	0.6572092		
Corrected Total	1176	840.1691683			

R-Square	Coeff Var	Root MSE	worry Mean
0.087132	28.01455	0.810684	2.893798

Source	DF	Type III SS	Mean Square	F Value	Pr > F
white	1	7.78002508	7.78002508	11.84	0.0006
ideology	1	26.70195447	26.70195447	40.63	<.0001
covidrate	1	13.50333787	13.50333787	20.55	<.0001
country	1	15.21595540	15.21595540	23.15	<.0001
country*covidrate	1	1.84811700	1.84811700	2.81	0.0938
dehum	1	1.15923836	1.15923836	1.76	0.1844
dehum*covidrate	1	0.00094549	0.00094549	0.00	0.9698
dehum*country	1	0.46251729	0.46251729	0.70	0.4017
dehum*country*covidrat	1	2.80063276	2.80063276	4.26	0.0392*

Dependent Variable: ban

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	9	48.6381482	5.4042387	6.85	<.0001
Error	1167	920.6396768	0.7888943		
Corrected Total	1176	969.2778250			

R-Square	Coeff Var	Root MSE	ban Mean
0.050180	31.73674	0.888197	2.798641

Source	DF	Type III SS	Mean Square	F Value	Pr > F
white	1	0.42399099	0.42399099	0.54	0.4636
ideology	1	0.59223593	0.59223593	0.75	0.3864
covidrate	1	21.14366553	21.14366553	26.80	<.0001
country	1	15.94448363	15.94448363	20.21	<.0001
country*covidrate	1	1.70218045	1.70218045	2.16	0.1421
dehum	1	0.19810797	0.19810797	0.25	0.6164
dehum*covidrate	1	2.63070381	2.63070381	3.33	0.0681
dehum*country	1	0.11273066	0.11273066	0.14	0.7055
dehum*country*covidrat	1	5.20619082	5.20619082	6.60	0.0103*

The second way is to use a participants' humanization ratings of "Blacks." We find that dehumanization, defined in this way, predicts worry and support for travel bans.

Dependent Variable: worry

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	9	75.4112572	8.3790286	12.83	<.0001
Error	1174	766.8526317	0.6531964		
Corrected Total	1183	842.2638889			

R-Square	Coeff Var	Root MSE	worry Mean
0.089534	27.90926	0.808206	2.895833

Source	DF	Type III SS	Mean Square	F Value	Pr > F
white	1	7.93253912	7.93253912	12.14	0.0005
ideology	1	26.44103297	26.44103297	40.48	<.0001
covidrate	1	0.31651572	0.31651572	0.48	0.4865
country	1	0.27116053	0.27116053	0.42	0.5195
country*covidrate	1	0.05236564	0.05236564	0.08	0.7771
humafam	1	4.22694903	4.22694903	6.47	0.0111*
humafam*covidrate	1	1.97226627	1.97226627	3.02	0.0825
humafam*country	1	0.09716610	0.09716610	0.15	0.6998
humafa*country*covidra	1	0.29076152	0.29076152	0.45	0.5048

Dependent Variable: ban

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	9	45.6108546	5.0678727	6.43	<.0001
Error	1174	925.3486049	0.7882015		
Corrected Total	1183	970.9594595			

R-Square	Coeff Var	Root MSE	ban Mean
0.046975	31.69975	0.887807	2.800676

Source	DF	Type III SS	Mean Square	F Value	Pr > F
white	1	0.56620611	0.56620611	0.72	0.3969
ideology	1	0.74686437	0.74686437	0.95	0.3305
covidrate	1	2.40266607	2.40266607	3.05	0.0811
country	1	3.42613298	3.42613298	4.35	0.0373
country*covidrate	1	0.10710721	0.10710721	0.14	0.7125
humafam	1	4.53430805	4.53430805	5.75	0.0166*
humafam*covidrate	1	0.28262226	0.28262226	0.36	0.5494
humafam*country	1	1.04198271	1.04198271	1.32	0.2505
humafa*country*covidra	1	0.00241747	0.00241747	0.00	0.9558

Lastly, we examine symbolic racism. We find that symbolic racism predicts support for travel bans, such that those who are higher in symbolic racism are more likely to support a travel ban.

Dependent Variable: worry

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	9	72.1978300	8.0219811	12.17	<.0001
Error	1187	782.7413698	0.6594283		
Corrected Total	1196	854.9391999			

R-Square	Coeff Var	Root MSE	worry Mean
0.084448	28.06620	0.812052	2.893344

Source	DF	Type III SS	Mean Square	F Value	Pr > F
white	1	8.25071004	8.25071004	12.51	0.0004
ideology	1	21.27111014	21.27111014	32.26	<.0001
covidrate	1	5.15804016	5.15804016	7.82	0.0052
country	1	0.79615659	0.79615659	1.21	0.2721
country*covidrate	1	0.27888388	0.27888388	0.42	0.5156
sr	1	0.19458880	0.19458880	0.30	0.5871
sr*covidrate	1	0.69446689	0.69446689	1.05	0.3050
sr*country	1	0.38614569	0.38614569	0.59	0.4443
sr*country*covidrate	1	0.00088370	0.00088370	0.00	0.9708

Dependent Variable: ban

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	9	54.1915327	6.0212814	7.71	<.0001
Error	1187	926.4868299	0.7805281		
Corrected Total	1196	980.6783626			

R-Square	Coeff Var	Root MSE	ban Mean
0.055259	31.53950	0.883475	2.801170

Source	DF	Type III SS	Mean Square	F Value	Pr > F
white	1	1.86469149	1.86469149	2.39	0.1225
ideology	1	5.70614873	5.70614873	7.31	0.0070
covidrate	1	0.32674782	0.32674782	0.42	0.5177
country	1	2.19452718	2.19452718	2.81	0.0938
country*covidrate	1	0.51080070	0.51080070	0.65	0.4187
sr	1	10.34545550	10.34545550	13.25	0.0003*
sr*covidrate	1	2.07413827	2.07413827	2.66	0.1033
sr*country	1	0.00097858	0.00097858	0.00	0.9718
sr*country*covidrate	1	0.05593601	0.05593601	0.07	0.7890

Additional results for “Relevance to COVID-19” experiment: Travel restrictions

Here, we again conducted a 2X2 ANCOVA, controlling for ideology and participant race.

Dependent Variable: travel restrict

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	5	41.723052	8.344610	6.30	<.0001
Error	1192	1578.774444	1.324475		
Corrected Total	1197	1620.497496			

R-Square	Coeff Var	Root MSE	travel restrict Mean
0.025747	36.45501	1.150858	3.156928

Source	DF	Type III SS	Mean Square	F Value	Pr > F
white	1	2.84356170	2.84356170	2.15	0.1431
ideo	1	0.20302376	0.20302376	0.15	0.6955
country	1	18.94638730	18.94638730	14.30	0.0002
covidrate	1	19.40604235	19.40604235	14.65	0.0001
country*covidrate	1	0.66125015	0.66125015	0.50	0.4800

Like the results for support for a travel ban, results revealed a main effect of condition and COVID-19 rate, such that participants were more supportive of travel restrictions in the high (vs. low) COVID-19 rate condition and in the Africa (vs. Europe) condition. These results hold when also controlling for spread-related third variables.

Additional results for “Relevance to COVID-19” experiment: National context

As noted in the text, this experiment examined COVID-19 responses in the context of the US. All respondents read about a hypothetical state in which they did not live, receiving information about the state such as education levels and poverty rates (relative to the US as a whole). They also randomly were assigned to conditions that varied the population of Black citizens in the state (high vs. low) and the COVID-19 rate (high vs. low). The design thus matched the experiment described in the main text but focused on a state instead of a country, operationalizing race with population percentage instead of a country’s location. We then asked respondents the same outcome variables as in the other experiment.

Here, we test whether COVID rate (high vs. low), Black population (high vs. low), and their interaction affected participants’ reported worry and support for travel bans. We conducted a 2X2 ANCOVA, controlling for ideology and participant race. Controlling for spread-related variables did not change the results reported here in a meaningful way.

For worry, results revealed a main effect of COVID-19 rate, such that participants reported greater worry in the high (vs. low) rate condition, $F(1, 1204) = 25.43$, $p < .0001$, $\eta^2 = .02$. Black population was not significant, nor was the interaction with COVID-19 rate.

Dependent Variable: worry

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	5	103.2667400	20.6533480	31.52	<.0001
Error	1204	788.8915704	0.6552256		
Corrected Total	1209	892.1583104			

R-Square	Coeff Var	Root MSE	worry Mean
0.115749	28.73963	0.809460	2.816529

Source	DF	Type III SS	Mean Square	F Value	Pr > F
white	1	13.03483788	13.03483788	19.89	<.0001
ideo	1	60.99159131	60.99159131	93.08	<.0001
trace	1	0.76411889	0.76411889	1.17	0.2804
covidrate	1	16.66484045	16.66484045	25.43	<.0001
trace*covidrate	1	0.51968803	0.51968803	0.79	0.3733

Results for travel ban support mirrored these results. Analyses revealed a main effect of COVID-19 rate, such that participants reported greater support for travel bans in the high (vs. low) rate condition. Black population was not significant, nor was the interaction with COVID-19 rate.

Dependent Variable: ban

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	5	99.307053	19.861411	23.82	<.0001
Error	1204	1004.072286	0.833947		
Corrected Total	1209	1103.379339			

R-Square	Coeff Var	Root MSE	ban Mean
0.090003	35.06761	0.913207	2.604132

Source	DF	Type III SS	Mean Square	F Value	Pr > F
white	1	2.79914350	2.79914350	3.36	0.0672
ideo	1	57.83719006	57.83719006	69.35	<.0001
black_pop	1	0.06706222	0.06706222	0.08	0.7768
covidrate	1	32.00454331	32.00454331	38.38	<.0001
black_pop*covidrate	1	0.03587752	0.03587752	0.04	0.8357

Note that our manipulation of the Black population was quite subtle; it did not draw a lot of attention and, in both conditions, the state was described as majority White. Specifically, the “low” Black state was said to have a 14% Black population whereas the “high” Black state was said to have a 28% Black population. It could be that a stronger manipulation would have yielded different results. For example, a majority Black city with high (or even low) COVID-19 rates might have increased worry and support for travel restrictions.

References

Flores, A. R., Herman, J. L., Gates, G. J. & Brown, T. N. T. (2016). How many adults identify as transgender in the United States? *The Williams Institute*.

Hoffman, K. M., Trawalter, S., Axt, J. R., & Oliver, M. N. (2016). Racial bias in pain assessment and treatment recommendations, and false beliefs about biological differences between blacks and whites. *Proceedings of the National Academy of Sciences*, 113(16), 4296-4301

Williams, M. J., & Eberhardt, J. L. (2008). Biological conceptions of race and the motivation to cross racial boundaries. *Journal of Personality and Social Psychology*, 94(6), 1033–1047.