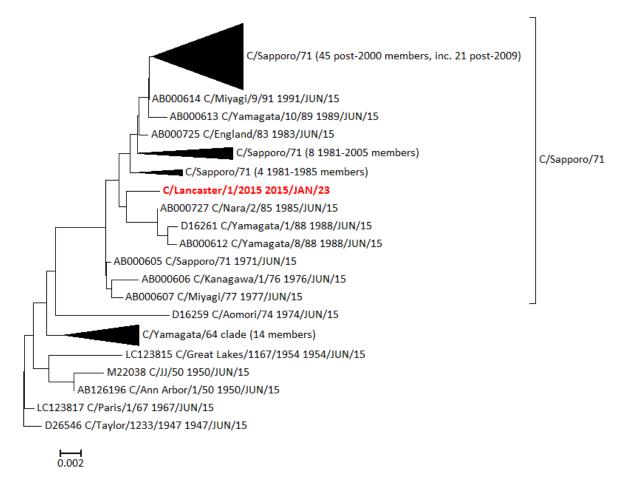
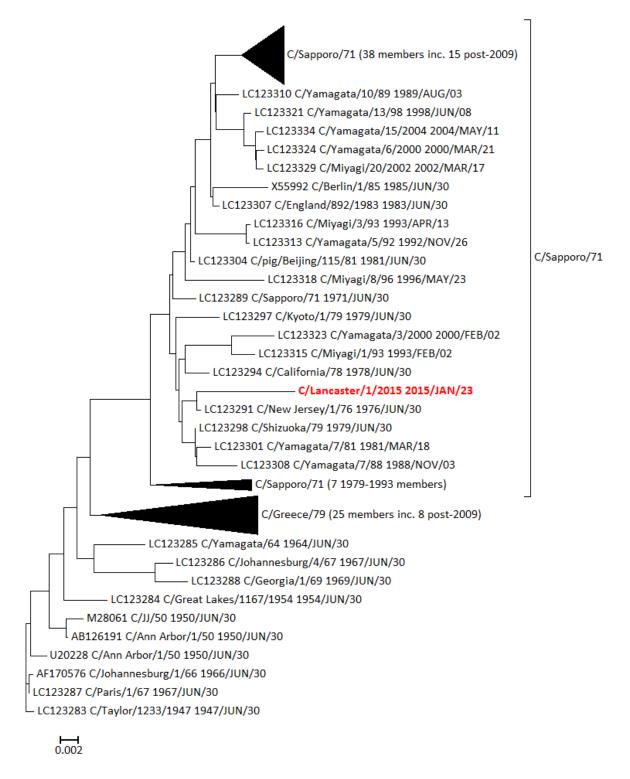
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Supplementary figures for:

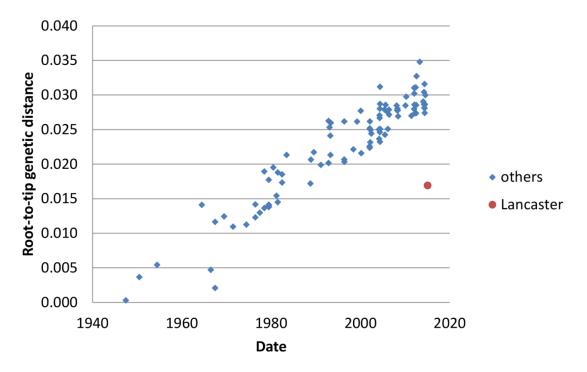
2 Influenza C in Lancaster, UK, in the 3 winter of 2014-2015 4 5 6 Kate V Atkinson^{1†}, Lisa A Bishop^{1,2}, Glenn Rhodes³, Nicolas Salez⁴, Neil R McEwan⁵, Matthew 7 J Hegarty⁵, Julie Robey⁶, Nicola Harding⁶, Simon Wetherell⁶, Robert M Lauder¹, Roger W 8 Pickup^{1,3}, Mark Wilkinson² & Derek Gatherer¹* 9 10 ¹ Division of Biomedical & Life Sciences, Faculty of Health & Medicine, Lancaster University, 11 Lancaster LA1 4YT, UK 12 ²Royal Lancaster Infirmary, Ashton Road, Lancaster LA1 4RP, UK ³Centre for Ecology & Hydrology, Lancaster Environment Centre, Lancaster University, 13 14 Lancaster LA1 4AP, UK 15 ⁴UMR D 190, Emergence des Pathologies Virales, Aix-Marseille University, 27 Bd Jean 16 Moulin, 13005 Marseille cedex 05, France 17 ⁵Institute of Biological, Environmental & Rural Sciences, Aberystwyth University, 18 Aberystwyth SY23 3DA, UK ⁶Queen Square Medical Practice, 2 Queen Square, Lancaster LA1 1RP, UK 19 20 21 † Present address: University College London Hospitals NHS Foundation Trust, London 22 * Contact for correspondence: Derek Gatherer, email: d.gatherer@lancaster.ac.uk, Tel: +44-23 24 1524-592900. Division of Biomedical & Life Sciences, Faculty of Health & Medicine, Lancaster University, Lancaster LA1 4YT, UK 25 26



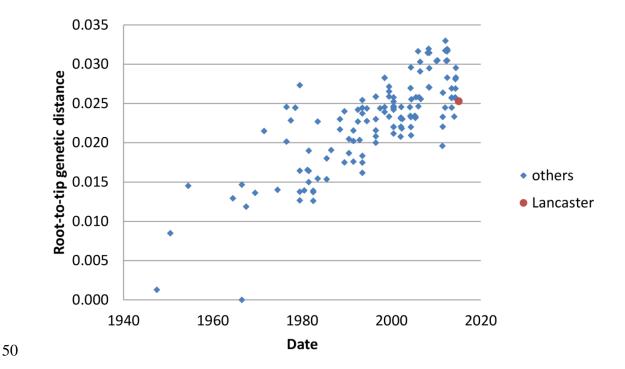
Supplementary Figure 1: Neighbour joining tree rooted on C/Taylor/1233/1947 for segment 6 (M1/CM2), annotated with clades derived from Gatherer ¹ and confirmed by BEAST analysis (see Supplementary Data Pack), demonstrating the closer relationship of C/Lancaster/1/2015 (red) to M1/CM2 segments of the C/Sapporo/71 clade from the 1980s than to recent isolates. Scale: substitutions per site.



Supplementary Figure 2: Neighbour joining tree rooted on C/Taylor/1233/1947 for segment 1 (PB2), annotated with clades derived from Gatherer ¹ and confirmed by BEAST analysis (see Supplementary Data Pack), demonstrating the closer relationship of C/Lancaster/1/2015 (red) to PB2 segments of the C/Sapporo/71 clade from the 1970s and 1980s than to recent isolates. Scale: substitutions per site.



Supplementary Figure 3: Root-to-tip distance in a neighbour joining tree for segment 5 (NP) of the influenza C genome. 96 full-length or near full-length genome segments (1809 bases) are used plus the 397 discontinuous bases of segment 5 derived from deep sequencing. C/Lancaster/1/2015 is less divergent from the root than it should be given its known sampling date, consistent with a perturbation of molecular clock-like behaviour in its lineage.



Supplementary Figure 4: Root-to-tip distance in a neighbour joining tree for segment 7 (NS1/NS2) segment of the influenza C genome. 134 full-length or near full-length genome segments (935 bases) are used plus the 288 discontinuous bases of segment 7 derived from deep sequencing. C/Lancaster/1/2015 has a degree of divergence from the root consistent with molecular clock-like behaviour in its lineage.

References

Gatherer, D. Tempo and mode in the molecular evolution of influenza C. *PLoS currents* **2**, RRN1199, doi:10.1371/currents.RRN1199 (2010).