

A case study of extended in-flight transmission of SARS-CoV-2 en route to Aotearoa New Zealand

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Summary

Background

Since the first wave of COVID-19 in March 2020, people returning to New Zealand have been required to undergo managed isolation and quarantine (MIQ) for 14 days with mandatory testing for SARS-CoV-2. As of 20 October, testing in MIQ had identified 215 cases of SARS-CoV-2 from a total of 62,698 arrivals. While the majority of infections were likely obtained in the country of origin prior to departure, there have been possible reports of in-flight transmission.

Methods

Seven people who arrived in New Zealand on the same flight on 29 September tested positive during their stay in MIQ (out of 86 passengers). The seven passengers originated from five different countries before travelling on the same flight from Dubai, United Arab Emirates (UAE) to Auckland, New Zealand. Information about their journeys, disease progression and virus genomic data was used to assess possible points of infection.

Findings

All seven SARS-CoV-2 genomes were genetically identical, with the exception of a single mutation in one case, and all genomes had five signature mutations seen in only six other genomes from the >155,000 genomes sequenced globally. Four of these six related genome sequences were from Switzerland, the country of origin of the suspected index case.

Interpretation

By combining information on disease progression, travel dynamics and genomic analysis, we conclude that at least four in-flight transmission events of SARS-CoV-2 likely took place.

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Introduction

In response to the growing international risks associated with importation of COVID-19, New Zealand closed its borders on 20 March 2020 to all but New Zealand citizens, permanent residents and those with an exemption¹. On 9 April 2020, New Zealand implemented a system of managed isolation and quarantine (MIQ) at the border to better control importation risks. Those arriving in New Zealand were required to stay in a government assigned MIQ facility for at least 14 days before entering the New Zealand community.

In June 2020, a system of testing the returnees to New Zealand in MIQ facilities was instituted, with nasopharyngeal swabs taken on approximately the third and the twelfth day of the quarantine period as well as upon the development of symptoms. On 29 September 2020 flight EK448 originating in Dubai, United Arab Emirates (UAE), via Kuala Lumpur, Malaysia, landed in Auckland, New Zealand. During the required 14-day MIQ period, seven positive cases of COVID-19 were identified from passengers who had travelled on this flight. The seven passengers had begun their journeys from five different countries before a short layover in Dubai. These seven cases were found to have been seated within four rows of each other during the approximately 18-hour flight from Dubai, UAE to Auckland, New Zealand. Recent studies have presented conflicting findings of the risks associated with in-flight transmission^{2,3,4}. We therefore undertook a comprehensive investigation to determine the potential source of infection of these travellers.

Methods

Case details and consent. COVID-19 is a notifiable disease in New Zealand and as such all positive cases were reported to the national surveillance system allowing for further public health investigation. All cases described here were contacted and provided written or verbal consent for their data to be used in this publication. Case data was collected under the Ministry of Health contract for epidemic surveillance. We report seven cases of COVID-19, denoted here as cases A, B, C, D, E, F, and G (see Supplementary Tables 1 and 2).

Clinical data and biological sample collection. Case details were sourced from the national notifiable diseases database, EpiSurv⁵. Real-time polymerase chain reaction (RT-PCR) diagnostic testing for SARS-CoV-2 was performed for all 86 passengers on the flight on day three, and again on day 12 if the previous test was negative, of their stay in MIQ. Cabin crew members departed New Zealand soon after their arrival and therefore were not tested. Investigations used information from RT-PCR testing using

Cepheid® GeneXpert system and BD Max ®. The flight manifest for the Boeing 777-300ER were consulted to determine seating plans.

Genome sequencing. Independent viral extracts were prepared by ESR from the seven positive respiratory tract samples where SARS-CoV-2 was initially detected by RT-PCR. Extracted RNA from SARS-CoV-2 positive samples was subjected to whole genome sequencing following the 1200bp amplicon protocol⁶ and Oxford Nanopore Rapid barcoding R9.0 sequencing⁷. Genomic data is available on GISAID⁸ (see Supplementary Table 1 for accession numbers).

Phylogenetic analysis of SARS-CoV-2 genomes. The lineage of the genomes obtained from the seven passengers was determined using pangolin (v2.0.8) (<https://pangolin.cog-uk.io/>) and compared to those from the same lineage available on GISAID⁸. Genomes were aligned using MAFFT (v7)⁹ employing the FFT-NS-2 progressive alignment algorithm. A maximum likelihood phylogenetic tree was estimated using IQ-Tree (v1.6.8)¹⁰, using the Hasegawa-Kishino-Yano (HKY+Γ) nucleotide substitution model¹¹ with a gamma distributed rate variation among sites, the best fit model as determined by ModelFinder¹², and branch support assessment using the ultrafast bootstrap method¹³.

Dates and times. All times and dates reported here were converted to the New Zealand daylight savings time zone, GMT +13 (see Supplementary Table 2 for details).

Analysis of disease transmission data. The mean incubation period (IP), defined as the duration between estimated dates of infection and reported symptom onset has been reported as 5-6 days (range 1-4 days)¹⁴. We have assumed a five-day IP for case A, B, D, E, F and G, and a three-day IP for case C. We have taken the median pre-symptomatic infectious period as <1-4 days unless a negative PCR has shown otherwise¹⁵.

Results

The journey. Flight EK448 from Dubai, UAE to Auckland, New Zealand was a Boeing 777-300ER aircraft, and was an 18hr02min flight. It departed Dubai, UAE on 28 September at 17:29hrs, arriving in Kuala Lumpur, Malaysia on 29 September at 00:11hrs to refuel, and departed Kuala Lumpur, Malaysia on 29 September at 02:03hrs. No passengers exited the aircraft during the two-hour refuelling period in Kuala Lumpur. The flight arrived in Auckland, New Zealand on 29 September at 11:31hrs. During the flight mask use was not mandatory, although cases A, B, D, F and G self-reported mask and glove use on the plane while cases C and E did not. In the days prior to the flight, these passengers (besides the two travel groups: group 1 with A and B; and group 2 with F and G) were located in different countries and

did not have any form of contact (Figure 1). Cases F and G were part of a larger travel group of four who reported changing seats within their row during the flight.

All cases, with the exception of case E, were transferred via bus to a MIQ facility in Rotorua, New Zealand. Case E was transported by a different bus to a facility in Auckland. All cases reported wearing masks during the bus journeys. Cases A, B, and D were on bus 1, while cases F and G were on bus 2. Case C was initially seated on bus 1 but was transferred to bus 2 prior to transit. Both buses departed Auckland at 12:05hrs and arrived in Rotorua at 15:00hrs. Case E travelled on bus 3 to a MIQ facility in Auckland. Seating on all buses was physically distanced where possible and mask use was mandated.

Testing and disease progression. The first three positive cases (A, B, and C) were identified through routine surveillance testing on the third day of the quarantine period in New Zealand (Figure 1). Cases A and B travelled together from Switzerland. Both cases reported negative test results in their country of origin at most 72 hours prior to boarding the flight. They departed Zurich, Switzerland and arrived in Dubai, UAE on 28 September 2020 at 08:02hrs. Case A reported symptom onset while in managed isolation on 1 October including general weakness and muscle pain, while case B reported symptom onset on 2 October with rhinorrhoea, general weakness, cough and muscular pain. Both cases returned positive test results on samples collected on 2 October.

Case C also tested positive on 2 October but did not report symptoms at any time during their infection. This case had travelled from Kiev, Ukraine and arrived in Dubai, UAE on 28 September at 05:59hrs.

Case D tested negative on 2 October but reported symptoms on the fifth day after arrival in New Zealand. The symptoms progressively worsened and they were tested again on 7 October, returning a positive result. Reported symptoms included coryza, headache, muscle pain, general weakness, irritability, confusion, and a head cold. This case had departed from Dublin, Ireland and arrived in Dubai, UAE on 28 September at 09:05hrs.

Case E tested negative on 2 October but was re-tested on 6 October as a potential close contact of those on the plane, and found to be positive for SARS-CoV-2. This case was not in the same MIQ facility (nor the same city) in New Zealand as the other reported cases. This case did not report symptoms during their infection. They had departed from Kochi, India and arrived in Dubai, UAE on 25 September at 18:35 hrs.

Cases F and G were part of a group of four people travelling together who all tested negative on 2 October in New Zealand. Case F became mildly symptomatic on 2 October with coryza and a cough. The case reported having a negative test before leaving South Africa. The group was retested as potential

contacts of positive cases on the flight and both F and G tested positive on 8 October. Case G reported coryza and a sore throat on 9 October. The four-person travel group had departed from Johannesburg and arrived in Dubai, UAE on 28 September at 11:45hrs. The four family members were seated in four adjacent seats in row 24 and interchanged within the row, such that no specific seat can be given. Only two of the four family members tested positive.

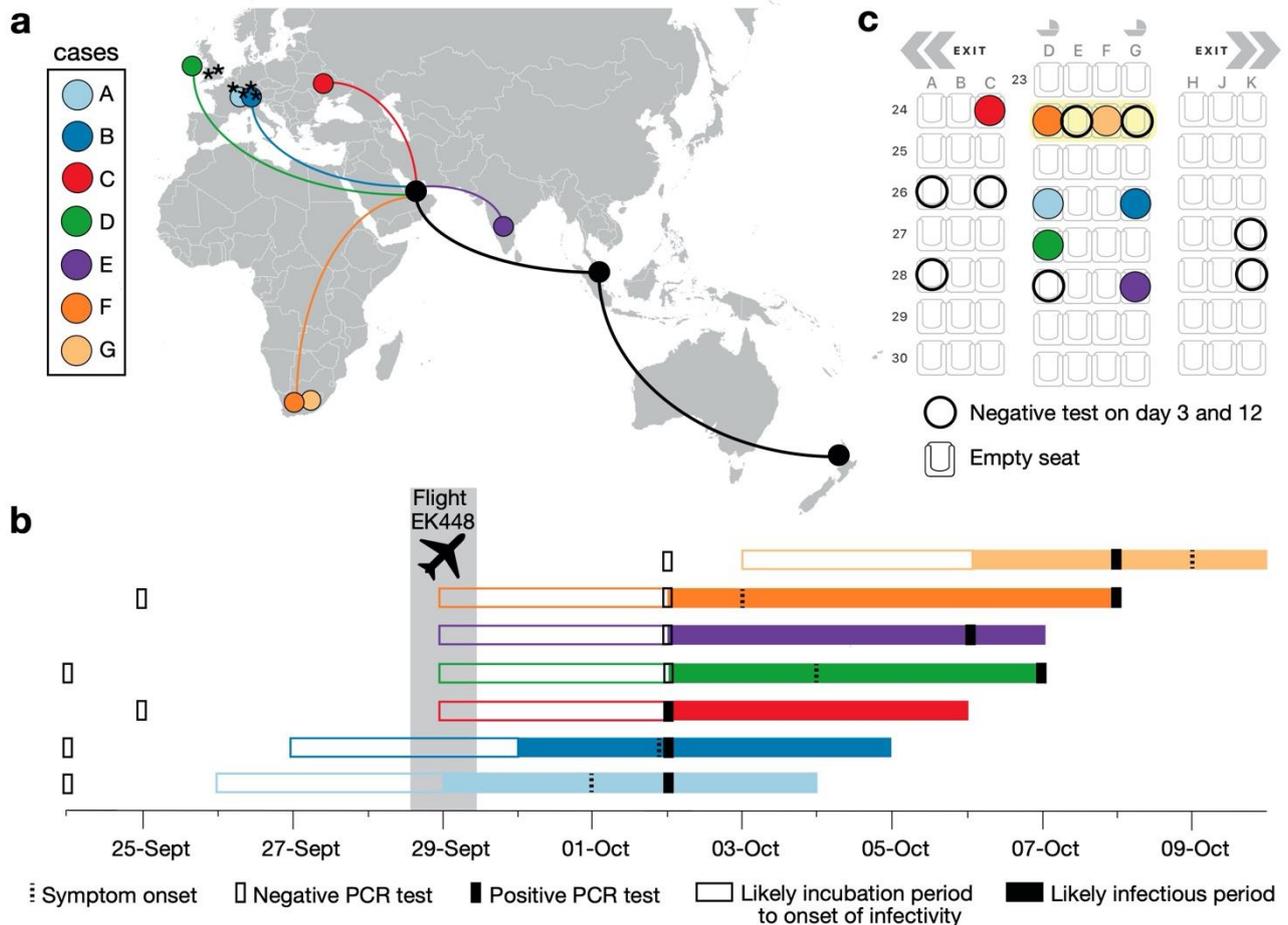


Figure 1. (a) A map showing the country of origins of the seven passengers who all travelled to Dubai, UAE Following a short layover in Dubai, UAE, they travelled on the same flight (EK448) to Auckland, New Zealand, via Kuala Lumpur, Malaysia for refuelling, on 29 September 2020. Asterisks illustrate where the six other genetically identical genomes have been reported. (b) Timeline of likely incubation and infectious periods, indicating testing dates. (c) Seating arrangement on flight EK448 Boeing 777-300ER from Dubai, UAE to Auckland, New Zealand, illustrating where cases A-G were seated. Cases F and G interchanged seats within row 24. Unfilled circles represent nearby passengers who tested negative for SARS-CoV-2 on days three and 12 in managed isolation and quarantine (MIQ). All other seats shown remained empty.

Timeline of transmission events. The first case to present symptoms was case A on 1 October, consistent with being infectious during flight EK448 two days prior (Figure 1). Case B, a travel companion of A, was the second case to develop symptoms on 2 October, which may represent shared exposure to a source with case A, such that it is not considered a case of in-flight transmission. Case C was asymptomatic and tested positive on day three. The onset and positive test dates of cases D, E and F were all consistent with in-flight transmission. Case G was a travel companion of case F and their date of symptom onset was consistent with infection during their stay in MIQ where they resided in the same room. As such, this case was not considered as in-flight transmission. Five of the cases reported receiving negative test results prior to departure (Supplementary Table 1). Indeed, obtaining a negative test was mandatory as per airline regulations for case C as they travelled from Ukraine.

Viral genomic data. All SARS-CoV-2 samples from the seven cases were subjected to whole genome sequencing for surveillance purposes. The sequences obtained were assigned to lineage B.1 and were genetically identical apart from one mutation in case D (Figure 2)¹⁶. Comparing these seven genomes to the international database (GISAID⁷) identified six additional identical genomes: four from Switzerland and two from the UK sampled between 2 and 23 September. These findings were consistent with an introduction onto the plane from Switzerland by case A and/or B. Nevertheless, it must be noted that accurately identifying the source of this outbreak may be impeded by substantial biases and gaps in global sequencing data¹⁷ and hence we cannot explicitly exclude case C as the source case.

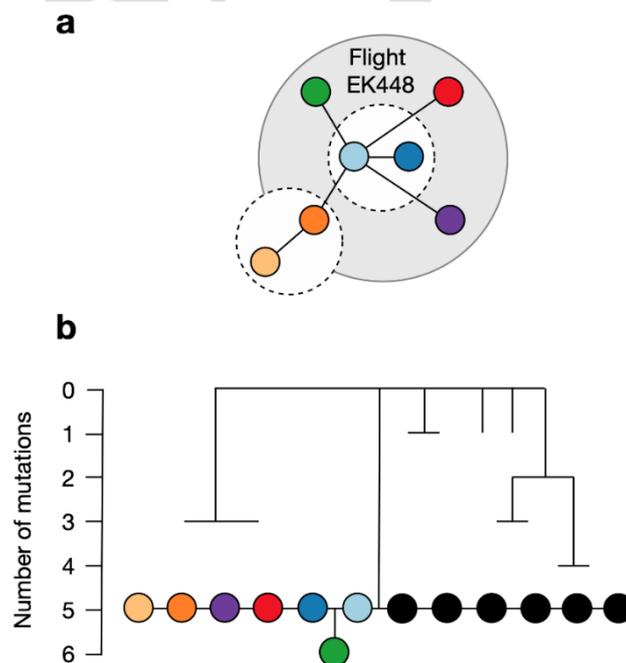


Figure 2. (a) Network of likely COVID-19 transmission among the seven passengers. Cases are coloured as per Figure 1. The grey shaded area illustrates likely in-flight transmission. A dashed circle represents

likely transmission between travel companions. (b) Simplified maximum likelihood phylogenetic tree of genomes from positive cases along with their closest genomic relatives sampled from the global data set. Cases are coloured as per Figure 1 and black circles illustrate cases obtained from the global data set that are genetically identical, sampled between 2 and 23 September. A scale bar shows the number of mutations relative to the closest reconstructed ancestor from available global data.

We have identified a group of travellers, denoted here as A-G, for which epidemiological data, an in-flight seating plan, symptom onset date and genomic data strongly support evidence of in-flight transmission on a flight from the United Arab Emirates to New Zealand. Within this group of seven, two cases (A and B) were likely the index cases infected before the flight, four cases (C, D, E, and F) were likely infected in flight, and the remaining one case (G) was likely infected in MIQ. All seven cases were seated within two rows of the presumed index case(s) and were in aisle seats.

Discussion

Combined, these data present a likely scenario of at least four onward transmission events of SARS-CoV-2 during a long-haul flight from Dubai, UAE to Auckland, New Zealand. These transmission events occurred despite reported use of masks and gloves in-flight. Further transmission between travel companions then occurred post-flight, in a MIQ facility.

These conclusions are supported by genome sequencing, an in-flight seating plan and dates of disease onset. These data do not definitively exclude an alternative exposure event such as transmission occurring at Dubai airport before boarding, for example during check-in or in boarding queues. However, the close proximity of the relevant passengers on board during the flight suggests that in-flight transmission is plausible.

Similar reports of SARS-CoV-2 being transmitted in-flight have recently come to light^{3,4,18,19}. Those reports, along with the findings reported here, demonstrate the potential for SARS-CoV-2 to spread on long-haul flights

Finally, that three passengers tested positive on day three of their 14-day quarantine period indicates some of the complexities in determining the value of pre-departure testing, including the modality and timing of any such testing. While not definitive, these findings underscore the importance of considering all international arrivals into New Zealand as potentially infected with SARS-CoV-2 even if pre-departure tests have been undertaken, social distancing and spacing have been followed and personal protective equipment has been used in flight.

References

1. Jefferies S, French N, Gilkison C, et al. (2020) COVID-19 in New Zealand and the impact of the national response: a descriptive epidemiological study. *Lancet Public Health*, 5, e612-23.
2. IATA (2020) Low risk of transmission (<https://www.iata.org/en/youandiata/travelers/health/low-risk-transmission/>), accessed November 2020.
3. Freedman, DO, Wilder-Smith, A (2020) In-flight transmission of SARS-CoV-2: a review of the attack rates and available data on the efficacy of face masks. *J Travel Med*, taaa178.
4. Murphy N, Boland M, Bambury N, et al. (2020) A large national outbreak of COVID-19 linked to air travel, Ireland, summer 2020. *Euro Surveill*, in press.
5. EpiSurv: national notifiable disease surveillance database (2020) <https://surv.esr.cri.nz/episurv/index.php>.
6. Quick, J (2020) nCoV-2019 sequencing protocol V3 (<https://www.protocols.io/view/ncov-2019-sequencing-protocol-v3-locost-bh42j8ye>), accessed 1 November 2020.
7. Freed NE, Vlková M, Faisal MB, et al. (2020) Rapid and inexpensive whole-genome sequencing of SARS-CoV-2 using 1200 bp tiled amplicons and Oxford Nanopore Rapid Barcoding. *Biol Methods Protoc*, 5(1).
8. Elbe, S, Buckland-Merrett, G (2017) Data, disease and diplomacy: GISAID's innovative contribution to global health. *Global Chall* 1, 33-46.
9. Katoh K, Standley DM (2013) MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Mol Biol Evol*, 30(4): 772-80.
10. Nguyen, LT, Schmidt, HA, von Haeseler, A et al. (2015) IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Mol Biol Evol*, 32, 268-274.
11. Hasegawa, M, Kishino, H, Yano, T (1985) Dating of the human-ape splitting by a molecular clock of mitochondrial DNA. *J Mol Evol*, 22, 160-174.
12. Kalyanamoorthy, S, Minh, BQ, Wong, TKF, et al. (2017) ModelFinder: fast model selection for accurate phylogenetic estimates. *Nat Methods*, 14, 587-589.
13. Hoang, DT, Chernomor, O, von Haeseler, A, et al. (2017) UFBoot2: Improving the ultrafast bootstrap approximation. *Mol Biol Evol*, 35, 518-522.

14. WHO (2020) Novel coronavirus situation report (<https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200121-sitrep-1-2019-ncov.pdf>), accessed 1 November 2020.
15. Byrne AW, McEvoy D, Collins AB, et al. (2020) Inferred duration of infectious period of SARS-CoV-2: rapid scoping review and analysis of available evidence for asymptomatic and symptomatic COVID-19 cases. *BMJ Open*, 10:e039856.
16. Rambaut A, Holmes EC, Hill V, et al. (2020) A dynamic nomenclature proposal for SARS-CoV-2 to assist genomic epidemiology. *Nat Micro*, 5, 1403-1407.
17. Geoghegan JL, Douglas J, Ren X, et al. (2020) The power and limitations of genomics to track COVID-19 outbreaks: a case study from New Zealand. *medRxiv*, doi: 10.1101/2020.10.28.20221853.
18. Choi EM, Chu D, Cheng P, et al. (2020) In-flight transmission of SARS-CoV-2. *Emerg Infect Dis*. 26(11), 2713-2716.
19. Speake H, Phillips A, Chong T et al. (2020) Flight-associated transmission of severe acute respiratory syndrome coronavirus 2 corroborated by whole-genome sequencing. *Emerg Infect Dis*. doi: 10.3201/eid2612.203910.
20. Commercial aircraft cabin aerosol dispersion tests (<https://www.ustranscom.mil/cmd/docs/TRANSCOM%20Report%20Final.pdf>), accessed 31 October 2020.

Supplementary Table 1. Detailed information regarding the seven positive cases of COVID-19.

	Case A	Case B	Case C	Case D	Case E	Case F	Case G
Genome	Identical	Identical	Identical #	1 additional mutation	Identical	Identical	Identical
Genome ID GISAID accession	20CV0408 EPI_ISL_582019	20CV0409 EPI_ISL_582020	20CV0410 EPI_ISL_582021	20CV0401 EPI_ISL_582018	20CV0398 EPI_ISL_582017	20CV0414 EPI_ISL_582022	20CV0415 EPI_ISL_582023
Pre-flight testing*	Negative test 24/9	Negative test 24/9	Negative test 25/9	Negative test 24/9	Not swabbed	Negative test 25/9	Not swabbed
Symptom onset	01/10/2020	02/10/2020	Asymptomatic	04/10/2020	Asymptomatic	3/10/2020	9/10/2020
Date tested positive	02/10/2020	02/10/2020	02/10/2020	07/10/2020	06/10/2020	8/10/2020	8/10/2020
Technology and Ct value	GeneXpert E-gene Ct 14.3, N2-gne Ct 16.4	GeneXpert E-gene Ct 27, N2-gene Ct 29.3	GeneXpert E-gene Ct 33.3, N2-gene Ct 36.8	GeneXpert E-gene Ct 18.5 N2-gene Ct 20.4	GeneXpert E-gene Ct 18.5, N2 gene Ct 22.3	BD Max N1-gene Ct 22.0 N2-gene Ct 22.3	BD Max N1-gene Ct 22.1 N2-gene Ct 19.1
Country of origin	Switzerland		Ukraine	Ireland	India	South Africa	
Transit info for Dubai	9hr 27 min layover		11hr 30 min layover	8hr 18 min layover	70 hr 54 min layover	5hr 44 mins layover	
Seat number on EK448	26G	26D	24C	27D	28G	24D/E/F/G	
Personal protective equipment (PPE) usage during travel*	Wore a face mask and gloves on plane and coach. Report they took mask off when sleeping and when seated.		Not reported	Wore a face mask and gloves on plane and coach	Not reported	Wore a face mask on plane and coach	
Bus** from airport to Managed Isolation Facility (MIF)	Bus 1		Bus 1 briefly, transported on bus 2	Bus 1	Bus 3	Bus 2	

partial genome obtained (1 amplicon failed resulting in 1200Ns) but has the 5 defining mutations of the cluster

* self-reported

** all buses socially distanced with mandated mask wearing

Supplementary Table 2. Flight arrival and departure times for the journeys of each case.

	Date/Time Zone (host country)	New Zealand Day Light Savings time zone GMT +13
Flight EK448	<p>Departed from Dubai on 28 September at 08:29hrs</p> <p>Arrived Kuala Lumpur 28 September 19:11hrs</p> <p>Departed Kuala Lumpur 28 September 21:03 hrs</p> <p>The flight arrived in Auckland, New Zealand on 29 September at 11:31hrs.</p>	<p>Departed from Dubai on 28 September 17:29 hrs.</p> <p>Arrived in Kuala Lumpur 29 September 00:11hrs</p> <p>Departed Kuala Lumpur 29 September 02:03hrs</p> <p>Flight arrived in Auckland New Zealand on 29 September 11:31hrs</p>
Case A & B	<p>Depart Zurich, Switzerland 27 September 15:25hrs</p> <p>Arrive Dubai, UAE 27 September 23:02hrs</p>	<p>Depart Zurich, Switzerland 28 September 02:25hrs</p> <p>Arrive Dubai, UAE 28 September 08:02hrs.</p>
Case C	<p>Departed from Kiev, Ukraine on 27 September to Dubai on EK2354 at 15:16hrs</p> <p>Arrived in Dubai on 27 September 20:59hrs</p>	<p>Departed from Kiev, Ukraine on 28 September 01:16hrs.</p> <p>Arrived in Dubai on 28 September 05:59hrs</p>
Case D	<p>EK162, which departed Dublin for Dubai on 27 September 14:10hrs.</p> <p>Arrived Dubai 28 September 00:05hrs</p>	<p>EK162, which departed Dublin for Dubai on 28 September 02:10hrs.</p> <p>Arrived Dubai 28 September 09:05hrs.</p>
Case E	<p>The case travelled on Flight 6E67 from Kochi, India, on 25 September 08:21hrs and landed in Dubai on 25 September at 10:35hrs.</p>	<p>The case travelled on Flight 6E67 from Kochi, India on 25 September 14:51hrs and landed in Dubai on 25 September at 18:35hrs</p>
Case F & G	<p>The cases flew on EK762 seat 29DEFG departed Johannesburg for Dubai on 27 September at 17:10hrs</p> <p>Arrived Dubai 28 September 02:45hrs</p>	<p>The cases flew on EK762 seat 29DEFG departed Johannesburg for Dubai on 28 September at 04:10hrs</p> <p>Arrived Dubai 28 September 11:45hrs</p>